

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 23, 2003, 23:32:40 ; Search time 2188.5 Seconds  
(without alignments)  
168.237 Million cell updates/sec

Title: US-09-214-836-2  
Sequence: 1 KVMQYQV 9

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL-frame+ p2n.model -DEV=xlh  
-O=/cgn2/USPTO.spool/US09214836/runat\_14082003\_085039\_7593/app\_query.fasta\_1.388  
-DB=GenEmbl -QPM=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCALL=GN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=25 -MODE=LOCAL  
-OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09214836 @CGN 1.1 3608 @runat\_14082003\_085039\_7593 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEIOURY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rdd:\*  
36: em\_htg\_man:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	55	94.8	697	9 HSA329943	AJ329943 Homo sapi
2	54	93.1	36	6 A46001	A46001 Sequence 9
3	54	93.1	36	6 AR269285	AR269285 Sequence
4	54	93.1	1986	6 AX133406	AX133406 Sequence
5	54	93.1	1986	6 AX133655	AX133655 Sequence
6	54	93.1	1986	6 AX192347	AX192347 Sequence
7	54	93.1	1986	6 BT007202	BT007202 Homo sapi
8	54	93.1	1986	12 HSU01874	HSU01874 Synthetic
9	54	93.1	2114	9 HUMGPMSS	M3295 Human 95 kd
10	54	93.1	2115	6 A45993	A45993 Sequence 1
11	54	93.1	2115	6 AR269281	AR269281 Sequence
12	54	93.1	2130	6 AR167365	AR167365 Sequence
13	54	93.1	2130	6 AX274950	AX274950 Sequence
14	54	93.1	2130	6 AX354933	AX354933 Sequence
15	54	93.1	2130	6 S73003	S73003 gp100-melan
16	54	93.1	2131	6 AX474662	AX474662 Sequence
17	54	93.1	2131	9 HUMPMEL	M77348 Human Pmel
18	54	93.1	2134	9 BC001414	BC001414 Homo sapi
19	54	93.1	2534	6 AX133528	AX133528 Sequence
20	54	93.1	2758	9 AK092881	AK092881 Homo sapi
21	51	87.9	64323	9 AL356976	AL356976 Homo DNA
22	51	87.9	170470	2 AC022696	AC022696 Homo sapi
23	51	86.2	1881	6 AX474660	AX474660 Sequence
24	50	86.2	1881	10 MMU14133	U14133 Mus muscu
25	50	86.2	2172	6 AR063067	AR063067 Sequence
26	50	86.2	2172	6 AR091800	AR091800 Sequence
27	50	86.2	2172	6 AR162997	AR162997 Sequence
28	50	86.2	2172	6 AR287974	AR287974 Sequence
29	50	86.2	2172	6 A45999	A45999 Sequence 7
30	49	84.5	24	6 AR269284	AR269284 Sequence
31	49	84.5	316	3 AF131719	AF131719 Polystoma
32	49	84.5	1223	3 AF382064	AF382064 Polystoma
33	49	84.5	12221	1 AE000312	AE000312 Escherich
34	49	84.5	12574	1 AE005454	AE005454 Escherich
35	49	84.5	13913	1 AE015246	AE015246 Shigella
36	49	84.5	16645	1 D90851	D90851 E.coli geno
37	49	84.5	18085	1 D90854	D90854 E.coli geno
38	49	84.5	106465	9 HSJ765F13	AL109853 Human DNA
39	49	84.5	107320	2 AC011391	AC011391 Homo sapi
40	49	84.5	110000	2 AC020884_1	Continuation (2 of
41	49	84.5	120584	9 AC011342	AC011342 Homo sapi
42	49	84.5	151712	9 AC008385	AC008385 Homo sapi
43	49	84.5	218444	2 AL365256	AL365256 Homo sapi
44	49	84.5	233305	2 AC025751	AC025751 Mus muscu
45	49	84.5	233305	2 AC025751	AC025751 Mus muscu

RESULT 1

ALIGNMENTS

HSA329943/c  
 LOCUS HSA329943 697 bp DNA linear PRI 18-JUL-2002  
 DEFINITION Homo sapiens genomic sequence surrounding Not1 site, clone  
 NLI-UN18R.  
 ACCESSION AJ329943  
 VERSION AJ329943.1 GI:15874361  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 697)  
 Kutzenko, A.S., Gzatzullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,  
 Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,  
 Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,  
 Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.  
 Not1 flanking sequences: a tool for gene discovery and verification  
 of the human genome  
 Nucleic Acids Res. 30 (14), 3163-3170 (2002)  
 TITLE  
 JOURNAL  
 MEDLINE 22131767  
 PUBMED 12136098  
 REFERENCE 2 (bases 1 to 697)  
 Zabarovsky, E.R.  
 AUTHORS  
 JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorigenesis Centre,  
 Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,  
 Sweden  
 FEATURES  
 source  
 1..697  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="NLI-UN18R"  
 BASE COUNT 174 a 259 c 90 g 174 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.42 Length: 697  
 Score: 55.00 Matches: 8  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 88.89% Mismatches: 0  
 Query Match: 94.83% Indels: 0  
 Gaps: 0  
 DB: 9  
 US-09-214-836-2 (1-9) x HSA329943 (1-697)  
 QY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
 Db 560 AAGGTCGTGGGGTCACTGAGAGTG 534  
 RESULT 2  
 LOCUS A46001 36 bp DNA linear PAT 07-MAR-1997  
 DEFINITION Sequence 9 from Patent EP068350.  
 ACCESSION A46001  
 VERSION A46001.1 GI:2300273  
 KEYWORDS  
 SOURCE  
 ORGANISM unidentified  
 unclassified  
 unclassified.  
 1 (bases 1 to 36)  
 REFERENCE  
 AUTHORS Adema, G.J. and Figdor, C.G.  
 TITLE Melanoma associated antigenic polypeptide, epitopes thereof and  
 vaccines against melanoma  
 JOURNAL Patent: EP 068350-A 9 23-AUG-1995;  
 AKZO NOBEL NV (NL)  
 COMMENT Other publication ZA 9501239 951019  
 Other publication JP 7278193 951024  
 Other publication FI 950665 950817  
 Other publication CA 2142575 950817  
 Other publication AU 1227295 950824.  
 FEATURES  
 source  
 1..36  
 Location/Qualifiers

/organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"  
 /cell\_type="MELANOCYT"  
 /cissue\_type="MELANOMA"  
 1..36  
 /note="unnamed protein product; Protein sequence is in  
 conflict with the conceptual translation"  
 /codon\_start=1  
 /protein\_id="CAA02870.1"  
 /db\_xref="GI:2300274"  
 /translation="VMKRWGQYMQVL"  
 BASE COUNT 9 a 8 c 11 g 8 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.282 Length: 36  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 Gaps: 0  
 DB: 6  
 US-09-214-836-2 (1-9) x AR269285 (1-36)  
 QY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
 Db 7 AAGACCTGGGCCCACTACTGCGAAGTT 33  
 RESULT 3  
 LOCUS AR269285 36 bp mRNA linear PAT 10-APR-2003  
 DEFINITION Sequence 9 from patent US 6500919.  
 ACCESSION AR269285  
 VERSION AR269285.1 GI:29700350  
 KEYWORDS  
 SOURCE  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 36)  
 Adema, G.J. and Figdor, C.G.  
 TITLE Melanoma associated antigenic polypeptide, epitopes thereof and  
 vaccines against melanoma  
 JOURNAL Patent: US 6500919-A 9 31-DEC-2002;  
 FEATURES  
 source  
 1..36  
 /organism="Unknown"  
 BASE COUNT 9 a 8 c 11 g 8 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.282 Length: 36  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 Gaps: 0  
 DB: 6  
 US-09-214-836-2 (1-9) x AR269285 (1-36)  
 QY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
 Db 7 AAGACCTGGGCCCACTACTGCGAAGTT 33  
 RESULT 4  
 LOCUS AX133406 1986 bp DNA linear PAT 15-MAY-2001  
 DEFINITION Sequence 1 from Patent WO0130847.  
 ACCESSION AX133406  
 VERSION AX133406.1 GI:14139665  
 KEYWORDS  
 SOURCE  
 ORGANISM synthetic construct

## REFERENCE

1 artificial sequences.  
 AUTHORS Bernstein,N., Tartaglia,J., Moingeon,P., Barber,B. and Tine,J.A.  
 TITLE Modified gp100 and uses thereof  
 JOURNAL Patent: WO 0130847-A 1 03-MAY-2001;  
 Aventis Pasteur Limited (CA)

## FEATURES

source  
 1..1986  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="modified gp 100"

BASE COUNT 431 a 552 c 552 g 451 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 8.74 Length: 1986  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: Gaps: 0

US-09-214-836-2 (1-9) x AX133406 (1-1986)

Qy 1 LysValTPGlyGlnTYTPGlnVal 9  
 Db 460 AAGACCTGGGCGCAATGCAAGTT 486

RESULT 5  
 LOCUS AX133655 1986 bp DNA linear PAT 15-MAY-2001  
 DEFINITION Sequence 109 from Patent WO0130382.  
 ACCESSION AX133655  
 VERSION AX133655.1 GI:14139697  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 synthetic construct  
 artificial sequences.

## REFERENCE

1  
 AUTHORS Bernstein,N., Tartaglia,J., Moingeon,P. and Barber,B.  
 TITLE Method of inducing and/or enhancing an immune response to tumor antigens  
 JOURNAL Patent: WO 0130382-A 109 03-MAY-2001;  
 Aventis Pasteur Limited (CA)

## FEATURES

source  
 1..1986  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="modified gp100"  
 1..1986  
 /note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="CAC38954.1"  
 /transl\_table=11  
 /translation="MDLVKRCILHLAVIGLLAVGATKVPKRNODMIGVSRQLTKAM  
 NRQIPEWTEKQRLDCWRGGVSLKVSNDGTLIGANASFIALNFPQSVLPDGOV  
 IWNNNTINSQVGVQVVPFQETDACLIPDGGPCPSGWSQKRSFYVWKWQYV  
 QVAGPVGSLIGTGRAMLGTHTMEVIVYHRSRSYVPLHSSSAFTIMQVPSVS  
 VSQLALDGNKHLNQLPLFALQHDPSGLAEADLSYTWDFGSSGTLISALVY  
 THTLEGPVTVQVLOALPLTSCGSPVGTGDGHRPTAEANTTAGOVPTTEVVG  
 TTPGAPLPSGTSSTVSQVPTTEVITRAVPMPTASSTGMPKRVUSVWGTLLAM  
 STPEATGMPARVSIIVLSGTTAQTTEVETTABELPIPEEGPDASSIMTESI  
 TGSIGPLDGTATLVRKQVPLDCAVIRGSFVTLIDIVGISASILQAVPGEED  
 AFELTVCCQGLPREACMEISPCGPPAQLCPVLPSPACQLVHLQILKGGGTVC  
 LNVSLADTNSLAVVSTOLIMGQAGAGOVPLIVGILLVMAVVLASLIYRRRLMKOD  
 FSVPOLHSSSHMLRLPRIFCSCIGENSPILSQGY"

BASE COUNT 431 a 552 c 552 g 451 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 8.74 Length: 1986  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: Gaps: 0

US-09-214-836-2 (1-9) x AX133655 (1-1986)

Qy 1 LysValTPGlyGlnTYTPGlnVal 9  
 Db 460 AAGACCTGGGCGCAATGCAAGTT 486

RESULT 6  
 LOCUS AX192347 1986 bp DNA linear PAT 15-AUG-2001  
 DEFINITION Sequence 1 from Patent WO0149317.  
 ACCESSION AX192347  
 VERSION AX192347.1 GI:15210325  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 synthetic construct  
 artificial sequences.

REFERENCE  
 AUTHORS Emhage,P., Barber,B.H., Sambhara,S. and Sia,C.D.  
 TITLE Enhancing the immune response to an antigen by presensitizing with an inducing agent prior to immunizing with the inducing agent and the antigen  
 JOURNAL Patent: WO 0149317-A 1 12-JUL-2001;  
 Aventis Pasteur Limited (CA)

## FEATURES

source  
 1..1986  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="modified gp 100"

BASE COUNT 431 a 552 c 552 g 451 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 8.74 Length: 1986  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: Gaps: 0

US-09-214-836-2 (1-9) x AX192347 (1-1986)

Qy 1 LysValTPGlyGlnTYTPGlnVal 9  
 Db 460 AAGACCTGGGCGCAATGCAAGTT 486

RESULT 7  
 LOCUS BT007202 1986 bp mRNA linear PRI 13-MAY-2003  
 DEFINITION Homo sapiens silver homolog (mouse) mRNA, complete cds.  
 ACCESSION BT007202  
 VERSION BT007202.1 GI:30583242  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 1986)  
 Kalline,N., Chen,X., Rolfe,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Pheasant,M. and Farmer,A.

TITLE Cloning of human full-length CDS in BD Creator(TM) System Donor  
 vector.

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1986)  
 AUTHORS Kalline,N., Chen,X., Rolfe,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
Phelan,M. and Farmer,A.

**TITLE**  
JOURNAL  
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow  
Circle, Palo Alto, CA 94303, USA

**COMMENT**  
This CDS clone is a part of a collection of human full length  
expression clones generated by BD Biosciences Clontech and the  
Harvard Institute of Proteomics. Each CDS has been cloned in two  
forms: with and without stop-codon (to allow fusion with C-terminal  
tag). The CDS has been directionally cloned using BD In-Fusion(TM)  
cloning system between the SalI and HindIII sites of the pDNR-DUAL  
vector. Additional sequences in the clone: 'ACC' after SalI site  
and before 'ATG' to provide Kozak consensus sequence; 'GG' after  
last codon and before HindIII site to maintain reading frame.  
Clone distribution: <http://bioinfo.clontech.com/orfclones>.

# FEATURES

## CDS

**source**  
1..1986  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="GH001991.0"  
/clone\_lib="BD Creator(TM) CDS library derived from MGC  
collection"  
/lab\_host="DH5alpha TI resistant"  
/note="Vector: pDNR-Dual"  
1..1986  
/codon\_start=1  
/product="silver homolog (mouse)"  
/protein\_id="AAP3866.1"  
/db\_xref="GI:30583243"  
/translation="MDLVLRKCLHLAVIGALLAVGATKVRPNODMLGVSRQLRTKAM  
NROYLPWTBAORLDCMRGGOVSLKNSNDGPTLIGANASFSIALNPFSGOKVLPDGOV  
IWNNTTINSQVWGQPVYPOETDDACIFPDGPGSGSQRSSRYVYWKMGQVY  
QVLAGPVSGISIGTRAMLGTHMEVTVYHRRGSRVYPLAHSSATFTTDOVPSVS  
VSQALDGNKHLRNQPLTFALQHLDPGSLADLSYTWDESGSLISRLLV  
THYLRGPVTAQVQLQALIPLTSCSSPVPTDGHRTAEAPNTTGAQVPTTEVG  
TTTGPAPAEPSGTSVQVPTTEVSTAPVQMPPTAESGMPKPVSEVWGTLAEI  
STPEATGTPAEVSIVLSGTTAAQVTTMETTARLELPPEBGPASSIMSTESI  
TSGSLPLDGTATRLVKRQVPLDCVLRYSFSAVTLIVQIGISAEILQAVPSGED  
APFLTVSCQGLPKEACMETISSPGCPAPRLCPVLPSPACQVLHQLILKGSSTYC  
LNVSLADTNSLAVVSTQIMPGQAGGQVPLVIGILLVMAVVLASLIYRRRLMKOD  
FSVPLPSSSHMRLPRIFCSCPIGENSPILSGQVY"

**BASE COUNT** 431 a 554 c 550 g 451 t  
**ORIGIN**  
Alignment Scores:  
Pred. No.: 8.74 Length: 1986  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
Gaps: 0

US-09-214-836-2 (1-9) x BT007202 (1-1986)

**Qy** 1 LysValTPGlyGlnTyrTPGlnVal 9  
Db 460 AAGACCTGGGCGCAATCTGCAAGTT 486

**RESULT 8** BT007991 1986 bp mRNA linear SYN 13-MAY-2003  
**LOCUS** BT007991  
**DEFINITION** Synthetic construct Homo sapiens silver homolog (mouse) mRNA.

**ACCESSION** BT007991  
**VERSION** BT007991.1 GI:30584820  
**KEYWORDS** FLI CDNA.  
**SOURCE** synthetic construct  
**ORGANISM** artificial sequences.

**REFERENCE** 1 (bases 1 to 1986)  
**AUTHORS** Koundinya,M., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,

Phelan,M. and Farmer,A.  
Cloning of human full-length CDSs in BD Creator(TM) System Donor  
vector

**TITLE**  
JOURNAL  
Unpublished  
2 (bases 1 to 1986)  
**REFERENCE**  
**AUTHORS** Koundinya,M., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
Phelan,M. and Farmer,A.

**COMMENT**  
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow  
Circle, Palo Alto, CA 94303, USA  
This CDS clone is a part of a collection of human full length  
expression clones generated by BD Biosciences Clontech and the  
Harvard Institute of Proteomics. Each CDS has been cloned in two  
forms: with and without stop-codon (to allow fusion with C-terminal  
tag). The CDS has been directionally cloned using BD In-Fusion(TM)  
cloning system between the SalI and HindIII sites of the pDNR-DUAL  
vector. Additional sequences in the clone: 'ACC' after SalI site  
and before 'ATG' to provide Kozak consensus sequence; 'GG' after  
last codon and before HindIII site to maintain reading frame.  
Clone distribution: <http://bioinfo.clontech.com/orfclones>.

# FEATURES

## CDS

**source**  
1..1986  
/organism="synthetic construct"  
/mol\_type="mRNA"  
/db\_xref="taxon:32630"  
/clone="GH001991.0"  
/clone\_lib="BD Creator(TM) CDS library derived from MGC  
collection"  
/lab\_host="DH5alpha TI resistant"  
/note="Vector: pDNR-Dual"  
1..1986  
/codon\_start=1  
/transl\_table=1  
/product="Homo sapiens silver homolog (mouse)"  
/protein\_id="AAP3663.1"  
/db\_xref="GI:30584821"  
/translation="MDLVLRKCLHLAVIGALLAVGATKVRPNODMLGVSRQLRTKAM  
NROYLPWTBAORLDCMRGGOVSLKNSNDGPTLIGANASFSIALNPFSGOKVLPDGOV  
IWNNTTINSQVWGQPVYPOETDDACIFPDGPGSGSQRSSRYVYWKMGQVY  
QVLAGPVSGISIGTRAMLGTHMEVTVYHRRGSRVYPLAHSSATFTTDOVPSVS  
VSQALDGNKHLRNQPLTFALQHLDPGSLADLSYTWDESGSLISRLLV  
THYLRGPVTAQVQLQALIPLTSCSSPVPTDGHRTAEAPNTTGAQVPTTEVG  
TTTGPAPAEPSGTSVQVPTTEVSTAPVQMPPTAESGMPKPVSEVWGTLAEI  
STPEATGTPAEVSIVLSGTTAAQVTTMETTARLELPPEBGPASSIMSTESI  
TSGSLPLDGTATRLVKRQVPLDCVLRYSFSAVTLIVQIGISAEILQAVPSGED  
APFLTVSCQGLPKEACMETISSPGCPAPRLCPVLPSPACQVLHQLILKGSSTYC  
LNVSLADTNSLAVVSTQIMPGQAGGQVPLVIGILLVMAVVLASLIYRRRLMKOD  
FSVPLPSSSHMRLPRIFCSCPIGENSPILSGQVY"

**BASE COUNT** 430 a 554 c 550 g 452 t  
**ORIGIN**  
Alignment Scores:  
Pred. No.: 8.74 Length: 1986  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
Gaps: 0

US-09-214-836-2 (1-9) x BT007991 (1-1986)

**Qy** 1 LysValTPGlyGlnTyrTPGlnVal 9  
Db 460 AAGACCTGGGCGCAATCTGCAAGTT 486

**RESULT 9** HSU01874 2026 bp mRNA linear PRI 26-MAY-1994  
**LOCUS** HSU01874  
**DEFINITION** Human me20m mRNA, complete cds.  
**ACCESSION** U01874  
**VERSION** U01874.1 GI:494939



KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2023)  
AUTHORS Mares, G.A., Marken, J.S., Neubauer, M., Aruffo, A., Hellstrom, I., Hellstrom, K.E. and Margardt, H.  
TITLE Cloning and expression of the gene for the melanoma-associated ME20 antigen  
JOURNAL DNA Cell Biol. 13 (2), 87-95 (1994)  
MEDLINE 94235165  
PubMed 8179825  
REFERENCE 2 (bases 1 to 2026)  
AUTHORS Neubauer, M.G.  
TITLE Direct Submission  
JOURNAL Submitted (16-SEP-1993) Michael G. Neubauer, Bristol-Myers Squibb Pharmaceutical Research Institute, 3005 1st Ave, Seattle, WA 98121, USA

FEATURES  
source Location/Qualifiers  
1. .2026  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="hfl2-2"  
/cell\_line="melanoma H3606"  
/clone\_lib="cdm8"  
7. .1995  
/standard\_name="melanoma-associated ME20 antigen"  
/codon\_start=1  
/product="me20m"  
/protein\_id="AA18479.1"  
/db\_xref="GI:494940"  
/translation="MDLVKRCILHLAVIGALLAVGATKVPKRNODMIGVSRQETKXW  
NROLYPWTBQRLDCRGQVSLKVSNDPTLIGANASFTILANPFSQVLPDGOY  
IWNNTTINSQVWGQPVYPOETDACLFPDGPCEGWSQKRSFVYWKTKVQYV  
QVGLGVPVSGISIGTRAMLGTHMEVYVYHRRGSRVYPLAHSSAFITIDQVPSVS  
VSQRLADGNGKHFILNROPFLFALQHPDPSGYLAADLSYMDGSSGTLISRALVY  
THYLEGPPVTAQVAVLOALPIITSCGSSPVGTTDGHRTAEAVNTTAAQVPTTEVVG  
TTPGCATPAEBSGTSVQVPTTEVISTAPQMTASTGTMTPEKVPVSEWGTILAM  
STPEATGMPAEVSIIVLSGTTAAQVTTTEVETTAELPIPEEGDASSIMTEBI  
TGSIGPLDGTATRLVKRQVPLDQVLYRGSFVTLIDIVGIESAEILQAVPSGEED  
AFELTVSCQGLPPEAKMEIISPGCPAPRLCQPVLPSPACOLVHLQILKSGSGTIC  
LNVSLADTNSLAVSTOLIMPGGAGIGQVPLIVGILVIMAVVLASLIYRRRLMQ  
DFSVPOLPHSSSHMLRLPRIFCSCPIENSLISGQY"

sig\_peptide 7. .78  
mat\_peptide 79. .1992  
/product="me20m"  
BASE COUNT 437 a 564 c 564 g 461 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.89 Length: 2026  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 9 Gaps: 0

US-09-214-836-2 (1-9) x HSU01874 (1-2026)  
Qy 1 Lyvalttrpglygintytrpglnval 9  
Db 466 AAGACCTGGGGCCCAACTGCAAGTT 492

RESULT 10  
LOCUS HUMGPMSS 2114 bp mRNA linear PRI 27-APR-1993  
DEFINITION Human 95 kD melanocyte-specific secreted glycoprotein mRNA, 3' end.  
ACCESSION M32295  
VERSION M32295.1 GI:183559  
KEYWORDS melanocyte-specific secreted glycoprotein.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2114)  
AUTHORS Vogel, A.  
TITLE Sequence of a melanocyte specific secreted glycoprotein  
JOURNAL Unpublished (1990)  
COMMENT Original source text: Human melanoma cell line, cDNA to mRNA, clone 8.  
Draft entry and computer-readable sequence for [1] kindly submitted by A.Vogel, 23-FEB-1990.

FEATURES  
source Location/Qualifiers  
1. .2114  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
<1. .2028  
/note="melanocyte-specific secreted glycoprotein"  
/codon\_start=1  
/protein\_id="AA15930.1"  
/db\_xref="GI:386754"  
/translation="RGIRKNTMDLVKRCILHLAVIGALLAVGATKVPKRNODMIGVSR  
QUTKAMNROLYPWTBQRLDCRGQVSLKVSNDPTLIGANASFTILANPFSQK  
VLPDGOYIWNNTTINSQVWGQPVYPOETDACLFPDGPCEGWSQKRSFVYWK  
KTWGQVYVGGPVSGISIGTRAMLGTHMEVYVYHRRGSRVYPLAHSSAFITID  
QVPSVSVSQRLADGNGKHFILNROPFLFALQHPDPSGYLAADLSYMDGSSGTL  
ISRALVYTHYLEGPPVTAQVAVLOALPIITSCGSSPVGTTDGHRTAEAVNTTAAQV  
PTTEVVGTTGQAPTAEPSTTSVQVPTTEVISTAPQMTASTGTMTPEKVPVSEW  
GITLAEMSTPEATGMPAEVSIIVLSGTTAAQVTTTEVETTAELPIPEEGDASS  
IMSTESI TGSIGPLDGTATRLVKRQVPLDQVLYRGSFVTLIDIVGIESAEILQAV  
VPSGEADAFELTVSCQGLPPEAKMEIISPGCPAPRLCQPVLPSPACOLVHLQILK  
GSGTICLAVSLADTNSLAVSTOLIMPGGAGIGQVPLIVGILVIMAVVLASLIY  
RLMKDPSPOLPHSSSHMLRLPASALPLVIRLAPSSVSGSSEVSHML"

BASE COUNT 469 a 586 c 575 g 484 t  
ORIGIN

Alignment Scores:  
Pred. No.: 9.22 Length: 2114  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 9 Gaps: 0

US-09-214-836-2 (1-9) x HUMGPMSS (1-2114)  
Qy 1 Lyvalttrpglygintytrpglnval 9  
Db 481 AAGACCTGGGGCCCAACTGCAAGTT 507

RESULT 11  
LOCUS A45993 2115 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 1 from Patent EP068350.  
ACCESSION A45993  
VERSION A45993.1 GI:2300268  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2115)  
AUTHORS Adema, G.J. and Fidor, C.G.  
TITLE Melanoma associated antigenic polypeptide, epitopes thereof and vaccines against melanoma  
JOURNAL Patent: EP 068350-A 1 23-AUG-1995; AKZO NOBEL NV (NL)  
COMMENT Other publication ZA 9501239 951019  
Other publication JP 7278193 951024  
Other publication FI 950665 950817  
Other publication CA 2142575 950817  
Other publication AU 1227295 950824.

FEATURES  
source Location/Qualifiers  
1. .2115

```
misc_signal
CDS
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
/cell_type="MELANOCYTE"
/tissue_type="MELANOMA"
1..81
22..2007
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAA02869.1"
/db_xref="GI:2300269"
/translation="MDLVLRCLHLAVIGALLAVGATKVPKRNODWLGVSRLQRTKAM
NRQLYPEWTEAQRDLQWRGQVSLKVSNDGPTLIGANASFSIALNFPQSKVLPDGOV
IWNVNTINGQVWGQGVPOETDQACIPDGGPCPSGMSOKRSFYVWKMGQYV
OVLGGPVSLGIGTRAMLGTHMEVTVYHRRGSRSVYPLAHSSSAFTITDOVPFVS
VSQRLADGKMKHFLRNQPLTFPALQHDPSGTLAEDISTYMDGSSGTLISALIV
THYLEPQVTAQVVLQALPLTSCGSPVGTIDGHRPLAEAPNTTAGOVPTTEVVG
TTPQAPPAEBSGTTSVQPTTEVISTAPVQMPAESEGTPEKVPVSEVWGTLAE
STPEATGMTPAEVSIVLSGTTAAQVTTTEWETLAEPLPEBEGPASSIMSTESI
TGSIGPLDGTATLRLVKROYPLDCVLYRGSFVTLDIYOGISAEILKQVSGEGD
AFELTVSCGGGLPKKACMEISSPGCPRAOLCOPVLPSPACQVLIHQILKSGSTYC
LNVSLADTNSLAIVSTQIIMPQEGAGQVPLIVGILVMAAVLASLITRRRLMKOD
FVSPQLPRSSSHMLRPLRIFCSPIGENSEPLISGOV"
262..264
1792..1870
/misc_signal
misc_signal
BASE COUNT 469 a 587 c 575 g 484 t
ORIGIN
/function="TRANSMEMBRANE REGION"
Alignment Scores:
Pred. No.: 9.22 Length: 2115
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 6 Gaps: 0
US-09-214-836-2 (1-9) x A45993 (1-2115)
Qy 1 LysValTTPGlyGlnTyrTTPGlnVal 9
Db 481 AAGACCTGGGGCCCACTACTGCAAGTT 507
RESULT 12
AR269281 2115 bp mRNA linear PAT 10-APR-2003
LOCUS AR269281
DEFINITION Sequence 1 from patent US 6500919.
ACCESSION AR269281
VERSION AR269281.1 GI:29700346
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2115)
AUTHORS Adema, G.J. and Figdor, C.G.
TITLE Melanoma associated antigenic polypeptide, epitopes thereof and
JOURNAL vaccines against melanoma
FEATURES
source
Location/Qualifiers
1..2115
/organism="unknown"
BASE COUNT 469 a 587 c 575 g 484 t
ORIGIN
Alignment Scores:
Pred. No.: 9.22 Length: 2115
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 6 Gaps: 0
US-09-214-836-2 (1-9) x AR269281 (1-2115)
```

```
Qy 1 LysValTTPGlyGlnTyrTTPGlnVal 9
Db 481 AAGACCTGGGGCCCACTACTGCAAGTT 507
RESULT 13
AR167365 2130 bp DNA linear PAT 17-DEC-2001
LOCUS AR167365
DEFINITION Sequence 1 from patent US 6287569.
ACCESSION AR167365
VERSION AR167365.1 GI:17903140
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2130)
AUTHORS Kippe, T.J. and Wu, Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 1 11-SEP-2001;
FEATURES
source
Location/Qualifiers
1..2130
/organism="unknown"
BASE COUNT 484 a 587 c 575 g 484 t
ORIGIN
Alignment Scores:
Pred. No.: 9.28 Length: 2130
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 6 Gaps: 0
US-09-214-836-2 (1-9) x AR167365 (1-2130)
Qy 1 LysValTTPGlyGlnTyrTTPGlnVal 9
Db 481 AAGACCTGGGGCCCACTACTGCAAGTT 507
RESULT 14
AX274950 2130 bp DNA linear PAT 29-OCT-2001
LOCUS AX274950
DEFINITION Sequence 1 from Patent WO0170767.
ACCESSION AX274950
VERSION AX274950.1 GI:16547582
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1
AUTHORS Nicolette, C.A.
TITLE Therapeutic anti-melanoma compounds
JOURNAL Patent: WO 0170767-A 1 27-SEP-2001;
GENZYME CORPORATION (US)
FEATURES
source
Location/Qualifiers
1..2130
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
22..2007
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAD10318.1"
/db_xref="GI:16547583"
/translation="MDLVLRCLHLAVIGALLAVGATKVPKRNODWLGVSRLQRTKAM
NRQLYPEWTEAQRDLQWRGQVSLKVSNDGPTLIGANASFSIALNFPQSKVLPDGOV
IWNVNTINGQVWGQGVPOETDQACIPDGGPCPSGMSOKRSFYVWKMGQYV
OVLGGPVSLGIGTRAMLGTHMEVTVYHRRGSRSVYPLAHSSSAFTITDOVPFVS
VSQRLADGKMKHFLRNQPLTFPALQHDPSGTLAEDISTYMDGSSGTLISALIV
THYLEPQVTAQVVLQALPLTSCGSPVGTIDGHRPLAEAPNTTAGOVPTTEVVG
TTPQAPPAEBSGTTSVQPTTEVISTAPVQMPAESEGTPEKVPVSEVWGTLAE
STPEATGMTPAEVSIVLSGTTAAQVTTTEWETLAEPLPEBEGPASSIMSTESI
```

TGSIGPLLDGTATLRVLRQVPLDCLVLRYSFSTLIDIVOGIESAEIIOAVPSGED  
 AFELTVSCOGGLPKPEACMEISPPCCPPAPRLCQPVLPSPACQVLIHQILKSGSTYC  
 LNVSLADTNSLAVSTOLIMGGGAGGGOPLVIGILVMAVAVLASLIYRRRLMKOD  
 FSVPLDHSSSHMLRLRIFRIFSCPIGNSPILSSGOY"

BASE COUNT 484 a 587 c 575 g 484 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 9.28 Length: 2130  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 6 Gaps: 0

US-09-214-836-2 (1-9) x AX274950 (1-2130)

Qy 1 LysValTTPGIyGIntYTPGInVal 9  
 Db 481 AAGACCTGGGGCCCAATCTGCAAGTT 507

RESULT 15  
 AX354933 2130 bp DNA linear PAT 06-FEB-2002  
 LOCUS AX354933 Sequence 1 from Patent WO0192294.  
 ACCESSION AX354933  
 VERSION AX354933.1 GI:18619617  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Nicolette, C.A.  
 TITLE Therapeutic anti-melanoma compounds  
 JOURNAL Patent: WO 0192294-A 1 06-DEC-2001;  
 GENZYME CORPORATION (US)

FEATURES  
 source 1..2130  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

BASE COUNT 484 a 587 c 575 g 484 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 9.28 Length: 2130  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 6 Gaps: 0

US-09-214-836-2 (1-9) x AX354933 (1-2130)

Qy 1 LysValTTPGIyGIntYTPGInVal 9  
 Db 481 AAGACCTGGGGCCCAATCTGCAAGTT 507

RESULT 16  
 S73003 2130 bp mRNA linear PRI 26-JAN-1995  
 LOCUS gpi100-melanocyte lineage-specific antigen/Pmel17 homolog [human,  
 DEFINITION mRNA, 2130 nt].  
 ACCESSION S73003.1 GI:639589  
 VERSION S73003.1  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Adema, G.J., de Boer, A.J., Vogel, A.M., Loenen, W.A. and Figdor, C.G.

TITLE Molecular characterization of the melanocyte lineage-specific  
 antigen gp100  
 JOURNAL J. Biol. Chem. 269 (31), 20126-20133 (1994)  
 MEDLINE 94327568  
 PUBMED 7519602  
 REMARK Genbank staff at the National Library of Medicine created this  
 entry [NCBI glibsq 154938] from the original journal article.  
 This sequence comes from Fig. 6.

FEATURES  
 source 1..2130  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

gene 1..2130  
 /gene="gpi100"  
 22..2007  
 /gene="gpi100"  
 /note="melanocyte lineage-specific antigen/Pmel17 homolog;  
 melanoma marker protein; This sequence comes from Fig. 6"  
 /codon\_start=1  
 /product="gpi100"  
 /protein\_id="AAC60634.1"  
 /db\_xref="GI:639590"

CDS

BASE COUNT 484 a 587 c 575 g 484 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 9.28 Length: 2130  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 9 Gaps: 0

US-09-214-836-2 (1-9) x S73003 (1-2130)

Qy 1 LysValTTPGIyGIntYTPGInVal 9  
 Db 481 AAGACCTGGGGCCCAATCTGCAAGTT 507

RESULT 17  
 AX474662 2131 bp DNA linear PAT 12-AUG-2002  
 LOCUS AX474662 Sequence 3 from Patent EP1222928.  
 ACCESSION AX474662  
 VERSION AX474662.1 GI:22214011  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Moelling, K., Nawrath, M. and Pavlovic, J.  
 TITLE Pharmaceutical compositions for treating or preventing cancer,  
 especially melanoma  
 JOURNAL Patent: EP 1222928-A 3 17-JUL-2002;  
 UNIVERSITAET ZUERICH INSTITUT FUER MEDIZINISCHE VIROLOGIE (CH)

FEATURES  
 source 1..2131  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"

## CDS

/db\_xref="taxon:9606"  
12..2018  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAD43667.1"  
/db\_xref="GI:22214012"  
/translation="MDLVLRKCLHLAVIGALLAVGATKVRNODMLGVSRQLRTKAM  
NRQLYPEWTEAQRDLDCRGVSLKVSNDGPTLLIGANASFSIALNFGSCQKVLPGQV  
IWNNTTINSQVWGCPVYPOSTDDACIFPDGPGSPSGSSGSKRSFVYWKWQGV  
QVAGPVSGLSITGRAMLGTHMEVYVYHRRGSRVPLAHSSAFITTDQVPSVS  
VSQALDGNKHFRLNQLPTFALQHDPSGTLAEADLSYTWDFGSSGTLISRAVY  
THYLEGPVTAQVAVLQAIPLTSCSSPVPGTTDGHRTAEAPNTTACQVPTTEVG  
TTTQGAFTAPBSGTSVQVPTTEVISTAPVOMPTASTGMPKPVSEVWGTTLAEM  
STPEAGMTPAEVSIIVLSGTTAAQVTTTEVETARLELPPEEGPDASIMSTESI  
TGSLLGLDGTATRLVKRQVPLDCVLRGSSVYLDIYQGESALILQAVSGED  
AFELTVSCQGLPKRACMETISSPGCPAPRLCQVLPSPACQVLVHQLKSGSGTYC  
LNSLADTNSLAVSTQLIMPVGLITGEGALGQVRLVIGLLVMAVAVLASLIYR  
RLMKQDFSVQPLPHSSSHMLRPLRIFCSCPIGENSPILSGQQV"

BASE COUNT 475 a 588 c 578 g 490 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.28 Length: 2131  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 6 Gaps: 0

US-09-214-836-2 (1-9) x AX474662 (1-2131)

QY 1 LysValTTPGLyGlnTyrTPGlnVal 9  
DB 471 AAGACCTGGGGCCCACTGCAAGTT 497

RESULT 18  
LOCUS HUMPMEL 2131 bp mRNA linear PRI 08-JAN-1995  
DEFINITION Human Pmel 17 mRNA, complete cds.  
ACCESSION M77348.1 GI:190105  
VERSION M77348.1  
KEYWORDS Pmel 17 protein; melanocyte.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 2131)  
Kwon,B.S., Chintamani,C., Kozak,C.A., Copeland,N.G.,  
Gilbert,D.J., Jenkins,N., Barton,D., Francke,U., Kobayashi,Y. and  
Kim,K.K.  
TITLE A melanocyte-specific gene, Pmel 17, maps near the silver coat  
color locus on mouse chromosome 10 and is in a syntenic region on  
human chromosome 12  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (20), 9228-9232 (1991)  
MEDLINE 92021023  
PubMed 1924386  
COMMENT Original source text: Homo sapiens skin cDNA to mRNA.  
FEATURES  
source location/Qualifiers  
1..2131  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="primary culture"  
/cell\_type="melanocyte"  
/tissue\_type="skin"  
1..2131  
/gene="Pmel 17"  
1..2121  
/gene="Pmel 17"  
12..2018  
/gene="Pmel 17"  
/codon\_start=1  
/product="Pmel 17 protein"

/protein\_id="AAA60121.1"  
/db\_xref="GI:190106"  
/translation="MDLVLRKCLHLAVIGALLAVGATKVRNODMLGVSRQLRTKAM  
NRQLYPEWTEAQRDLDCRGVSLKVSNDGPTLLIGANASFSIALNFGSCQKVLPGQV  
IWNNTTINSQVWGCPVYPOSTDDACIFPDGPGSPSGSSGSKRSFVYWKWQGV  
QVAGPVSGLSITGRAMLGTHMEVYVYHRRGSRVPLAHSSAFITTDQVPSVS  
VSQALDGNKHFRLNQLPTFALQHDPSGTLAEADLSYTWDFGSSGTLISRAVY  
THYLEGPVTAQVAVLQAIPLTSCSSPVPGTTDGHRTAEAPNTTACQVPTTEVG  
TTTQGAFTAPBSGTSVQVPTTEVISTAPVOMPTASTGMPKPVSEVWGTTLAEM  
STPEAGMTPAEVSIIVLSGTTAAQVTTTEVETARLELPPEEGPDASIMSTESI  
TGSLLGLDGTATRLVKRQVPLDCVLRGSSVYLDIYQGESALILQAVSGED  
AFELTVSCQGLPKRACMETISSPGCPAPRLCQVLPSPACQVLVHQLKSGSGTYC  
LNSLADTNSLAVSTQLIMPVGLITGEGALGQVRLVIGLLVMAVAVLASLIYR  
RLMKQDFSVQPLPHSSSHMLRPLRIFCSCPIGENSPILSGQQV"

BASE COUNT 475 a 588 c 578 g 490 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.28 Length: 2131  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 9 Gaps: 0

US-09-214-836-2 (1-9) x HUMPMEL (1-2131)

QY 1 LysValTTPGLyGlnTyrTPGlnVal 9  
DB 471 AAGACCTGGGGCCCACTGCAAGTT 497

RESULT 19  
LOCUS BC001414 2134 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, silver (mouse homolog) like, clone MGC:2169  
IMAGE:3139788, mRNA, complete cds.  
ACCESSION BC001414  
VERSION BC001414.1 GI:12655122  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 2134)  
Strausberg,R.  
Direct Submission  
Submitted (12-DEC-2000) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland,  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,  
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,  
Lim,M., Maduro,Q.L., Mastaglio,C., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Snyder,B., Stantittop,S., Thomas,P.J.,  
Tiongson,E.E., Touchman,D.W., Tsurgon,C., Vogt,J.L., Walker,M.A.,  
Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>  
Series: IRAL Plate: 4 Row: 1 Column: 8  
This clone was selected for full length sequencing because it



Db 1124 AAGACCTGGGCGCACTACTGCGCAGTT 1150

RESULT 22  
LOCUS AL356976/c 64323 bp DNA linear PRI 11-JUN-2002  
DEFINITION Human DNA sequence from clone RP4-700P11 on chromosome 1p32.1-32.3, complete sequence.

ACCESSION AL356976  
VERSION AL356976.3 GI:21425222  
KEYWORDS HTG  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 64323)  
AUTHORS Van Hellmond, Z.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
On Jun 13, 2002 this sequence version replaced gi:20386813.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>  
RP4-700P11 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pCYPAC2.

FEATURES  
source  
1..64323  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/map="p32.1-32.3"  
/clone="RP4-700P11"  
/clone\_lib="RPCI-4"  
BASE COUNT 17962 a 14719 c 15018 g 16624 t  
ORIGIN

Alignment Scores: 552 Length: 64323  
Pred. No.: 51.00 Matches: 8  
Score: 88.89% Conservatve: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 87.93% Indels: 0  
DB: 9 Gaps: 0

US-09-214-836-2 (1-9) x AL356976 (1-64323)

CY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 36114 AAGGCTGGGCTCACTACTGCGGAGTG 36088  
+

RESULT 23  
LOCUS AC022696/c 170470 bp DNA linear HTG 24-AUG-2002  
DEFINITION Homo sapiens chromosome 12 clone RP11-799J2 map 12, WORKING DRAFT  
SEQUENCE, 31 unordered pieces.

ACCESSION AC022696  
VERSION AC022696.3 GI:7249173  
KEYWORDS HTG; HTGS PHASE1; HTGS \_DRAFT.  
SOURCE HTG  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 170470)  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 12, clone RP11-799J2  
unpublished  
2 (bases 1 to 170470)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bede, F., Boguslavsky, L., Bouckgalter, B., Brown, A., Burkett, G., Castle, A., Choe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearlano, K., Dewar, K., Domino, M., Doyle, M., Fennestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardina, S., Grant, G., Hago, B., Heatford, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczy, J., Levine, R., Liu, G., Locke, K., MacDonald, P., Margulis, N., McPheters, R., Melgrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tsafaye, S., Theodore, J., Tirrell, A., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 170470)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bede, F., Boguslavsky, L., Bouckgalter, B., Brown, A., Burkett, G., Castle, A., Choe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Grant, G., Hago, B., Heatford, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczy, J., Levine, R., Liu, G., Locke, K., MacDonald, P., Margulis, N., McPheters, R., Melgrim, J., Meneus, L., Morrow, J., Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tsafaye, S., Theodore, J., Tirrell, A., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 16, 2000 this sequence version replaced gi:6984437.  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
Genome Center  
Center: Whitehead Institute/MIT Center for Genome Research  
Center code: WITR  
Web site: <http://www-seg.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L5293

```

Center clone name: 799_J_2
----- Summary Statistics -----
Sequencing Vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 157750 bases at least Q40
Consensus quality: 163812 bases at least Q30
Consensus quality: 165978 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 167470; sum-of-contigs
Quality coverage: 4.3 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1396: contig of 1396 bp in length
* 1397 1496: gap of 100 bp
* 1497 2649: contig of 1153 bp in length
* 2650 2749: gap of 100 bp
* 2750 4677: contig of 1928 bp in length
* 4678 4778: gap of 100 bp
* 4779 7400: contig of 2623 bp in length
* 7401 7501: gap of 100 bp
* 7502 9731: contig of 2231 bp in length
* 9732 9831: gap of 100 bp
* 9832 12715: contig of 2884 bp in length
* 12716 12815: gap of 100 bp
* 12816 15665: contig of 2850 bp in length
* 15666 15765: gap of 100 bp
* 15766 18113: contig of 2348 bp in length
* 18114 18213: gap of 100 bp
* 18214 21335: contig of 3122 bp in length
* 21336 21435: gap of 100 bp
* 21436 23658: contig of 2223 bp in length
* 23659 23758: gap of 100 bp
* 23759 27219: contig of 3461 bp in length
* 27220 27319: gap of 100 bp
* 27320 28943: contig of 1624 bp in length
* 28944 29044: gap of 100 bp
* 29045 32644: contig of 3601 bp in length
* 32645 32744: gap of 100 bp
* 32745 35824: contig of 3080 bp in length
* 35825 35925: gap of 100 bp
* 35926 39691: contig of 3767 bp in length
* 39692 39791: gap of 100 bp
* 39792 44173: contig of 4382 bp in length
* 44174 44273: gap of 100 bp
* 44274 48765: contig of 4492 bp in length
* 48766 48865: gap of 100 bp
* 48866 53583: contig of 4718 bp in length
* 53584 53684: gap of 100 bp
* 53685 60015: contig of 6332 bp in length
* 60016 60115: gap of 100 bp
* 60116 65089: contig of 4974 bp in length
* 65090 65189: gap of 100 bp
* 65190 70726: contig of 5537 bp in length
* 70727 70826: gap of 100 bp
* 70827 75813: contig of 4987 bp in length
* 75814 75913: gap of 100 bp
* 75914 83356: contig of 7443 bp in length
* 83357 83456: gap of 100 bp
* 83457 89398: contig of 5942 bp in length
* 89399 89498: gap of 100 bp
* 89499 95293: contig of 5795 bp in length
* 95294 95393: gap of 100 bp
* 95394 106536: contig of 11143 bp in length
* 106537 106636: gap of 100 bp

```

```

FEATURES
source
* 106637 114952: contig of 8316 bp in length
* 114953 115052: gap of 100 bp
* 115053 121344: contig of 6292 bp in length
* 121345 121444: gap of 100 bp
* 121445 130004: contig of 8560 bp in length
* 130005 130104: gap of 100 bp
* 130105 142220: contig of 12116 bp in length
* 142221 142320: gap of 100 bp
* 142321 170470: contig of 28150 bp in length.
Location/Qualifiers
1. 170470
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/map="12"
/clone="RP11-799J2"
/clone_1b="RPC1-11 Human Male BAC"
1. 1396
/feature="assembly_fragment"
1497. 2649
/feature="assembly_fragment"
2750. 4677
/feature="assembly_fragment"
4778. 7400
/feature="assembly_fragment"
7501. 9731
/feature="assembly_fragment"
9832. 12715
/feature="assembly_fragment"
12816. 15665
/feature="assembly_fragment"
15766. 18113
/feature="assembly_fragment"
18214. 21335
/feature="assembly_fragment"
21436. 23658
/feature="assembly_fragment"
23759. 27219
/feature="assembly_fragment"
27320. 28943
/feature="assembly_fragment"
27320. 28943
/feature="assembly_fragment"
vector_end:SP6
vector_side:left"
29044. 32644
/feature="assembly_fragment"
32745. 35824
/feature="assembly_fragment"
35925. 39691
/feature="assembly_fragment"
39792. 44173
/feature="assembly_fragment"
44274. 48765
/feature="assembly_fragment"
48866. 53583
/feature="assembly_fragment"

```

## Alignment Scores:

```

Pred. No.: 1.27e+03 Length: 170470
Score: 51.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 87.93% Indels: 0
DB: 2 Gaps: 0

```

US-09-214-836-2 (1-9) x ACO22696 (1-170470)

Oy 1 LysValTrpGlyGlnTrpGlnVal 9

Db 115899 AAGCTCTGGGCTGAGTCTGGGAGTGG 115873

RESULT 24  
AX474660

LOCUS AX474660 1881 bp DNA linear PAT 12-AUG-2002  
DEFINITION Sequence 1 from Patent EP122928.  
ACCESSION AX474660  
VERSION AX474660.1 GI:22214009  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Moelling, K., Nawrath, M. and Pavlovic, J.  
TITLE Pharmaceutical compositions for treating or preventing cancer,  
especially melanoma  
JOURNAL Patent: EP 122928-A 1 17-JUL-2002;  
Universitaet Zuerich Institut fuer Medizinische Virologie (CH)  
FEATURES  
Source  
Location/Qualifiers  
1..1881  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
1..1881  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAD43666.1"  
/db\_xref="GI:22214010"  
/translation="MWGVRSFLPVLYSALLAVGALEGRNODMLGVPRLVTKTW  
NRQLYPEWTEVOGNCWGRGQVLRVINDPFLVGNASSTILAHFPGSKVLPDGV  
IWANNITINSQWGGQPVYPOEPDCAVFPDGGPCSPGPRPRSPVYVKTWGTKW  
QVLGQPVRSISATRAKGLTHMEVTVYHRRGQSQSVPLAHASSTFTITDQVPSVS  
VSQALDGEKTHFLRNHPLIFALQHDPSGLAEADLSYMDPGDGTLLISRALDV  
THYLESGSYTAOVVLOAALPLVSCSSPVGTTDGMPLAEPAGTTSRGCTTKVVG  
TTPOGMPPTQSGTIVQMPTEVTATSEOMLTSAVIDTTLAEVSTTEGTTPTPR  
SGTTVAQATTTEGPDSPLPTQSGTSGISPLDDPTTLMVKRQVPLDCVLYRGSF  
SLADIVQIGTESAEILQAVPESGDALVELTVCQGGUPKACMDISSPGCPPRQRLC  
QSVPPSPCQVLHGVLYKGGSGTYCLNVSADANSIAVASTQLVVPGDGLQAPLL  
VGILLVAVVAVLASLILIGIDLRSAQFPKCHMVALTAPASGLRARGLGENSEPILLSQ  
QV"  
BASE COUNT 417 a 537 c 500 g 427 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 39.7 Length: 1881  
Score: 50.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 86.21% Indels: 0  
DB: Gaps: 0  
US-09-214-836-2 (1-9) x AX474660 (1-1881)  
QY 1 LysValTTPGLyGlnTyTTPGlnVal 9  
DB 460 AAGACCTGGGGAATACTGGCAAGTT 486  
RESULT 25  
MMU14133 1881 bp mRNA linear ROD 06-JUL-1995  
LOCUS Mus musculus pmel17 protein mRNA, complete cds.  
ACCESSION U14133  
VERSION U14133.1 GI:887940  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Kwon, B.-S., Halaban, R., Ponnazhagan, S., Kim, K., Chintamaneni, C.,  
Bennett, D. and Pickard, R.T.  
TITLE Mouse silver mutation is caused by a single base insertion in the  
JOURNAL putative cytoplasmic domain of Pmel 17  
MEDLINE Nucleic Acids Res. 23 (1), 154-158 (1995)  
PUBMED 95175358  
7870580

REFERENCE 2 (bases 1 to 1881)  
AUTHORS Kwon, B.-S.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-1994) Byoung S. Kwon, Indiana University School  
of Medicine, Microbiology and Immunology, 635 Barnhill Dr,  
Indianapolis, IN 46202, USA  
FEATURES  
Source  
Location/Qualifiers  
1..1881  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57Bl/6"  
/db\_xref="taxon:10090"  
/chromosome="10"  
/map="chromosome 10 si locus"  
/clone="pmel17-10"  
/sex="female"  
/cell\_line="primary culture"  
/cell\_type="melanocyte"  
/tissue\_type="skin"  
1..1881  
/gene="pmel17"  
1..1881  
/gene="pmel17"  
/product="Pmel17 protein"  
/protein\_id="AA69538.1"  
/db\_xref="GI:887941"  
/translation="MWGVRSFLPVLYSALLAVGALEGRNODMLGVPRLVTKTW  
NRQLYPEWTEVOGNCWGRGQVLRVINDPFLVGNASSTILAHFPGSKVLPDGV  
IWANNITINSQWGGQPVYPOEPDCAVFPDGGPCSPGPRPRSPVYVKTWGTKW  
QVLGQPVRSISATRAKGLTHMEVTVYHRRGQSQSVPLAHASSTFTITDQVPSVS  
VSQALDGEKTHFLRNHPLIFALQHDPSGLAEADLSYMDPGDGTLLISRALDV  
THYLESGSYTAOVVLOAALPLVSCSSPVGTTDGMPLAEPAGTTSRGCTTKVVG  
TTPOGMPPTQSGTIVQMPTEVTATSEOMLTSAVIDTTLAEVSTTEGTTPTPR  
SGTTVAQATTTEGPDSPLPTQSGTSGISPLDDPTTLMVKRQVPLDCVLYRGSF  
SLADIVQIGTESAEILQAVPESGDALVELTVCQGGUPKACMDISSPGCPPRQRLC  
QSVPPSPCQVLHGVLYKGGSGTYCLNVSADANSIAVASTQLVVPGDGLQAPLL  
VGILLVAVVAVLASLILIGIDLRSAQFPKCHMVALTAPASGLRARGLGENSEPILLSQ  
QV"  
BASE COUNT 417 a 537 c 500 g 427 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 39.7 Length: 1881  
Score: 50.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 86.21% Indels: 0  
DB: Gaps: 0  
US-09-214-836-2 (1-9) x MMU14133 (1-1881)  
QY 1 LysValTTPGLyGlnTyTTPGlnVal 9  
DB 460 AAGACCTGGGGAATACTGGCAAGTT 486  
Search completed: August 24, 2003, 02:54:11  
Job time : 2212.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_p2n model

Run on: August 23, 2003, 23:25:17 ; Search time 196.5 Seconds  
(without alignments)  
123.638 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KWGQYQV 9

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlh  
-Q/cgrr2/US09214836/runat 14082003 085039 7585/app query.fasta\_1.398  
-DB=N.geneseq.19Jun03 -QMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=25  
-MODE=LOCAL -OUTFMT=PCT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09214836 @CGN 1.1 401 @runat 14082003 085039 7585 -NCPU=6 -ICPU=3  
-NO MMAP -IARGUMENTARY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEXTIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
N.GeneSeq.19Jun03:  
1: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1987.DAT.\*  
9: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1988.DAT.\*  
10: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1989.DAT.\*  
11: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1995.DAT.\*  
17: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1996.DAT.\*  
18: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2002.DAT.\*  
25: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Match Length	DB ID	Description
1	54	93.1	36	AA05466
2	54	93.1	51	AA05466
3	54	93.1	90	AA05466
4	54	93.1	90	AA05466
5	54	93.1	90	AA05466
6	54	93.1	1986	AA07346
7	54	93.1	1986	AA07346
8	54	93.1	1986	AA07346
9	54	93.1	2130	AA096055
10	54	93.1	2130	AA096055
11	54	93.1	2130	AA096055
12	54	93.1	2131	AA096055
13	54	93.1	2131	AA096055
14	54	93.1	2131	AA096055
15	54	93.1	2534	AA096055
16	54	93.1	16638	AA096055
17	50	86.2	1881	AA096055
18	50	86.2	2172	AA096055
19	49	84.5	24	AA096055
20	49	84.5	24	AA096055
21	49	84.5	24	AA096055
22	49	84.5	24	AA096055
23	49	84.5	24	AA096055
24	48	82.8	7094	AA096055
25	48	82.8	7094	AA096055
26	46	79.3	174	AA096055
27	46	79.3	1664976	AA096055
28	45	77.6	2000	AA096055
29	45	77.6	3570	AA096055
30	45	77.6	7855	AA096055
31	44	75.9	591	AA096055
32	44	75.9	591	AA096055
33	44	75.9	591	AA096055
34	44	75.9	591	AA096055
35	44	75.9	591	AA096055
36	44	75.9	591	AA096055
37	44	75.9	591	AA096055
38	44	75.9	1786	AA096055
39	44	75.9	1807	AA096055
40	44	75.9	15044	AA096055
41	44	75.9	15046	AA096055
42	44	75.9	42571	AA096055
43	44	75.9	130480	AA096055
44	44	75.9	260209	AA096055
45	43	74.1	417	AA096055

## ALIGNMENTS

RESULT 1	ALIGNMENTS
AA05466	AA05466 standard; cDNA to mRNA, 36 BP.
AA05466	AA05466
25-JAN-1996	(first entry)
Sequence encoding immunogenic peptide of melanoma antigen gp100.	
Melanoma; antigen; vaccine; immunogen; primer; probe; detection;	
identification; tumour; gp100; ss.	
Homo sapiens.	
Key	Location/Qualifiers
FT	1..36
CDS	

KW multifactorial disease; autoimmune disease; infection;  
 KM nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US35498.  
 XX  
 PR 28-DEC-1999; 99US-0173419.  
 PR 27-DEC-2000; 2000US-0173419.  
 XX  
 PA (CDRA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach M;  
 XX  
 DR WPI, 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX  
 PS Claim 1; Page 1443; 4143p; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.  
 XX  
 SQ Sequence 51 BP; 15 A; 17 C; 9 G; 10 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 0.522 Length: 51  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 22 Gaps: 0  
 XX  
 US-09-214-836-2 (1-9) x AAL26956 (1-51)  
 OY 1 lysvaltptgilyglnrttptglnval 9  
 ID 37 AAGACCTGGGGTCATATCTGCAAGTT 11  
 XX  
 ABK36650 standard; DNA; 90 BP.  
 XX  
 ABK36650;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Human DNA encoding gp100 segment 10.  
 XX  
 KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; parasitic infection;  
 KW Trypanosoma; Toxoplasma; Giardia; ds.

XX Homo sapiens.  
 OS  
 XX MO200190197-A1.  
 PN  
 XX 29-NOV-2001.  
 PD  
 XX  
 XX 25-MAY-2001; 2001WO-AU00622.  
 PF  
 XX 26-MAY-2000; 2000AU-0007761.  
 PR  
 XX (AUSU ) UNIV AUSTRALIAN NAT.  
 PA  
 XX Thomson SA, Ramshaw IA;  
 PI  
 XX WPI: 2002-147575/19.  
 DR P-PSDB; AAU84830.  
 XX  
 XX New synthetic polypeptides having several different segments of at  
 PT least one parent polypeptide linked together differently compared to  
 PT the linkage in the parent polypeptide, for inducing immune response  
 PT against a pathogen or cancer  
 XX  
 XX Example 3; Fig 27; 364pp; English.  
 PS  
 XX The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for  
 CC designing the synthetic polypeptides. The synthetic polypeptides and  
 CC polynucleotides are referred to as a Savine. The synthetic polypeptide is  
 CC useful for modulating immune responses preferably directed against a  
 CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,  
 CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone  
 CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.  
 CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present  
 CC sequence encodes a peptide derived from a parent protein used to  
 CC construct a savine of the invention.  
 CC  
 XX SQ Sequence 90 BP; 23 A; 17 C; 32 G; 18 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0.968 Length: 90  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-214-836-2 (1-9) x ABK36650 (1-90)  
 Oy 1 lysValTrpGlyGlnTyrTrpGlnVal 9  
 Db 61 AAGACATCGGACACATATTCGCAAGTG 87  
 RESULT 4  
 ABK36651  
 ID ABK36651 standard; DNA; 90 BP.  
 XX  
 AC ABK36651;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX

DE Human DNA encoding gp100 segment 11.  
 XX  
 XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; parasitic infection;  
 KW Trypanosoma; Toxoplasma; Giardia; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200190197-A1.  
 PN  
 XX 29-NOV-2001.  
 PD  
 XX 25-MAY-2001; 2001WO-AU00622.  
 PF  
 XX 26-MAY-2000; 2000AU-0007761.  
 PR  
 XX (AUSU ) UNIV AUSTRALIAN NAT.  
 PA  
 XX Thomson SA, Ramshaw IA;  
 PI  
 XX WPI: 2002-147575/19.  
 DR P-PSDB; AAU84831.  
 XX  
 XX New synthetic polypeptides having several different segments of at  
 PT least one parent polypeptide linked together differently compared to  
 PT the linkage in the parent polypeptide, for inducing immune response  
 PT against a pathogen or cancer  
 XX  
 XX Example 3; Fig 27; 364pp; English.  
 PS  
 XX The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for  
 CC designing the synthetic polypeptides. The synthetic polypeptides and  
 CC polynucleotides are referred to as a Savine. The synthetic polypeptide is  
 CC useful for modulating immune responses preferably directed against a  
 CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,  
 CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone  
 CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.  
 CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present  
 CC sequence encodes a peptide derived from a parent protein used to  
 CC construct a savine of the invention.  
 CC  
 XX SQ Sequence 90 BP; 17 A; 26 C; 29 G; 18 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 0.968 Length: 90  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-214-836-2 (1-9) x ABK36651 (1-90)  
 Oy 1 lysValTrpGlyGlnTyrTrpGlnVal 9  
 Db 16 AAAACCTGGGCGCAATCTGCAAGTC 42  
 RESULT 5  
 AAD07346

ID	AA007346 standard; DNA; 1986 BP.	
XX		
AC	AA007346;	
XX		
DT	18-SEP-2001 (first entry)	
XX		
DE	Modified tumour-associated antigen, GP100 DNA.	
XX		
KM	Tumour-associated antigen; TAA; GP100 antigen; cytostatic; gene therapy;	
KW	immune response; tetanus toxoid; TT; diphtheria toxoid; DT; prophylactic;	
KM	vaccine; cancer; therapeutic; ds.	
XX		
OS	Synthetic.	
XX		
FI	Key	Location/Qualifiers
FT	CDS	1..1986
FT		/*tag= a
FT		/product= "Modified tumour-associated antigen, GP100"
XX		
PN	WO200149317-A2.	
XX		
PD	12-JUL-2001.	
XX		
PF	05-JAN-2001; 2001WO-CA000005.	
XX		
PR	05-JAN-2000; 2000US-0174587.	
XX		
PA	(AVET ) AVENTIS PASTEUR LTD.	
XX		
PI	Emtage P, Barber BH, Sambhara S, Sia CDY;	
XX		
PI	WPI. 2001-441790/47.	
DR	P-PSDB; AAEO5116.	
XX		
PT	Enhancing immune response to antigen such as tumor antigen for treating	
PT	cancer in an animal involves administering an inducing agent to the	
PT	animal followed by administering inducing agent-antigen mixture	
XX		
PS	Example 1; Fig 1; 62pp; English.	
XX		
CC	The invention relates to a method of enhancing an immune response against	
CC	tumour-associated antigens (TAAe), such as GP100 and carcinoembryonic	
CC	antigen (CEA) in an animal. The method involves priming of the animal	
CC	with an inducing agent such as tetanus toxoid (TT) or diphtheria toxoid	
CC	(DT), subsequently followed by administration of an inducing agent-	
CC	antigen mixture. The method provides the enhancement or augmentation of	
CC	the immune response to the antigen and/or improves a vaccination protocol	
CC	by allowing use of less antigen. The immunisation of the animal with	
CC	tumour-associated antigen is useful for the prophylactic or therapeutic	
CC	treatment of cancer. The present DNA sequence encodes modified tumour-	
CC	associated antigen, GP100 related to the invention.	
XX		
SQ	Sequence 1986 BP; 431 A; 552 C; 552 G; 451 T; 0 other;	
	Alignment Scores:	
	Pred. No.:	28.2
	Score:	54.00
	Percent Similarity:	88.89%
	Best Local Similarity:	88.89%
	Query Match:	93.10%
	DB:	22
		Gaps: 0
	US-09-214-836-2 (1-9) x AA007346 (1-1986)	
OY	1 LysValTrpGlyGlnTyrTrpGlnVal 9	
Db	460 AAGACCTGGGGCCCAATACCTGGCAAGTT 486	
	RESULT 6	
	AAH22098	
ID	AAH22098 standard; cDNA; 1986 BP.	
XX		
AC	AAH22098;	

[illegible]

XX Virus.  
OS Synthetic.  
XX  
XX WO200130382-A1.  
XX  
XX 03-MAY-2001.  
XX  
XX 20-OCT-2000; 2000WO-CAN01253.  
XX  
XX 22-OCT-1999; 99US-0160879.  
PR 07-AUG-2000; 2000US-0223325.  
XX  
XX  
PA (AVERT ) AVENTIS PASTEUR LTD.  
XX  
XX Bernstein N, Tartaglia J, Moingeon P, Barber B,  
PI WPI; 2001-308587/32.  
DR P-PsDB; AAB97816.  
XX  
PT Inducing immune response to tumor antigen, useful in immunotherapy of  
XX cancer, by administering the antigen to a lymphatic site -  
XX  
XX Disclosure; Fig 6; 60pp; English.

XX The present invention describes a method for inducing an immune response,  
CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or  
CC nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys/  
CC (Macaca fascicularis) were injected with a modified form of gp100 antigen  
CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals  
CC of (a) developed a cell-mediated response (indicated by production of  
CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but  
CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far  
CC greater antibody response to gp100. The method is used in immunotherapy  
CC of a wide range of cancers through induction of a specific immune  
CC response (humoral and cellular) against the tumour antigens. When  
CC administered to a lymphatic site, Ag (or (II)) induces a stronger immune  
CC response than administration by other routes and may also break tolerance  
CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to  
CC AAB97815 represent peptides derived from gp100 which stimulate interferon  
CC (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given  
CC in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)  
CC protein given in AAB97817; and AAB97818 represents a CDA modified antigen  
CC peptide, all of which are used in the exemplification of the present  
CC invention.

SQ Sequence 1986 BP; 431 A; 552 C; 552 G; 451 T; 0 other;  
XX

Alignment Scores:  
Pred. No.: 28.2 Length: 1986  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 22 Gaps: 0

US-09-214-836-2 (1-9) x AAH20120 (1-1986)

Oy 1 LysValTrrPglVglnTyTrpGlnVal 9  
Db 460 AAGACCTGGGGCCCAATACTGGCAAGTT 486

RESULT 8  
AAO96055 ID AAO96055 standard; cDNA to mRNA; 2115 BP.  
XX  
XX AAO96055;  
XX  
XX 22-JAN-1996 (first entry)  
XX  
XX DT  
XX  
XX Sequence encoding melanoma associated antigen gp100.  
DE  
XX Melanoma; antigen; vaccine; immunogen; primer; probe; detection;  
XM

XX	identification; tumour; gp100; ds.
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	/tag= a
FT	/product= Melanoma associated antigen gp100.
FT	1..81
FT	misc_signal
FT	/tag= b
FT	1792..1870
FT	misc_feature
FT	/tag= c
FT	/label= Transmembrane domain.
FT	262..264
FT	misc_binding
FT	/tag= d
FT	/bound_molecTy= Carbohydrate.
FT	337..339
FT	misc_binding
FT	/tag= e
FT	352..354
FT	misc_binding
FT	/tag= f
FT	982..984
FT	misc_binding
FT	/tag= g
FT	1723..1725
FT	misc_binding
FT	/tag= h
XX	
PN	EP668350-A1.
PD	23-AUG-1995.
XX	
PF	14-FEB-1995;
PP	95EP-0200348.
PR	21-DEC-1994;
PR	94EP-0203709.
PR	16-FEB-1994;
PA	94EP-0200337.
PA	(ALKU ) AKZO NOBEL NV.
PI	
PI	Adema GJ, Fijdor CG;
XX	
DR	WP1; 1995-284790/38.
DR	P-PSDB; AAR78646.
PT	Melanoma associated antigen gp100 - used in vaccines and for the detection of tumours
XX	
PS	Claim 2; Page 19-22; 40pp; English.
CC	
CC	Immunogenic peptides derived from the melanoma associated antigen may be used in the production of vaccine. Nucleotide sequences encoding the immunogenic peptides may be used as primers and probes in the detection of melanoma cells. Tumour infiltrating lymphocytes capable of binding to the melanoma associated antigen can be cultured ex vivo and returned to melanoma particles, and when radiolabelled, they may be used to identify tumour deposits.
XX	
SQ	Sequence 2115 BP; 469 A; 587 C; 575 G; 484 T; 0 other;
Alignment Scores:	
Pred. No.:	30.2
Score:	54.00
Percent Similarity:	88.89%
Best Local Similarity:	88.89%
Query Match:	93.10%
DB:	16
US-09-214-836-2 (1-9) x AAQ96055 (1-2115)	
Oy	1 LysValTrpGlyGlnTyrTrpGlnVal 9
Db	481 AAGACCTGGGGCCCAATACGCGCAAGTT 507
RESULT 9	
ABQ76195	
ID	ABQ76195 standard; DNM; 2130 BP.

XX	Major histocompatibility complex; MHC; human; melanoma antigen; gp100;
KW	HLA-A2 binding domain; mutation; antigen presenting cell; vaccine;
KM	immune effector cell; cancer; antibody; ss.
XX	
OS	Homo sapiens.
XX	
FH	Location/Qualifiers
FT	Key 22..2007
CDS	
FT	/tag= a
FT	/product= "gp100"
XX	
PM	M02001.70767-A2.
XX	
PD	27-SEP-2001.
XX	
PF	19-MAR-2001; 2001WO-US08919.
XX	
PR	20-MAR-2000; 2000US-190750P.
PR	12-DEC-2000; 2000US-255019P.
XX	
PA	(GENZ ) GENZYME CORP.
PI	Nicorette CA;
DR	WPI; 2001-611469/70.
DR	P-PSEI; AAB47500.
XX	
PS	Disclosure; Page 60-63; 67pp; English.
XX	
CC	This sequence encodes human melanoma antigen gp100. Peptides of the invention based on the sequence of residues 209-217 of human melanoma antigen gp100, which represents the putative HLA-A2 binding domain, are designed to enhance binding to major histocompatibility complex (MHC) molecules and to enhance immunoregulatory properties relative to their natural counterparts. The mutations in the claimed peptides confer tighter binding to the MHC. These peptides are useful for inducing an immune response in a subject, where they are delivered in the context of an MHC molecule which presents the compound on the surface of an antigen presenting cell. The peptide sequences are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterized by expression of the melanoma antigen gp100. They are useful for diagnosis and treatment of diseases such as cancer, in particular against human melanoma and for generating antibodies that specifically recognize and bind the compounds
XX	
SQ	Sequence 2130 BP; 484 A; 587 C; 575 G; 484 T; 0 other;
XX	
Alignment Scores:	
Pred. No.:	30.4 Length: 2130
Score:	54.00 Matches: 8
Percent Similarity:	88.89% Conservative: 0
Best Local Similarity:	88.89% Mismatches: 1
Query Match:	93.10% Indels: 0
DB:	22 Gaps: 0
US-09-214-836-2 (1-9) x AAH43500 (1-2130)	
OY	1 LyEvAlTrpGlyGlnTrpTrpGlnVal 9
Db	 481 AAGACCTGGGGCCAATACCGCAAGTT 507
RESULT 11	
AAS14396	
ID	AAS14396 standard; cDNA; 2130 BP.
XX	
AC	AAS14396;
XX	
DT	26-MAR-2002 (first entry)

XX CDNA encoding human melanoma antigen gp100.  
 DE Human; anti-melanoma compound; melanoma antigen gp100; APC; MHC;  
 KW immune effector cell; antigen presenting cell; anti-cancer;  
 KW major histocompatibility complex; gp100 tumour antigen; cytostatic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 22.2007  
 FT CDS /tag=a  
 FT /product= "Melanoma antigen gp100"  
 FT  
 XX W0200192294-A2.  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX 21-MAY-2001; 2001WO-US16417.  
 XX  
 XX 31-MAY-2000; 2000US-208955P.  
 XX  
 XX 09-FEB-2001; 2001US-267877P.  
 XX  
 XX (GENZ ) GENZYME CORP.  
 XX  
 XX Nicolette CA;  
 XX  
 XX PI  
 XX WPI: 2002-106301/14.  
 XX  
 XX P-PSDB; AAU09695.  
 XX  
 XX Novel anti-melanoma compound or peptide useful for inducing immune  
 PT response in a subject, for treating melanoma, as components of  
 PT anti-cancer vaccines and to expand immune effector cells specific for  
 PT cancers -  
 XX  
 XX  
 XX Disclosure; Page 64-65; 69pp; English.  
 XX  
 XX The present invention relates to anti-melanoma compounds comprising a  
 CC peptide sequence based on human melanoma antigen gp100. Also described  
 CC are antibodies that recognise and bind to these compounds,  
 CC polynucleotides that encode these compounds, and immune effector cells  
 CC that have been raised in vitro or in vivo in the presence of an antigen  
 CC presenting cell (APC) that presents the compound. Such an APC may be  
 CC the major histocompatibility complex (MHC) molecule. The anti-melanoma  
 CC compounds are useful for inducing an immune response in a subject, by  
 CC delivering the compound to the subject in the context of an MHC molecule  
 CC which presents the compound on the surface of an APC. The anti-melanoma  
 CC compound is delivered as a polynucleotide that encodes it. The compounds  
 CC are useful to generate antibodies that specifically recognise and bind  
 CC to them, for the treatment of melanoma, as components of anti-cancer  
 CC vaccines, and to expand immune effector cells that are specific for  
 CC cancers characterised by expression of gp100 tumour antigen, melanoma.  
 CC The compounds are also useful in diagnostic methods for such diseases.  
 CC The present sequence encodes human melanoma antigen gp100.  
 CC  
 XX  
 XX Sequence 2130 BP; 484 A; 587 C; 575 G; 484 T; 0 other;  
 XX  
 XX  
 XX Alignment Scores:  
 Pred. No.: 30.4 Length: 2130  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-214-836-2 (1-9) x AAS14396 (1-2130)  
 QY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
 Db 481 AAGACCTGGGGCCCAATCTGCGCAAGTT 507  
 RESULT 12  
 AAT03760

ID AAT03760 standard; DNA; 2131 BP.  
 XX  
 XX AAT03760;  
 AC  
 XX 25-MAR-1996 (first entry)  
 DT  
 XX Melanoma-specific immunogen, pMEL17.  
 DE  
 XX Melanoma; immunogen; epitope; homologue; vaccine; immunotherapy;  
 KW cytotoxic T cell; lymphocyte; HLA-A2; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W09522561-A2.  
 XX  
 XX 24-AUG-1995.  
 XX  
 XX 16-FEB-1995; 95WO-US01991.  
 XX  
 XX 29-APR-1994; 94US-0234784.  
 XX  
 XX 16-FEB-1994; 94US-0197399.  
 XX  
 XX (UYVI-) UNIV VIRGINIA PATENT FOUND.  
 XX  
 XX Cox AL, Engelhard VH, Hunt DF, Shabanowitz J, Slingluff CL;  
 XX  
 XX WPI: 1995-302688/39.  
 XX  
 XX Melanoma-specific immunogen comprises epitope(s) homologous with  
 PT pMEL17 - are highly potent stimulators of HLA-A2+CTL's useful in  
 PT adoptive immuno-therapy  
 PT  
 XX  
 XX Disclosure; Page 19-20; 148pp; English.  
 XX  
 XX A melanoma-specific immunogen homologous with pMEL-17 (AAT03760)  
 CC comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the  
 CC group AAR82098-R82194 capable of eliciting a CTL response. The epitopes  
 CC AAR82098- AAR82108 are of particular interest. The immunogen can be used  
 CC for partial protection in mammals against melanoma peptides which are  
 CC homologous with pMEL-17 are highly potent stimulators of HLA-A2+  
 CC CTLs in several cell lines and can be used in immunotherapy or  
 CC incorporated into immunogenic conjugates as vaccines.  
 CC  
 XX  
 XX Sequence 2131 BP; 474 A; 589 C; 577 G; 491 T; 0 other;  
 XX  
 XX  
 XX Alignment Scores:  
 Pred. No.: 30.4 Length: 2131  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 16 Gaps: 0  
 US-09-214-836-2 (1-9) x AAT03760 (1-2131)  
 QY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
 Db 471 AAGACCTGGGGCCCAATCTGCGCAAGTT 497  
 RESULT 13  
 AAT96726  
 ID AAT96726 standard; cDNA; 2131 BP.  
 AC  
 XX AAT96726;  
 AC  
 XX 08-APR-1998 (first entry)  
 DT  
 XX pMEL17 cDNA.  
 DE  
 XX Melanoma; immunogen; cytotoxic T lymphocyte; CTL;  
 KW human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3;  
 KW HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection; ss.  
 XX

```

OS Homo sapiens.
XX
XX WO3734613-A1.
XX
XX 25-SEP-1997.
XX
XX 17-MAR-1997; 97WO-US04958.
XX
XX 04-OCT-1996; 96US-0027627.
XX 19-MAR-1996; 96US-0013972.
XX
XX (U9V1-) UNIV VIRGINIA PATENT FOUND.
XX
XX Cox AL, Engelhard VH, Hendrikson RC, Hunt DF, Kittlesen D;
PI Shabanowitz J, Skipper J, Slingluff CJ,
XX
XX WPI; 1997-479982/44.
XX
XX Melanoma-specific immunogens of pmel-17 and tyrosinase - useful in
PT vaccination for producing melanoma-specific cytotoxic T lymphocytes
XX
XX Disclosure; Pages 30-31; 106pp; English.
XX
XX A novel melanoma specific immunogen comprises at least 1 melanoma
CC specific cytotoxic T lymphocyte (CTL) epitope, where at least
CC 1 of the epitopes is substantially homologous to a human leukocyte
CC antigen-A1 (HLA-A1) and HLA-A3 restricted epitope of a melanoma
CC antigen, either pmel-17, i.e. the protein encoded by present
CC sequence, or tyrosinase. The immunogen can be used in vaccines for
CC protection against melanoma in mammals.
XX
XX Sequence 2131 BP; 475 A; 588 C; 578 G; 490 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 30.4 Length: 2131
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 18 Gaps: 0

US-09-214-836-2 (1-9) x AAT96726 (1-2131)
Oy 1 LysValTrpGlyGlnTyrTrpGlnVal 9
DB 471 AAGACCTGGGGCCAACTACTGCAAGTT 497

RESULT 14
AAL49164
ID AAL49164 standard; cDNA; 2131 BP.
XX
XX AAL49164;
XX
XX 29-OCT-2002 (first entry)
XX
XX Human gp100 coding sequence.
XX
XX Human; gp100; cancer; vaccine; melanoma; tumour-associated antigen;
KM cytosolic; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 12..2018
FT /*tag= a
FT /product= "gp100"
XX
XX EPI222928-A2.
XX
XX 17-JUL-2002.
XX
XX 09-JAN-2002; 2002EP-0000185.
XX

```

```

PR 16-JAN-2001; 2001EP-0100914.
XX
XX (U9ZU-) UNIV ZUERICH INST MEDIZINISCHE VIROLOGIE.
XX
XX Moelling K, Nawrath M, Pavlovic J;
XX
XX WPI; 2002-610269/66.
XX
XX P-PSDB; AAO18863.
XX
XX Pharmaceutical composition useful for treating cancer, comprises
PT nucleic acid molecule encoding tumor associated antigen and peptide
PT comprising a region corresponding to epitope of tumor associated
PT antigen
XX
XX Disclosure; Page 21-24; 34pp; English.
XX
XX The present invention relates to a pharmaceutical composition which
CC comprises a nucleic acid molecule encoding a tumour-associated antigen
CC and at least one peptide comprising a region corresponding to a putative
CC cytotoxic T cell, helper T cell or B cell epitope of a tumour-associated
CC antigen and/or cells pulsed with such peptide(s). In particular, the
CC tumour-associated antigen may be gp100. The composition is useful for the
CC treatment of cancer, especially melanoma. The present sequence is for the
CC human gp100 coding sequence.
XX
XX Sequence 2131 BP; 475 A; 588 C; 578 G; 490 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 30.4 Length: 2131
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 24 Gaps: 0

US-09-214-836-2 (1-9) x AAL49164 (1-2131)
Oy 1 LysValTrpGlyGlnTyrTrpGlnVal 9
DB 471 AAGACCTGGGGCCAACTACTGCAAGTT 497

RESULT 15
AAH22099
ID AAH22099 standard; DNA; 2534 BP.
XX
XX AAH22099;
XX
XX 17-AUG-2001 (first entry)
XX
XX Plasmid C5H6gp100M H6 promoted human gp100M nucleotide sequence.
XX
XX Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
KM modified gp100; vaccine; gene therapy; cancer; circular; cyclic; ds.
XX
XX Homo sapiens.
XX
XX Vaccinia virus.
XX
XX WO200130847-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-CA01254.
XX
XX 22-OCT-1999; 99US-0160879.
XX 07-AUG-2000; 2000US-0223325.
XX
XX (AVET) AVENTIS PASTEUR LTD.
XX
XX Berinsein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
XX
XX WPI; 2001-316326/33.
XX
XX New isolated and purified gp100 useful for the prophylactic treatment
PT

```



PT of cancer -  
 XX  
 PS Example 2; Fig 3; 89pp; English.  
 XX  
 CC The present invention describes an isolated and purified modified gp100  
 CC molecule (gp100M) capable of modulating an immune response in an animal.  
 CC gp100M has cytostatic activity and can be used in vaccine production and  
 CC gene therapy. Nucleic acids and proteins of the invention are useful as  
 CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and  
 CC AAH98098 to AAH98206 represent sequence used in the exemplification of  
 CC the present invention. More specifically AAH98098 and AAH98205 represent  
 CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to  
 CC AAH22106 represent primers used in the present invention; AAH22099  
 CC represents the plasmid nucleotide sequence comprising the Vaccinia virus  
 CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human  
 CC gp100M protein given in AAH22106.  
 XX  
 SO Sequence 2534 BP; 622 A; 632 C; 657 G; 623 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 36.7 Length: 2534  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: Gaps: 0  
 US-09-214-836-2 (1-9) x AAH22099 (1-2534)  
 Qy 1 LysValTrpGlyGlnVal 9  
 Db 836 AAGACCTGGGGCAATCTGCAAGTT 862  
 RESULT 16  
 ABK36828  
 ID ABK36828 standard; DNA; 16638 BP.  
 AC ABK36828;  
 XX  
 XX 08-MAY-2002 (first entry)  
 DT  
 XX  
 DE Human DNA for melanocyte differentiation antigens savine.  
 XX  
 XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; parasitic infection;  
 KW Trypanosoma; Toxoplasma; Giardia; ds.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200190197-A1.  
 PN  
 XX  
 PD 29-NOV-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-AU00622.  
 PF  
 XX 26-MAY-2000; 2000AU-000761.  
 PR  
 XX (AUSU ) UNIV AUSTRALIAN NAT.  
 PA  
 XX Thomson SA, Ramshaw IA;  
 PI  
 XX WPI: 2002-147575/19.  
 DR P-PSDB; AAU85008.  
 XX  
 XX New synthetic polypeptides having several different segments of at  
 PT least one parent polypeptide linked together differently compared to  
 PT the linkage in the parent polypeptide, for inducing immune response  
 PT against a pathogen or cancer -  
 XX Example 3; Fig 27; 364pp; English.  
 XX

CC The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for  
 CC designing the synthetic polypeptides. The synthetic polypeptides and  
 CC polynucleotides are referred to as a Savine. The synthetic polypeptide is  
 CC useful for modulating immune responses preferably directed against a  
 CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,  
 CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone  
 CC liver, osteophagus, brain, testicle, uterus), as potentiating agents.  
 CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present  
 CC sequence encodes a savine protein of the invention.  
 SO Sequence 16638 BP; 3840 A; 5297 C; 3944 G; 3557 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 285 Length: 16638  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: Gaps: 0  
 US-09-214-836-2 (1-9) x ABK36828 (1-16638)  
 Qy 1 LysValTrpGlyGlnVal 9  
 Db 7252 AAAACCTGGGGCAATCTGCGAGTTC 7278  
 RESULT 17  
 AAL49163  
 ID AAL49163 standard; cDNA; 1881 BP.  
 AC AAL49163;  
 XX  
 XX 29-OCT-2002 (first entry)  
 DT  
 XX  
 DE Murine gp100 coding sequence.  
 XX  
 XX Mouse; gp100; cancer; vaccine; melanoma; tumour-associated antigen;  
 KW cytosolic; gene; ss.  
 KW  
 XX Mus musculus.  
 OS  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 1..1881  
 FT /\*tag= "a"  
 FT /product= "gp100"  
 XX  
 XX BP1222928-A2.  
 XX  
 XX 17-JUL-2002.  
 PD  
 XX 09-JAN-2002; 2002EP-0000185.  
 PF  
 XX 16-JAN-2001; 2001EP-0100914.  
 PR  
 XX (VUZU-) UNIV ZUERICH INST MEDIZINISCHE VIROLOGIE.  
 PA  
 XX Moelling K, Nawrath M, Pavlovic J;  
 PI  
 XX WPI: 2002-610269/66.  
 DR P-PSDB; AAO18862.  
 XX

XX Pharmaceutical composition useful for treating cancer, comprises  
PT nucleic acid molecule encoding tumor associated antigen and peptide  
PT comprising a region corresponding to epitope of tumor associated  
PT antigen -  
XX  
XX  
XX Disclosure; Page 16-19; 34pp; English.  
XX  
CC The present invention relates to a pharmaceutical composition which  
CC comprises a nucleic acid molecule encoding a tumour-associated antigen  
CC and at least one peptide comprising a region corresponding to a putative  
CC cytotoxic T cell, helper T cell or B cell epitope of a tumour-associated  
CC antigen and/or cells pulsed with such peptide(s). In particular, the  
CC tumour-associated antigen may be gp100. The composition is useful for the  
CC treatment of cancer, especially melanoma. The present sequence is the  
CC murine gp100 coding sequence.  
XX  
SQ Sequence 1881 BP; 417 A; 537 C; 500 G; 427 T; 0 other;  
Alignment Scores:  
Pred. No.: 114 Length: 1881  
Score: 50.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 86.21% Indels: 0  
DB: 24 Gaps: 0  
US-09-214-836-2 (1-9) x AAL49163 (1-1881)  
Oy 1 LysValTPGIyGIntYrTPGInVal 9  
Db 460 AAGACCTGGGGAAATACTGGCAAGTT 486  
RESULT 18  
AAT02716  
ID AAT02716 standard; cDNA; 2172 BP.  
XX  
AC AAT02716;  
XX  
DT 20-APR-1996 (first entry)  
XX  
DE MART-1 melanoma antigen cDNA25.  
XX  
KW cDNA25; MART-1; melanoma antigen recognised by T-cells;  
KW gp100 antigen derivative; melanoma; metastatic melanoma;  
KW tumour-associated antigen; immunogen; diagnosis; prognosis;  
KW prophylaxis; therapy; vaccine; ds.  
XX  
OS Mammalian.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 38..2038  
FT /\*tag= a  
FT /note= "cDNA25 melanoma antigen"  
XX  
XX WO9529193-A2.  
XX  
PD 02-NOV-1995.  
XX  
PF 21-APR-1995; 95WO-US05063.  
XX  
PR 05-APR-1995; 95US-0417174.  
PR 22-APR-1994; 94US-0231565.  
XX  
PA (USSH ) US SEC DEPT HEALTH.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
XX WPI: 1995-382963/49.  
XX P-PSDB; AAR84854.  
XX  
PT DNA encoding melanoma antigens recognised by T-lymphocytes - also  
PT vectors, host cells and antibodies, used to detect, treat and

PT immunise animal against melanoma.  
XX  
XX Disclosure; Fig 4A-4B; 184pp; English.  
XX  
XX The nucleic acid encodes cDNA25, a melanoma antigen (MART-1)  
CC which is recognized by T-lymphocytes. cDNA25 is a derivative of  
CC the melanocyte-melanoma-specific antigen gp100 (see AAR84855).  
CC Antigen cDNA25 is a source of immunogenic peptides (see AAR84199)  
CC which are optionally modified (see AAR84200-R84211) and used in  
CC medicaments, especially vaccines, for the treatment or prevention  
CC (by immunization) of melanoma. Antibodies against cDNA25 and its  
CC immunogenic peptides may be used in the detection and isolation  
CC of the antigen from a sample, the detection of which is indicative  
CC of a disease state (melanoma or metastatic melanoma).  
XX  
SQ Sequence 2172 BP; 512 A; 594 C; 578 G; 488 T; 0 other;  
Alignment Scores:  
Pred. No.: 134 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 86.21% Indels: 0  
DB: 16 Gaps: 0  
US-09-214-836-2 (1-9) x AAT02716 (1-2172)  
Oy 1 LysValTPGIyGIntYrTPGIn 8  
Db 498 AAGACCTGGGGCCCAATCTGGCAA 521  
RESULT 19  
AAS45525  
ID AAS45525 standard; cDNA; 2172 BP.  
XX  
AC AAS45525;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE DNA encoding Melanoma antigen cDNA25.  
XX  
KW Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;  
KW diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;  
KW in vivo tumour rejection; ss.  
XX  
OS Homo sapiens.  
XX  
XX US6270778-B1.  
XX  
PD 07-AUG-2001.  
XX  
PF 12-MAR-1999; 99US-0267439.  
XX  
PR 05-MAY-1998; 98US-0073138.  
PR 22-APR-1994; 94US-0231565.  
PR 05-APR-1995; 95US-0417174.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
XX WPI: 2001-595403/67.  
XX P-PSDB; AAU28912.  
XX  
PT Immunogenic peptide useful in vaccines comprises specific amino acids  
PT of new melanoma antigen recognised by T lymphocytes -  
XX  
XX Example 3; Figure 4; 73pp; English.  
XX  
CC The invention relates to a novel immunogenic peptide comprising 5-20  
CC contiguous amino acids of new melanoma antigen recognised by T  
CC lymphocytes (MART-1). The peptide sequence contains at least one amino  
CC acid modification of MART-1. The peptide is used in diagnostic and

CC therapeutic methods as an immunogen or vaccine to prevent or treat  
CC melanoma, and for in vivo tumour recognition and rejection. AAG5524-  
CC AAG5528 represent MAF-1 coding sequences, PCR primers, and related  
CC sequences of the invention.

XX  
SQ Sequence 2172 BP, 512 A, 594 C, 578 G, 488 T, 0 other;

#### Alignment Scores:

Pred. No.:	134	Length:	2172
Score:	50.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	86.21%	Indels:	0
DB:	22	Gaps:	0

US-09-214-836-2 (1-9) x AAG5525 (1-2172)

OY 1 LysValITpGIyGIntYITpGln 8

DB 498 AAGACCTGGGCGCAATACCTGCGCA 521

#### RESULT 20

AAT05465 AAT05465 standard; CDNA to mRNA; 24 BP.

AC AAT05465;

DT 25-JAN-1996 (first entry)

XX Sequence encoding immunogenic peptide of melanoma antigen gp100.

XX Melanoma; antigen; vaccine; immunogen; primer; probe; detection;

KW identification; tumour; gp100; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 1..24

FT /\*tag= a

FT /product= Immunogenic peptide.

XX EPE68350-A1.

XX 23-AUG-1995.

PF 14-FEB-1995; 95EP-0200348.

PR 21-DEC-1994; 94EP-0203709.

PR 16-FEB-1994; 94EP-0200337.

XX (ALKU) AKZO NOBEL NV.

PI Adema GJ, Figdor CG;

DR WPI; 1995-284790/38.

DR P-PSDB; AAR78641.

XX Melanoma associated antigen gp100 - used in vaccines and for the

PT detection of tumours

XX Claim 7; Page 26; 40pp; English.

XX Immunogenic peptides derived from the melanoma associated antigen

CC (See AAR7633-45) may be used in the production of vaccines.

CC Nucleotide sequences encoding the immunogenic peptides may be used

CC as primers and probes in the detection of melanoma cells. Tumour

CC infiltrating lymphocytes capable of binding to the melanoma

CC associated antigen can be cultured ex vivo and returned to melanoma

CC particles, and when radiolabelled, they may be used to identify

Alignment Scores:

Pred. No.:	1,42	Length:	24
Score:	49.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	84.48%	Indels:	0
DB:	16	Gaps:	0

US-09-214-836-2 (1-9) x AAT05465 (1-24)

OY 3 TrpGIyGIntYITpGlnVal 9

DB 4 TGGGCGCAATACCTGCGCAAGTT 24

#### RESULT 21

AAS80038 AAS80038 standard; CDNA; 3669 BP.

AC AAS80038;

DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #15842.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PSDB; ABG15851.

XX Claim 1; SEQ ID No 15842; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAG54197-AAG54564 represent novel human

CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 3669 BP; 868 A; 974 C; 1037 G; 790 T; 0 other;  
Alignment Scores:  
Pred. No.: 341 Length: 3669  
Score: 49.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 84.48% Indels: 0  
DB: 23 Gaps: 0  
US-09-214-836-2 (1-9) x AAS80038 (1-3669)  
QY 2 ValTPGIYGIINTYTRPGIn 8  
Db 1696 GTGTGGGGCAATCTGSCAA 1716  
RESULT 22  
AAS94092  
ID AAS94092 standard; cDNA; 3669 BP.  
XX AC AAS94092;  
XX DT 13-FEB-2002 (first entry)  
XX DE DNA encoding novel human diagnostic protein #29896.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KM food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI: 2001-639362/73.  
XX DR P-PSDB; ABG23905.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity -  
XX PS Claim 1; SEQ ID No 29896; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and  
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX CC and gene mapping, and in recombinant production of (II). The  
XX CC polynucleotides are also used in diagnostics as expressed sequence tags  
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques  
XX CC to restore normal activity of (II) or to treat disease states involving  
XX CC (II). (II) is useful for generating antibodies against it, detecting or  
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as  
XX CC a food supplement. (II) and its binding partners are useful in medical  
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating  
XX CC disorders involving aberrant protein expression or biological activity.  
XX CC The polypeptide and polynucleotide sequences have applications in  
XX CC diagnostics, forensics, gene mapping, identification of mutations  
XX CC responsible for genetic disorders or other traits to assess biodiversity  
XX CC and to produce other types of data and products dependent on DNA and  
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human  
XX CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 3669 BP; 868 A; 974 C; 1037 G; 790 T; 0 other;  
Alignment Scores:  
Pred. No.: 341 Length: 3669  
Score: 49.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 84.48% Indels: 0  
DB: 23 Gaps: 0  
US-09-214-836-2 (1-9) x AAS94092 (1-3669)  
QY 2 ValTPGIYGIINTYTRPGIn 8  
Db 1696 GTGTGGGGCAATCTGSCAA 1716  
RESULT 23  
AAS94313  
ID AAS94313 standard; cDNA; 3670 BP.  
XX AC AAS94313;  
XX DT 13-FEB-2002 (first entry)  
XX DE DNA encoding novel human diagnostic protein #30117.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KM food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI: 2001-639362/73.  
XX DR P-PSDB; ABG30126.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
XX PT diagnostics, gene mapping, identification of mutations  
XX PT responsible for genetic disorders or other traits and to assess  
XX PT biodiversity -  
XX PS Claim 1; SEQ ID No 30117; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and  
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX CC and gene mapping, and in recombinant production of (II). The  
XX CC polynucleotides are also used in diagnostics as expressed sequence tags  
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques  
XX CC to restore normal activity of (II) or to treat disease states involving  
XX CC (II). (II) is useful for generating antibodies against it, detecting or  
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as  
XX CC a food supplement. (II) and its binding partners are useful in medical  
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating  
XX CC disorders involving aberrant protein expression or biological activity.  
XX CC The polypeptide and polynucleotide sequences have applications in  
XX CC diagnostics, forensics, gene mapping, identification of mutations  
XX CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 3670 BP; 870 A; 973 C; 1037 G; 790 T; 0 other;

Alignment Scores:

Pred. No.:	341	Length:	3670
Score:	49.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	84.48%	Indels:	0
DB:	23	Gaps:	0

US-09-214-836-2 (1-9) x AAS94313 (1-3670)

Qy 2 ValTTPGlyGlnTyrTPGln 8

Db 1696 GTGTGGGGCAATCTGCGCA 1716

RESULT 24

AB224215/C

ID AB224215 standard; DNA; 7094 BP.

XX AB224215;

XX 14-APR-2003 (first entry)

XX Human LCE gene related DNA (GenBank Identifier No. GI#1044344).

XX LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;

XX cancer; human; gene; ds.

XX Homo sapiens.

XX WO200299068-A2.

XX 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US17739.

XX 05-JUN-2001; 2001US-296076P.

XX 10-OCT-2001; 2001US-328605P.

XX 15-FEB-2002; 2002US-357253P.

XX 01-MAR-2002; 2002US-361196P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX Karim FD, Keyes LN, Kobalizer TI;

XX WPI; 2003-167338/16.

XX P-PSDB; ABB82959.

XX Identifying a candidate p53 pathway modulating agent for

XX diagnosing/treating cancer comprises detecting a test agent-biased

XX activity of an assay system comprising a purified long chain fatty acyl

XX elongase (LCE) polypeptide or nucleic acid -

XX Disclosure; Page 46-50; 69pp; English.

XX The invention relates to identifying a candidate p53 pathway modulating

XX agent that involves assaying a purified LCE (long chain fatty acyl

XX elongase) polypeptide or nucleic acid or its functionally active fragment

XX or derivative, with a test agent. The methods are useful for identifying

XX a candidate p53 pathway modulating agent, modulating a p53 pathway of a

XX cell, or a mammalian cell, diagnosing a disease in a patient, identifying

XX a candidate branching morphogenesis modulating agent, and modulating

XX branching morphogenesis in a mammalian cell. The diseases that can be

XX diagnosed are breast, colon, lung or ovary cancer having greater than

CC 25% expression level. The method is useful for manufacturing a medicament

CC for diagnosing or treating breast, colon, lung or ovary cancer. Sequences

CC AB224215-222 represent DNA sequences related to human LCE gene.

XX Sequence 7094 BP; 1713 A; 1902 C; 1683 G; 1791 T; 5 other;

Alignment Scores:

Pred. No.:	1.01e+03	Length:	7094
Score:	48.00	Matches:	6
Percent Similarity:	88.89%	Conservative:	2
Best Local Similarity:	82.67%	Mismatches:	1
Query Match:	82.76%	Indels:	0
DB:	25	Gaps:	0

US-09-214-836-2 (1-9) x AB224215 (1-7094)

Qy 1 LysValTTPGlyGlnTyrTPGlnVal 9

Db 5040 AAAATATGGGGAAGTATGGAGGGTC 5014

RESULT 25

AAC18543

XX AAC18543 standard; CDNA; 174 BP.

XX AAC18543;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 22618.

XX Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EPI033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

XX Dunas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX Claim 1; SEQ ID 22618; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from

XX cDNAs encoding secreted proteins. No ORF has yet been conclusively

XX identified within the present sequence. The 5' ESTs were prepared from

XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

XX sequences usually correspond mainly to the 3' untranslated region (UTR)

XX of the mRNA because they are often obtained from oligo-dT primed cDNA

XX libraries. Such ESTs are not well suited for isolating cDNA sequences

XX derived from the 5' ends of mRNAs and even in those cases where longer

XX cDNA sequences have been obtained, the full 5' UTR is rarely included.

XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be

XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used

XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX They are used to obtain upstream regulatory sequences and to design

XX expression and secretion vectors.

XX Alignment Scores:

XX Sequence 174 BP; 49 A; 31 C; 38 G; 55 T; 1 other;

Pred. NO.:	36.8	Length:	174
Score:	46.00	Matches:	5
Percent Similarity:	77.78%	Conservative:	2
Best Local Similarity:	55.56%	Mismatches:	0
Query Match:	79.31%	Indels:	0
DB:	21	Gaps:	0

US-09-214-836-2 (1-9) x AAC18543 (1-174)

Oy	1	LysValITpGIyGINTYTTpGlnVal 9
		::
Db	58	AAATATGGGAAATTACTGGAAATATT 84

Search completed: August 24, 2003, 01:40:53  
 Job time : 204.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 24, 2003, 01:25:55 ; Search time 47 Seconds  
(without alignments)  
84.520 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KVMQGYWQV 9

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Xgapop 10.0 , Xgapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 56978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09214836/runat\_14082003\_085041\_7665/app\_query.fasta\_1.398  
-DB=Issued\_Patents\_NA -QPMT=fastap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0  
-LIST=45 -DOCALLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=25  
-MODE=LOCAL -OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USRR=US09214836 @CEN 1 1 76 @runat\_14082003\_085041\_7665 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	93.1	36	4	US-08-388-852B-9
2	54	93.1	2115	4	US-08-388-852B-1
3	54	93.1	2130	3	US-09-056-105-1
4	50	86.2	2172	2	US-08-417-174-26
5	50	86.2	2172	2	US-08-231-565A-26
6	50	86.2	2172	2	US-09-007-961-26
7	50	86.2	2172	3	US-09-267-439-26
8	50	86.2	2172	4	US-09-073-138-26
9	49	84.5	224	4	US-08-388-852B-7
10	46	79.3	1664976	4	US-08-916-421B-1
11	44	75.9	42571	4	US-09-810-347-3
12	44	75.9	129908	4	US-09-585-858-1

13	43	74.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
14	42	72.4	951	4	US-09-615-192A-240	Sequence 240, App
15	42	72.4	1826	4	US-09-620-312D-485	Sequence 485, App
16	42	72.4	98844	4	US-09-791-211-10	Sequence 10, Appli
17	42	72.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
18	42	72.4	1830121	4	US-09-557-884-1	Sequence 1, Appli
19	42	72.4	1830121	4	US-09-643-990A-1	Sequence 1, Appli
20	41	70.7	2268	2	US-08-890-853-1	Sequence 1, Appli
21	41	70.7	2268	2	US-09-099-125A-1	Sequence 1, Appli
22	41	70.7	2268	2	US-09-099-124A-1	Sequence 1, Appli
23	41	70.7	2268	2	US-09-197-008-1	Sequence 1, Appli
24	41	70.7	2268	3	US-09-032-476-1	Sequence 1, Appli
25	41	70.7	2268	3	US-08-890-854-1	Sequence 1, Appli
26	41	70.7	2268	3	US-09-023-324-1	Sequence 1, Appli
27	41	70.7	2268	4	US-09-109-986-1	Sequence 1, Appli
28	41	70.7	2271	3	US-08-910-820-8	Sequence 8, Appli
29	41	70.7	2271	4	US-09-844-908-8	Sequence 8, Appli
30	41	70.7	2931	3	US-09-168-629-14	Sequence 14, Appli
31	41	70.7	3966	3	US-09-215-131-1	Sequence 1, Appli
32	41	70.7	3966	3	US-09-222-734-1	Sequence 1, Appli
33	41	70.7	4143	4	US-08-826-134-6	Sequence 6, Appli
34	41	70.7	5350	4	US-08-826-134-3	Sequence 3, Appli
35	41	70.7	10706	1	US-08-411-389-1	Sequence 1, Appli
36	40	69.0	190	1	US-08-594-031-95	Sequence 112, App
37	40	69.0	217	1	US-08-594-031-112	Sequence 112, App
38	40	69.0	223	1	US-08-594-031-116	Sequence 116, App
39	40	69.0	260	1	US-08-594-031-119	Sequence 119, App
40	40	69.0	262	1	US-08-594-031-93	Sequence 93, Appli
41	40	69.0	286	1	US-08-594-031-121	Sequence 121, App
42	40	69.0	335	1	US-08-594-031-92	Sequence 92, Appli
43	40	69.0	335	1	US-08-594-031-94	Sequence 94, Appli
44	40	69.0	335	1	US-08-594-031-96	Sequence 96, Appli
45	40	69.0	335	1	US-08-594-031-123	Sequence 123, App

## ALIGNMENTS

RESULT 1  
US-08-388-852B-9  
Sequence 9, Application US/08388852B  
Patent No. 6500919  
GENERAL INFORMATION:  
APPLICANT: Adema, Gosse Jan, Figdor, Carl Gustav.  
TITLE OF INVENTION: Melanoma associated antigenic polypeptide.  
TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Adema, Gosse Jan, Figdor, Carl Gustav  
STREET: Philips van Leydenlaan 25  
CITY: Nijmegen  
STATE: Brabant  
COUNTRY: the Netherlands  
ZIP: 6525 EX  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentcin Release #1.0, Version #1.30 (EFO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,852B  
FILING DATE: February 15, 1995  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE: Melanoma  
TISSUE TYPE: Melanocyte  
CELL TYPE: Melanocyte

```
FEATURE:
NAME/KEY: CDS
LOCATION: 1...36
FEATURE:
NAME/KEY: protein bind
LOCATION: 1...33
FEATURE:
NAME/KEY: protein bind
LOCATION: 1...36
FEATURE:
NAME/KEY: protein bind
LOCATION: 7...33
FEATURE:
NAME/KEY: protein bind
LOCATION: 10...36
US-08-388-852B-9

Alignment Scores:
Pred. No.: 0.0406 Length: 36
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-08-388-852B-9 (1-36)

Cy 1 LysValTrpGlyGlnTyrTrpGlnVal 9
Db 7 AAGACCTGGGGCCAACTGCGCAAGTT 33

RESULT 2
US-08-388-852B-1
Sequence 1, Application US/08388852B
Patent No. 6500919
GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan, Figdor, Carl Gustav.
TITLE OF INVENTION: Melanoma associated antigenic polypeptide,
TITLE OF INVENTION: Melanoma associated antigenic polypeptide,
TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Adema, Gosse Jan, Figdor, Carl Gustav
STREET: Phillips van Leydenlaan 25
CITY: Nijmegen
STATE: Brabant
COUNTRY: the Netherlands
ZIP: 6525 EX
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,852B
FILING DATE: February 15, 1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: Melanoma
CELL TYPE: Melanocyte
FEATURE:
NAME/KEY: CDS
LOCATION: 22...2005
FEATURE:
NAME/KEY: misc_signal
LOCATION: 1...81
```

```
FEATURE:
NAME/KEY: misc feature
LOCATION: 1792...1870
OTHER INFORMATION: /function = "transmembrane region"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 262...264
OTHER INFORMATION: /bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 337...339
OTHER INFORMATION: /bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 352...354
OTHER INFORMATION: /bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 982...984
OTHER INFORMATION: /bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 1723...1725
OTHER INFORMATION: /bound moiety = "carbohydrate"
US-08-388-852B-1

Alignment Scores:
Pred. No.: 3.76 Length: 2115
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-08-388-852B-1 (1-2115)

Cy 1 LysValTrpGlyGlnTyrTrpGlnVal 9
Db 481 AAGACCTGGGGCCAACTGCGCAAGTT 507

RESULT 3
US-09-056-105-1
Sequence 1, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 2130
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-1

Alignment Scores:
Pred. No.: 3.79 Length: 2130
Score: 54.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 93.10% Indels: 0
DB: 3 Gaps: 0

US-09-214-836-2 (1-9) x US-09-056-105-1 (1-2130)

Cy 1 LysValTrpGlyGlnTyrTrpGlnVal 9
```



Db 481 AAGACCTGGGGCCCAATCTGCGCAAGTT 507  
RESULT 4  
US-08-417-174-26  
Sequence 26, Application US/08417174  
Patent No. 5844075  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-08-417-174-26  
Alignment Scores:  
Pred. No.: 17.8 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 86.21% Indels: 0  
Gaps: 0  
US-09-214-836-2 (1-9) x US-08-417-174-26 (1-2172)  
Qy 1 LyeValTPGlyGlnTYTTPGln 8  
Db 498 AAGACCTGGGGCCCAATCTGCGCA 521  
RESULT 5  
US-08-231-565A-26  
Sequence 26, Application US/08231565A  
Patent No. 5874560  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS

TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,565A  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-08-231-565A-26  
Alignment Scores:  
Pred. No.: 17.8 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 86.21% Indels: 0  
Gaps: 0  
US-09-214-836-2 (1-9) x US-08-231-565A-26 (1-2172)  
Qy 1 LyeValTPGlyGlnTYTTPGln 8  
Db 498 AAGACCTGGGGCCCAATCTGCGCA 521  
RESULT 6  
US-09-007-961-26  
Sequence 26, Application US/09007961  
Patent No. 5994523  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/007,961  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-09-007-961-26

Alignment Scores:  
Pred. No.: 17.8 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 86.21% Indels: 0  
DB: 2 Gaps: 0

US-09-214-836-2 (1-9) x US-09-007-961-26 (1-2172)

Qy 1 LysValTPrGlyGlnTyrTrpGln 8  
Db 498 AAGACCTGGGGCCAACTACTGGCAA 521

RESULT 7  
US-09-267-439-26  
Sequence 26, Application US/09267439  
Patent No. 6270778  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-09-267-439-26

Alignment Scores:  
Pred. No.: 17.8 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 86.21% Indels: 0  
DB: 3 Gaps: 0

US-09-214-836-2 (1-9) x US-09-267-439-26 (1-2172)

Qy 1 LysValTPrGlyGlnTyrTrpGln 8  
Db 498 AAGACCTGGGGCCAACTACTGGCAA 521

RESULT 8  
US-09-073-138-26  
Sequence 26, Application US/09073138  
Patent No. 6537560  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,138  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-09-073-138-26

Alignment Scores:

Pred. No.:	17.8	Length:	2172
Score:	50.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	86.21%	Indels:	0
DB:	4	Gaps:	0

US-09-214-836-2 (1-9) x US-09-073-138-26 (1-2172)

Qy 1 LysValTTPGlyGlnTTPGln 8

Db 498 AAGACCTGGGCAATCTGCA 521

RESULT 9

US-08-388-852B-7  
Sequence 7, Application US/08388852B  
Patent No. 6500919

GENERAL INFORMATION:

APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.

TITLE OF INVENTION: Melanoma associated antigenic polypeptide.

TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav

STREET: Philips van Leydenlaan 25

CITY: Nijmegen

STATE: Brabant

COUNTRY: the Netherlands

ZIP: 6525 EX

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,852B

FILING DATE: February 15, 1995

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHEICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

TISSUE TYPE: Melanoma

CELL TYPE: Melanocyte

FEATURE:

NAME/KEY: CDS

LOCATION: 1...24

US-08-388-852B-7

US-09-214-836-2 (1-9) x US-08-388-852B-7 (1-24)

Alignment Scores:

Pred. No.:	0.174	Length:	24
Score:	49.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	84.48%	Indels:	0
DB:	4	Gaps:	0

US-09-214-836-2 (1-9) x US-08-388-852B-7 (1-24)

Qy 3 TTPGlyGlnTTPGlnVal 9

Db 4 TGGGGCAATCTGCAAGTT 24

RESULT 10

US-08-316-421B-1/c

Sequence 1, Application US/08916421B

Patent No. 6503729

US-09-214-836-2 (1-9) x US-08-316-421B-1/c

Sequence 1, Application US/08916421B

Patent No. 6503729

GENERAL INFORMATION:

APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus

Patent No. 6503729

TITLE OF INVENTION: jannaschii

FILE REFERENCE: PB275

CURRENT APPLICATION NUMBER: US/08/916,421B

CURRENT FILING DATE: 1997-08-22

PRIOR APPLICATION NUMBER: US 60/024,428

PRIOR FILING DATE: 1996-08-22

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 1664976

TYPE: DNA

ORGANISM: Methanococcus jannaschii

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (28222)..(28222)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (28257)..(28258)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (84773)..(84773)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (84808)..(84808)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (84812)..(84812)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (98120)..(98120)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (98159)..(98159)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (98239)..(98239)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (98266)..(98266)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (103998)..(103998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (148948)..(148948)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (163385)..(163385)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (191989)..(191989)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (234187)..(234187)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (234220)..(234220)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc\_feature

LOCATION: (234814)..(234814)

OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (309398)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (309418)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (312837)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (312993)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (319226)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (559167)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (559241)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (600992)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (622708)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (657081)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (657203)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (674435)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (682442)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (713652)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (741684)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (779455)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (779676)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (855339)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (871619)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1084830)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1096846)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1119881)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1130881)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1310988)..  
OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature  
LOCATION: (1313224)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1349473)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1349491)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1470091)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1569020)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1602912)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1603734)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1637998)..  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1664854)..  
OTHER INFORMATION: n equals a, t, c, or g

US-08-916-421B-1

Alignment Scores:  
Pred. No.: 1.24e+05 Length: 1664976  
Score: 46.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 79.31% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-08-916-421B-1 (1-1664976)

Qy 1 LysValTrpGlyGlnTrpGln 8

Db 1092170 AAGGTTGGGAGAGCTATTGGAG 1092147

RESULT 11

US-09-810-347-3  
Sequence 3, Application US/09810347  
Patent No. 6461847

GENERAL INFORMATION:  
APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: C1001169

CURRENT APPLICATION NUMBER: US/09/810.347

CURRENT FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 42571

TYPE: DNA

ORGANISM: Human

US-09-810-347-3

Alignment Scores:  
Pred. No.: 4.77e+03 Length: 42571  
Score: 44.00 Matches: 6  
Percent Similarity: 87.50% Conservative: 1  
Best Local Similarity: 75.00% Mismatches: 1  
Query Match: 75.86% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-09-810-347-3 (1-42571)

```

Oy      1 LysValTTPGlyGlnTyrTyrPipIn 8
Db      39699 AAGATTGGGGGCAATCGTGCAC 39722

RESULT 12
US-09-585-858-1/c
; Sequence 1, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigrundur Hjorleifsdottir
; APPLICANT: Gudmundur O. Hrengvasson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevartsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 129908
; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-09-585-858-1

Alignment Scores:
Pred. No.:      1.64e+04      Length:      129908
Score:          44.00         Matches:      6
Percent Similarity: 85.71%    Conservative: 0
Best Local Similarity: 85.71% Mismatches:      1
Query Match:    75.86%       Indels:          0
DB:             4            Gaps:            0

US-09-214-836-2 (1-9) x US-09-585-858-1 (1-129908)

Oy      1 LysValTTPGlyGlnTyrTyrPipIn 7
Db      113704 AAGGTGGGGAGATTACTGG 113684

RESULT 13
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Built et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g

```

```

; NAME/KEY: misc_feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature

```

```

LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1345473)..(1345473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)

```

```

OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
Alignment Scores:
Pred. No.: 3.45e+05
Score: 43.00
Percent Similarity: 77.78%
Best Local Similarity: 55.56%
Query Match: 74.14%
DB: 4
Gaps: 0

US-09-214-836-2 (1-9) x US-08-916-421B-1 (1-1664976)
Oy 1 LyseValTrpGlyGlnTyrTrpGlnVal 9
Db 1205138 AAAATTGGGGAAGCTTTTGGAAATGTC 1205164

RESULT 14
US-09-615-192A-240
Sequence 240, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615.192A
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 240
LENGTH: 951
TYPE: DNA
ORGANISM: Pinus radiata
US-09-615-192A-240

Alignment Scores:
Pred. No.: 149
Score: 42.00
Percent Similarity: 88.89%
Best Local Similarity: 55.56%
Query Match: 72.41%
DB: 4
Gaps: 0

US-09-214-836-2 (1-9) x US-09-615-192A-240 (1-951)
Oy 1 LyseValTrpGlyGlnTyrTrpGlnVal 9
Db 778 CGTTACTGGGAGCAGCATATGCGCGTA 804

RESULT 15
US-09-620-312D-485/C
Sequence 485, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Aseundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui

```

APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yunging  
APPLICANT: Wang, Dunxui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Dumanac, Radoje T.  
TITLE OF INVENTION: No. 656962e1 Nucleic Acids and  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pf\_fl\_genes Version 1.0  
SEQ ID NO 485  
LENGTH: 1826  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (755)..(1726)  
US-09-620-312D-485

Alignment Scores:  
Pred. No.: 308 Length: 1826  
Score: 42.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 50.00% Mismatches: 0  
Query Match: 72.41% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-09-620-312D-485 (1-1826)

Qy 1 LysValTrpGlyGlnTyrTrpGln 8  
Db 80 AGGATTGGGCGTATTCGATTCGAG 57

RESULT 16  
US-09-791-211-10/C  
Sequence 10, Application US/09791211  
Patent No. 6448080  
GENERAL INFORMATION:  
APPLICANT: Donna T. Ward  
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION  
FILE REFERENCE: RTS-0205  
CURRENT APPLICATION NUMBER: US/09/791,211  
CURRENT FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 90  
SEQ ID NO 10  
LENGTH: 98844  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 24962  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 64383  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 65468  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 65469  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 65470  
OTHER INFORMATION: unknown  
NAME/KEY: unsure

LOCATION: 65471  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 87130  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 89049  
OTHER INFORMATION: unknown  
OTHER INFORMATION:  
US-09-791-211-10

Alignment Scores:  
Pred. No.: 2,58e+04 Length: 98844  
Score: 42.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 3  
Best Local Similarity: 66.67% Mismatches: 0  
Query Match: 72.41% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-09-791-211-10 (1-98844)

Qy 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 12368 AAGGTTGGGAGATTTCATTCAGTA 12342

RESULT 17  
US-08-545-528D-1/C  
Sequence 1, Application US/08545528D  
Patent No. 6537773  
GENERAL INFORMATION:  
APPLICANT: Frazer et al.  
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitium Genome, Fragment:  
FILE REFERENCE: PB193P1  
CURRENT APPLICATION NUMBER: US/08/545,528D  
PRIOR FILING DATE: 1995-10-19  
PRIOR APPLICATION NUMBER: US 08/488,018  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/473,545  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 580073  
TYPE: DNA  
ORGANISM: Mycoplasma genitalium  
US-08-545-528D-1

Alignment Scores:  
Pred. No.: 1,72e+05 Length: 580073  
Score: 42.00 Matches: 5  
Percent Similarity: 85.71% Conservative: 1  
Best Local Similarity: 71.43% Mismatches: 1  
Query Match: 72.41% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-08-545-528D-1 (1-580073)

Qy 1 LysValTrpGlyGlnTyrTrp 7  
Db 162611 AAATATGGGTCATCTACTCG 162591

RESULT 18  
US-09-557-884-1/C  
Sequence 1, Application US/09557884  
Patent No. 6506581  
GENERAL INFORMATION:  
APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557,884  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB186P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1

Alignment Scores:  
Pred. No.: 5.05e+05 Length: 1830121  
Score: 42.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 71.43% Mismatches: 0  
Query Match: 72.41% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-09-557-884-1 (1-1830121)

QY 1 LysValITpGlyGIntYtTp 7  
:::|||||:::|||||

Db 710242 CGAGTTGGGGAATAATTGG 710222

RESULT 19  
US-09-643-990A-1/c  
Sequence 1, Application US/09643990A  
Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1

Alignment Scores:  
Pred. No.: 5.05e+05 Length: 1830121  
Score: 42.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 71.43% Mismatches: 0  
Query Match: 72.41% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-2 (1-9) x US-09-643-990A-1 (1-1830121)

QY 1 LysValITpGlyGIntYtTp 7  
:::|||||:::|||||

Db 710242 CGAGTTGGGGAATAATTGG 710222

RESULT 20  
US-08-890-853-1  
Sequence 1, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Woronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342



INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2268 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-890-853-1

## Alignment Scores:

Pred. No.:	574	Length:	2268
Score:	41.00	Matches:	6
Percent Similarity:	85.71%	Conservative:	0
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	70.69%	Indels:	0
DB:	2	Gaps:	0

US-09-214-836-2 (1-9) x US-08-890-853-1 (1-2268)

Qy 1 LysValTrpGlyGlnTyrTrp 7  
Db 1282 AAGGTGGGGCCAGGTCTGG 1302

## RESULT 21

US-09-099-125A-1  
Sequence 1, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2268 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-099-125A-1

## Alignment Scores:

Pred. No.:	574	Length:	2268
Score:	41.00	Matches:	6
Percent Similarity:	85.71%	Conservative:	0
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	70.69%	Indels:	0

DB: 2 Gaps: 0

US-09-214-836-2 (1-9) x US-09-099-125A-1 (1-2268)

Qy 1 LysValTrpGlyGlnTyrTrp 7  
Db 1282 AAGGTGGGGCCAGGTCTGG 1302

## RESULT 22

US-09-099-124A-1  
Sequence 1, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2268 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-099-124A-1

## Alignment Scores:

Pred. No.:	574	Length:	2268
Score:	41.00	Matches:	6
Percent Similarity:	85.71%	Conservative:	0
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	70.69%	Indels:	0
DB:	2	Gaps:	0

US-09-214-836-2 (1-9) x US-09-099-124A-1 (1-2268)

Qy 1 LysValTrpGlyGlnTyrTrp 7  
Db 1282 AAGGTGGGGCCAGGTCTGG 1302

## RESULT 23

US-09-197-008-1  
Sequence 1, Application US/09197008  
Patent No. 5977341  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Bret M. Cowser

TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION  
FILE REFERENCE: RTS-0019  
CURRENT APPLICATION NUMBER: US/09/197,008  
CURRENT FILING DATE: 1998-11-20  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO: 1  
LENGTH: 2268  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2268)  
US-09-197-008-1

Alignment Scores:  
Pred. No.: 574 Length: 2268  
Score: 41.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 2 Gaps: 0

US-09-214-836-2 (1-9) x US-09-197-008-1 (1-2268)

Qy 1 LysValTrpGlyGlnTyrTrp 7  
Db 1282 AAGGTGTGGGGCCAGCTGTGG 1302

RESULT 24  
US-09-032-476-1  
Sequence 1, Application US/09032476  
Patent No. 6235492  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2268 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-032-476-1

Alignment Scores:  
Pred. No.: 574 Length: 2268  
Score: 41.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 3 Gaps: 0

US-09-214-836-2 (1-9) x US-09-032-476-1 (1-2268)

Qy 1 LysValTrpGlyGlnTyrTrp 7  
Db 1282 AAGGTGTGGGGCCAGCTGTGG 1302

RESULT 25  
US-08-890-854-1  
Sequence 1, Application US/08890854  
Patent No. 6235512  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2268 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-890-854-1

Alignment Scores:  
Pred. No.: 574 Length: 2268  
Score: 41.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 3 Gaps: 0

US-09-214-836-2 (1-9) x US-08-890-854-1 (1-2268)

Qy 1 LysValTrpGlyGlnTyrTrp 7  
Db 1282 AAGGTGTGGGGCCAGCTGTGG 1302

Search completed: August 24, 2003, 04:11:04  
Job time : 765 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 24, 2003, 02:54:20 ; Search time 150.5 Seconds

(without alignments)  
134.442 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KVMGQYQV 9

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1517243 segs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09214836/runat\_14082003\_085045\_7758/app\_query.fasta\_1.398  
-DB=Published Applications NA -OFMT=fastap -SUFFIX=trmpb -MINMATCH=0.1  
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62  
-TRANS=numan40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MTLEN=0  
-MAXLEN=2000000000 -USER=US09214836 @CGN 1 1 290 @runat\_14082003\_085045\_7758  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSELOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PTCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PTCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09 NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10 NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	54	93.1	2130 9 US-09-862-260A-1	Sequence 1, Appl1

2	54	93.1	2130 10 US-09-812-238B-1	Sequence 1, Appl1
3	54	93.1	2130 14 US-10-207-655-76	Sequence 76, Appl1
4	54	93.1	2131 13 US-10-047-539-3	Sequence 3, Appl1
5	54	93.1	23770 14 US-10-035-637-8	Sequence 8, Appl1
6	50	86.2	1881 13 US-10-047-539-1	Sequence 1, Appl1
7	50	86.2	2172 12 US-09-898-860-26	Sequence 26, Appl1
8	46	79.3	719 13 US-10-027-632-26627	Sequence 26627, A
9	45	77.6	215 10 US-09-960-352-10302	Sequence 10302, A
10	45	77.6	812 13 US-10-027-632-7570	Sequence 7570, Ap
11	45	77.6	2000 10 US-09-938-842K-3977	Sequence 3977, Ap
12	45	77.6	3406 13 US-10-027-632-115796	Sequence 115796, A
13	45	77.6	3406 13 US-10-027-632-115797	Sequence 115797, A
14	45	77.6	2140405 13 US-10-027-632-76212	Sequence 76212, A
15	44	75.9	591 9 US-09-864-761-7654	Sequence 7654, Ap
16	44	75.9	1786 10 US-09-822-830A-106	Sequence 106, App
17	44	75.9	15044 9 US-09-764-869-1790	Sequence 1790, Ap
18	44	75.9	15044 9 US-10-091-504-1790	Sequence 1790, Ap
19	44	75.9	15046 9 US-09-764-869-1791	Sequence 1791, Ap
20	44	75.9	15046 14 US-10-091-504-1791	Sequence 1791, Ap
21	44	75.9	42571 14 US-10-224-413-3	Sequence 3, Appl1
22	44	75.9	129908 14 US-10-270-875-1	Sequence 1, Appl1
23	44	75.9	129908 14 US-10-270-878-1	Sequence 1, Appl1
24	44	75.9	129908 14 US-10-270-786-1	Sequence 1, Appl1
25	44	75.9	129908 14 US-10-270-710-1	Sequence 1, Appl1
26	44	75.9	129908 14 US-10-270-859-1	Sequence 1, Appl1
27	44	75.9	129908 15 US-10-270-846-1	Sequence 1, Appl1
28	44	75.9	260209 12 US-10-025-966A-23	Sequence 23, Appl1
29	44	75.9	260209 12 US-10-265-071-23	Sequence 23, Appl1
30	44	75.9	1223197 13 US-10-027-632-179264	Sequence 179264, A
31	43	74.1	417 11 US-09-918-995-8569	Sequence 8569, Ap
32	43	74.1	814 13 US-10-027-632-170393	Sequence 170393, A
33	42	72.4	404 11 US-09-918-995-6693	Sequence 6693, Ap
34	42	72.4	526 9 US-10-027-632-255189	Sequence 255189, A
35	42	72.4	535 13 US-10-027-632-254454	Sequence 254454, A
36	42	72.4	598 13 US-10-027-632-254455	Sequence 254455, A
37	42	72.4	598 13 US-10-027-632-254456	Sequence 254456, A
38	42	72.4	648 13 US-10-027-632-184958	Sequence 184958, A
39	42	72.4	714 13 US-10-027-632-110313	Sequence 110313, A
40	42	72.4	837 13 US-10-027-632-131880	Sequence 131880, A
41	42	72.4	837 13 US-10-027-632-131881	Sequence 131881, A
42	42	72.4	886 14 US-10-198-846-6249	Sequence 6249, Ap
43	42	72.4	921 9 US-09-925-299-33	Sequence 33, Appl1
44	42	72.4	921 11 US-09-925-299-33	Sequence 33, Appl1
45	42	72.4	921 11 US-09-925-299-33	Sequence 33, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-862-260A-1  
Sequence 1, Application US/09862260A  
Patent No. US20020082217A1  
GENERAL INFORMATION:  
APPLICANT: Niccollette, Charles A.  
TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
FILE REFERENCE: 126881210200  
CURRENT APPLICATION NUMBER: US/09/862,260A  
CURRENT FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/208,955  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/267,877  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2130  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-862-260A-1

Alignment Scores: 12.5 Length: 2130  
Pred. No.: 54.00 Matches: 8

Percent Similarity: 88.89%  
Best Local Similarity: 88.89%  
Query Match: 93.10%  
DB: 9  
Conservative: 0  
Matches: 1  
Indels: 0  
Gaps: 0

US-09-214-836-2 (1-9) x US-09-862-260A-1 (1-2130)

Qy 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 481 AAGACCTGGGGCCATACCTGCAAGTT 507

RESULT 2  
US-09-812-238B-1  
; Sequence 1, Application US/09812238B  
; Patent No. US20020169132A1  
; GENERAL INFORMATION:

; APPLICANT: Nicolette, Charles  
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
; FILE REFERENCE: GZ 2094.00  
; CURRENT APPLICATION NUMBER: US/09/812,238B  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2130  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (22)...(2004)  
US-09-812-238B-1

Alignment Scores:

Pred. No.: 12.5  
Score: 54.00  
Percent Similarity: 88.89%  
Best Local Similarity: 88.89%  
Query Match: 93.10%  
Length: 2130  
Matches: 8  
Conservative: 0  
Mismatch: 1  
Indels: 0  
Gaps: 0

US-09-214-836-2 (1-9) x US-09-812-238B-1 (1-2130)

Qy 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 481 AAGACCTGGGGCCATACCTGCAAGTT 507

RESULT 3

US-10-207-655-76  
; Sequence 76, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 76  
; LENGTH: 2130  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-207-655-76

Alignment Scores:

Pred. No.: 12.5  
Score: 54.00  
Percent Similarity: 88.89%  
Best Local Similarity: 88.89%  
Query Match: 93.10%  
Length: 2130  
Matches: 8  
Conservative: 0  
Mismatch: 1  
Indels: 0  
Gaps: 0

US-09-214-836-2 (1-9) x US-10-207-655-76 (1-2130)

Qy 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 481 AAGACCTGGGGCCATACCTGCAAGTT 507

RESULT 4  
US-10-047-539-3  
; Sequence 3, Application US/10047539  
; Publication No. US20020177547A1  
; GENERAL INFORMATION:

; APPLICANT: MOLLING, KARIN  
; APPLICANT: PAVLOVIC, JOVAN  
; APPLICANT: NAMRATH, MICHAEL  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING  
; FILE REFERENCE: VOS-27  
; CURRENT APPLICATION NUMBER: US/10/047,539  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
; PRIOR FILING DATE: 2001-01-16  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2131  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (12)..(2018)  
US-10-047-539-3

Alignment Scores:

Pred. No.: 12.5  
Score: 54.00  
Percent Similarity: 88.89%  
Best Local Similarity: 88.89%  
Query Match: 93.10%  
Length: 2131  
Matches: 8  
Conservative: 0  
Mismatch: 1  
Indels: 0  
Gaps: 0

US-09-214-836-2 (1-9) x US-10-047-539-3 (1-2131)

Qy 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 471 AAGACCTGGGGCCATACCTGCAAGTT 497

RESULT 5

US-10-035-637-8/c  
; Sequence 8, Application US/10035637  
; Publication No. US20030031667A1  
; GENERAL INFORMATION:  
; APPLICANT: Keiler, Tibor  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC  
; FILE REFERENCE: MKI-166CP  
; CURRENT APPLICATION NUMBER: US/10/035,637  
; CURRENT FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 09/851,614  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: USSN 60/203,126  
; PRIOR FILING DATE: 2000-05-08  
; PRIOR APPLICATION NUMBER: USSN 60/230,739  
; PRIOR FILING DATE: 2000-09-07  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 23770  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (16489)...(17094)

US-10-035-637-8

Alignment Scores:

Pred. No.:	143	Length:	23770
Score:	54.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	93.10%	Indels:	0
DB:	14	Gaps:	0

US-09-214-836-2 (1-9) x US-10-035-637-8 (1-23770)

Qy 1 LysValTrpGlyGlnTyrTrpGlnVal 9

Db 10671 AAGACCTGGGGCCCAATCTGCGCAAGTT 10645

RESULT 6

US-10-047-539-1

Sequence 1, Application US/10047539

Publication No. US20020177547A1

GENERAL INFORMATION:

APPLICANT: MOLLING, KARIN

APPLICANT: PAVLOVIC, JOVAN

APPLICANT: NAMRATH, MICHAEL

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING

FILE REFERENCE: VOS-27

CURRENT APPLICATION NUMBER: US/10/047,539

CURRENT FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: EP 01 10 0914.9

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1881

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1881)

US-10-047-539-1

Alignment Scores:

Pred. No.:	47.7	Length:	1881
Score:	50.00	Matches:	7
Percent Similarity:	88.89%	Conservative:	1
Best Local Similarity:	77.78%	Mismatches:	1
Query Match:	86.21%	Indels:	0
DB:	13	Gaps:	0

US-09-214-836-2 (1-9) x US-10-047-539-1 (1-1881)

Qy 1 LysValTrpGlyGlnTyrTrpGlnVal 9

Db 460 AAGACCTGGGGGAAATCTGCGCAAGTT 486

RESULT 7

US-09-898-860-26

Sequence 26, Application US/09898860

Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 2172

TYPE: nucleotide

STRANDEDNESS: Double

TOPOLOGY: Unknown

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-898-860-26

Alignment Scores:

Pred. No.:	55.2	Length:	2172
Score:	50.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	86.21%	Mismatches:	1
Query Match:	86.21%	Indels:	0
DB:	12	Gaps:	0

US-09-214-836-2 (1-9) x US-09-898-860-26 (1-2172)

Qy 1 LysValTrpGlyGlnTyrTrpGln 8

Db 498 AAGACCTGGGGCCCAATCTGCGCA 521

RESULT 8

US-10-027-632-26627

Sequence 26627, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/199,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26627
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-26627

Alignment Scores:
Pred. No.: 78.3 Length: 719
Score: 46.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 79.31% Indels: 0
DB: 13 Gaps: 0

US-09-214-836-2 (1-9) x US-10-027-632-26627 (1-719)

Cy 1 LysValTPGlyGlnTTPGln 8
|||:|||||:|||||
Db 138 AAGGTGGGGTGGAGCAGCGAG 161

RESULT 9
US-09-960-352-10302
; Sequence 10302, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10302
; LENGTH: 215
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 44-LIB34-021-Q1-E1-C8
US-09-960-352-10302

Alignment Scores:
Pred. No.: 33.4 Length: 215
Score: 45.00 Matches: 7
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 77.59% Indels: 0
DB: 10 Gaps: 0

US-09-214-836-2 (1-9) x US-09-960-352-10302 (1-215)

Cy 1 LysValTPGlyGlnTTPGlnVal 9
|||:|||||:|||||
Db 166 AAGCAATGGGACATACCTGCTGCTC 192

RESULT 10
US-10-027-632-7570/c
; Sequence 7570, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7570
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-7570

Alignment Scores:
Pred. No.: 128 Length: 812
Score: 45.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.59% Indels: 0
DB: 13 Gaps: 0

US-09-214-836-2 (1-9) x US-10-027-632-7570 (1-812)

Cy 1 LysValTPGlyGlnTTPGln 7
|||:|||||:|||||
Db 466 AAGGTGGGGAAATATCTGG 446

RESULT 11
US-09-938-842A-3977/c
; Sequence 3977, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3977
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3977

Alignment Scores:
Pred. No.: 317 Length: 2000
Score: 45.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 77.59% Indels: 0
DB: 10 Gaps: 0

US-09-214-836-2 (1-9) x US-09-938-842A-3977 (1-2000)

Cy 1 LysValTPGlyGlnTTPGln 8
|||:|||||:|||||
Db 1066 AAATGTGGGACCCCTATGGCAA 1043

RESULT 12
US-10-027-632-115796
```



```
; Sequence 115796, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115796
; LENGTH: 3406
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-115796

Alignment Scores:
Pred. No.: 543 Length: 3406
Score: 45.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 77.59% Indels: 0
Gaps: 0
DB: 13

US-09-214-836-2 (1-9) x US-10-027-632-115796 (1-3406)
QY 1 LysValTrpGlyGlnTyrTrpGln 8
Db 3224 AAGATTGGGGGACATTTGGGAA 3247

RESULT 13
US-10-027-632-115797
; Sequence 115797, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115797
; LENGTH: 3406
; TYPE: DNA
```

```
; ORGANISM: Human
US-10-027-632-115797

Alignment Scores:
Pred. No.: 543 Length: 3406
Score: 45.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 77.59% Indels: 0
Gaps: 0
DB: 13

US-09-214-836-2 (1-9) x US-10-027-632-115797 (1-3406)
QY 1 LysValTrpGlyGlnTyrTrpGln 8
Db 3224 AAGATTGGGGGACATTTGGGAA 3247

RESULT 14
US-10-027-632-76212/c
; Sequence 76212, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76212
; LENGTH: 2140405
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(2140405)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-76212

Alignment Scores:
Pred. No.: 3,41e+05 Length: 2140405
Score: 45.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.59% Indels: 0
Gaps: 0
DB: 13

US-09-214-836-2 (1-9) x US-10-027-632-76212 (1-2140405)
QY 3 TrpGlyGlnTyrTrpGlnVal 9
Db 273786 TGGGGAAGATTTGGCAAGTG 273766

RESULT 15
US-09-864-761-7654/c
; Sequence 7654, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
```

QY 1 LysValTyrGlnTyrTyrGln 8  
|||:::||||| |||||

Pred. No.:	3.5e+03	Length:	1504
Score:	44.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	75.86%	Indels:	0
DB:	9	Gaps:	0

US-09-214-836-2 (1-9) X US-09-764-869-1790 (1-15044)

OY 2 ValTTPGlyGlnTYTTP 7  
Db 11435 GTCTGGGTCAGTATTGG 11452

## RESULT 18

US-10-091-504-1790  
; Sequence 1790, Application US/10091504  
; Publication No. US20030059908A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007C1  
; CURRENT APPLICATION NUMBER: US/10/091,504  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 2442  
; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1790  
; LENGTH: 15044  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-091-504-1790

## Alignment Scores:

Pred. No.:	3.51e+03	Length:	15044
Score:	44.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	75.86%	Indels:	0
DB:	14	Gaps:	0

US-09-214-836-2 (1-9) x US-10-091-504-1790 (1-15044)

OY 2 ValTTPGlyGlnTYTTP 7  
Db 11435 GTCTGGGTCAGTATTGG 11452

## RESULT 19

US-09-764-869-1791  
; Sequence 1791, Application US/09764869  
; Patent No. US20020061521A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007  
; CURRENT APPLICATION NUMBER: US/09/764,869  
; CURRENT FILING DATE: 2001-01-17  
; Prior Application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 2442  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1791  
; LENGTH: 15046  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (9942)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-869-1791

## Alignment Scores:

Pred. No.:	3.51e+03	Length:	15046
Score:	44.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	75.86%	Indels:	0
DB:	9	Gaps:	0

US-09-214-836-2 (1-9) x US-09-764-869-1791 (1-15046)

OY 2 ValTTPGlyGlnTYTTP 7  
Db 11436 GTCTGGGTCAGTATTGG 11453

## RESULT 20

US-10-091-504-1791  
; Sequence 1791, Application US/10091504  
; Publication No. US20030059908A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007C1  
; CURRENT APPLICATION NUMBER: US/10/091,504  
; CURRENT FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 2442  
; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1791  
; LENGTH: 15046  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9942)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-091-504-1791

## Alignment Scores:

Pred. No.:	3.51e+03	Length:	15046
Score:	44.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	75.86%	Indels:	0
DB:	14	Gaps:	0

US-09-214-836-2 (1-9) x US-10-091-504-1791 (1-15046)

OY 2 ValTTPGlyGlnTYTTP 7  
Db 11436 GTCTGGGTCAGTATTGG 11453

## RESULT 21

US-10-224-413-3  
; Sequence 3, Application US/10224413  
; Publication No. US2003003167A1  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; FILE REFERENCE: CL001169  
; CURRENT APPLICATION NUMBER: US/10/224,413  
; CURRENT FILING DATE: 2002-08-21  
; Prior Application Number: 09/810,347  
; Prior Filing Date: 2001-03-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 42571  
; TYPE: DNA  
; ORGANISM: Human  
US-10-224-413-3

## Alignment Scores:

Pred. No.:	1e+04	Length:	42571
Score:	44.00	Matches:	6
Percent Similarity:	87.50%	Conservative:	1
Best Local Similarity:	75.00%	Mismatches:	1
Query Match:	75.86%	Indels:	0
DB:	14	Gaps:	0

US-09-214-836-2 (1-9) x US-10-224-413-3 (1-42571)

OY 1 LyseValTTPGlyGlnTYTTPGln 8  
Db 39699 AAGATTGGGGGCAATGTCGCAA 39722

RESULT 22  
US-10-270-875-1/c  
; Sequence 1, Application US/10270875  
; Publication No. US20030082741A1  
; GENERAL INFORMATION:  
; APPLICANT: Sigridur Hjorleifsdottir  
; APPLICANT: Gudmundur O. Hregvildsson  
; APPLICANT: Olafur H. Fridjonsson  
; APPLICANT: Arnthor Avararson  
; APPLICANT: Jakob K. Kristjansson  
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic  
; FILE REFERENCE: 2739.1001-001  
; CURRENT APPLICATION NUMBER: US/10/270,875  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: US/09/585,858  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/137,120  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 129908  
; TYPE: DNA  
; ORGANISM: Bacteriophage RM378  
US-10-270-875-1

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 129908  
Score: 44.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 75.86% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x US-10-270-875-1 (1-129908)

OY 1 LysValTPgLyGlnTYrTp 7  
Db 113704 AAGGTGGGAGATTACTGG 113684

RESULT 23  
US-10-270-878-1/c  
; Sequence 1, Application US/10270878  
; Publication No. US20030082790A1  
; GENERAL INFORMATION:  
; APPLICANT: Sigridur Hjorleifsdottir  
; APPLICANT: Gudmundur O. Hregvildsson  
; APPLICANT: Olafur H. Fridjonsson  
; APPLICANT: Arnthor Avararson  
; APPLICANT: Jakob K. Kristjansson  
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic  
; FILE REFERENCE: 2739.1001-001  
; CURRENT APPLICATION NUMBER: US/10/270,878  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: US/09/585,858  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 129908  
; TYPE: DNA  
; ORGANISM: Bacteriophage RM378  
US-10-270-878-1

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 129908  
Score: 44.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 75.86% Indels: 0

DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x US-10-270-878-1 (1-129908)

OY 1 LysValTPgLyGlnTYrTp 7  
Db 113704 AAGGTGGGAGATTACTGG 113684

RESULT 24  
US-10-270-786-1/c  
; Sequence 1, Application US/10270786  
; Publication No. US20030087392A1  
; GENERAL INFORMATION:  
; APPLICANT: Sigridur Hjorleifsdottir  
; APPLICANT: Gudmundur O. Hregvildsson  
; APPLICANT: Olafur H. Fridjonsson  
; APPLICANT: Arnthor Avararson  
; APPLICANT: Jakob K. Kristjansson  
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic  
; FILE REFERENCE: 2739.1001-001  
; CURRENT APPLICATION NUMBER: US/10/270,786  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: US/09/585,858  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/137,120  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 129908  
; TYPE: DNA  
; ORGANISM: Bacteriophage RM378  
US-10-270-786-1

Alignment Scores:  
Pred. No.: 3.07e+04 Length: 129908  
Score: 44.00 Matches: 6  
Percent Similarity: 85.71% Conservative: 0  
Best Local Similarity: 85.71% Mismatches: 1  
Query Match: 75.86% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x US-10-270-786-1 (1-129908)

OY 1 LysValTPgLyGlnTYrTp 7  
Db 113704 AAGGTGGGAGATTACTGG 113684

RESULT 25  
US-10-270-710-1/c  
; Sequence 1, Application US/10270710  
; Publication No. US20030092128A1  
; GENERAL INFORMATION:  
; APPLICANT: Sigridur Hjorleifsdottir  
; APPLICANT: Gudmundur O. Hregvildsson  
; APPLICANT: Olafur H. Fridjonsson  
; APPLICANT: Arnthor Avararson  
; APPLICANT: Jakob K. Kristjansson  
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic  
; FILE REFERENCE: 2739.1001-001  
; CURRENT APPLICATION NUMBER: US/10/270,710  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: US/09/585,858  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/137,120  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 129908  
; TYPE: DNA

ORGANISM: Bacteriophage RM378  
US-10-270-710-1

Alignment Scores:

Pred. No.:	3.07e+04	Length:	129908
Score:	44.00	Matches:	6
Percent Similarity:	85.71%	Conservative:	0
Best Local Similarity:	85.71%	Mismatches:	1
Query Match:	75.86%	Indels:	0
DB:	14	Gaps:	0

US-09-214-836-2 (1-9) x US-10-270-710-1 (1-129908)

QY 1 LysValTrpGlyGlnTyrTrp 7  
DB 113704 AAGGTGGGGAGATTAAGTGG 113684

Search completed: August 24, 2003, 05:43:33  
Job time : 580.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 24, 2003, 01:08:28 ; Search time 1896.5 Seconds  
(without alignments)  
115.339 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KVMQYQV 9

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Zgapop 6.0, Zgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgm2\_1/USPFO\_spool/US09214836/runat\_14082003\_085040\_7605/app\_query.fasta.1.398  
-DB=EST -QMT=fastap -SUFF1=trst -MINMATCH=0.1 -LOOCL=0 -LOOEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pc -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09214836 @CGN 1.1 3596 @runat\_14082003\_085040\_7605 -NCPU=6 -ICPU=3  
-NO MAP -LARGOUIRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_esthu:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	54	93.1	304	13	B0678421	B0678421 AGENCOURT
2	54	93.1	384	12	BM708487	BM708487 UI-E-C11-
3	54	93.1	436	14	CB792319	CB792319 AMGNNUC:N
4	54	93.1	503	10	BE387921	BE387921 601282169
5	54	93.1	506	10	BE389161	BE389161 601285960
6	54	93.1	506	12	BM707920	BM707920 UI-E-C11-
7	54	93.1	515	10	BE407844	BE407844 601300882
8	54	93.1	523	10	BE276871	BE276871 601178433
9	54	93.1	531	10	BE280517	BE280517 601155392
10	54	93.1	546	10	BE408811	BE408811 601303333
11	54	93.1	577	14	CA397722	CA397722 CS94912.Y
12	54	93.1	585	10	BE281030	BE281030 601136355
13	54	93.1	587	14	CA392552	CA392552 CS26407.Y
14	54	93.1	587	14	CA396509	CA396509 CS78910.Y
15	54	93.1	594	12	BG762070	BG762070 602718443
16	54	93.1	595	10	BE743315	BE743315 601573227
17	54	93.1	603	12	BG767860	BG767860 602741357
18	54	93.1	603	12	BE384038	BE384038 601272829
19	54	93.1	604	12	BG761374	BG761374 602718257
20	54	93.1	605	14	CA397065	CA397065 CS85110.Y
21	54	93.1	606	12	BM722309	BM722309 UI-E-B00-
22	54	93.1	611	14	CA397499	CA397499 CS91007.Y
23	54	93.1	616	10	BE389689	BE389689 601281927
24	54	93.1	619	14	CA396195	CA396195 CS75802.Y
25	54	93.1	622	10	BE384085	BE384085 601272888
26	54	93.1	632	10	BE895835	BE895835 601432764
27	54	93.1	628	10	BE276204	BE276204 601144476
28	54	93.1	630	12	BG769568	BG769568 602744465
29	54	93.1	640	12	BG766391	BG766391 602739133
30	54	93.1	640	14	CA379865	CA379865 659059 NC
31	54	93.1	649	10	BG477442	BG477442 602523678
32	54	93.1	650	9	AL134961	AL134961 DKFZP762E
33	54	93.1	655	10	BE388095	BE388095 601284411
34	54	93.1	657	12	BG768036	BG768036 602743812
35	54	93.1	660	10	BF978563	BF978563 602149002
36	54	93.1	666	12	BG760391	BG760391 602716813
37	54	93.1	667	12	BG764284	BG764284 602736160
38	54	93.1	671	14	CA389877	CA389877 CS103906-
39	54	93.1	673	12	BG766458	BG766458 602739218
40	54	93.1	678	12	BG761457	BG761457 602718663
41	54	93.1	680	10	BE277419	BE277419 601179283
42	54	93.1	684	10	BF689653	BF689653 602187053
43	54	93.1	684	12	BG770571	BG770571 602734295
44	54	93.1	690	10	BE408713	BE408713 601304079
45	54	93.1	698	12	BG766715	BG766715 602740007

#### ALIGNMENTS

RESULT 1  
LOCUS B0678421  
DEFINITION B0678421 304 bp mRNA, linear, EST 15-JUN-2002  
ACCESSION AGENCOURT\_8281395 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6258718  
VERSION B0678421  
KEYWORDS B0678421.1 GI:21791100  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 304)

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCTD/DRP

**FEATURES** CNA Library Preparation: Rubin Laboratory  
 CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: L1CM2415 row: a column: 23  
 High quality sequence stop: 303.  
 Location/Qualifiers

**BASE COUNT** 59 a 89 c 86 g 70 t  
**ORIGIN**

1..304  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6258718"  
 /tissue\_type="melanotic melanoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 112"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

**Alignment Scores:**  
 Pred. No.: 32.1 Length: 304  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 13 Gaps: 0

US-09-214-836-2 (1-9) x BQ678421 (1-304)

**Cy** 1 LysValTPGjYgInTYTTPGlnVal 9  
**Db** 13 AAGACCTGGGGCCAACTGCGCAGTT 39

**RESULT 2** BM708487 384 bp mRNA linear EST 28-FEB-2002  
**LOCUS** UI-E-C11-afu-b-14-0-UI-r1 UI-E-C11 Homo sapiens cDNA clone  
**DEFINITION** UI-E-C11-afu-b-14-0-UI 5', mRNA sequence.

**ACCESSION** BM708487  
**VERSION** BM708487.1 GI:19021745  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

**REFERENCE** Bonaldo, M.F., Lennon, G. and Soares, M.B.  
**AUTHORS** Normalization and subtraction: two approaches to facilitate gene  
**TITLE** discovery

**JOURNAL** Genome Res. 6 (9), 791-806 (1996)  
**MEDLINE** 97044477  
**PUBMED** 8889548

**COMMENT** Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565

Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
 Tissue Procurement: Dr. Gregg Hageman  
 CNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics ([www.resgen.com](http://www.resgen.com)).  
 Seq primer: M13 Reverse.

**FEATURES** Location/Qualifiers

1..384  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-C11-afu-b-14-0-UI"  
 /tissue\_type="RPE and Choroid"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-C11"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-C11 is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

**BASE COUNT** 89 a 91 c 113 g 91 t  
**ORIGIN**

**Alignment Scores:**  
 Pred. No.: 44.7 Length: 384  
 Score: 54.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 12 Gaps: 0

US-09-214-836-2 (1-9) x BM708487 (1-384)

**Cy** 1 LysValTPGjYgInTYTTPGlnVal 9  
**Db** 277 AAGACCTGGGGCCAACTGCGCAGTT 303

**RESULT 3** CB792319 436 bp mRNA linear EST 16-MAY-2003  
**LOCUS** AMGNMNC:NRHY4-00003-D6-A W Rat. Hypothalamus (10464) Rattus  
**DEFINITION** norvegicus cDNA clone nrhy4-00003-d6 5', mRNA sequence.

**ACCESSION** CB792319  
**VERSION** CB792319.1 GI:29880712  
**KEYWORDS** EST.  
**SOURCE** Rattus norvegicus (Norway rat)  
**ORGANISM** Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

**REFERENCE** 1 (bases 1 to 436)  
**AUTHORS** Amgen EST Program.  
**TITLE** Amgen Rat EST Program  
**JOURNAL** Unpublished  
**COMMENT** Contact: Dan Fitzpatrick  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00003 row: d column: 6.





Db 454 AAGACCTGGGCGCAATGCGCAAGTT 480

RESULT 6  
LOCUS BM707920 506 bp mRNA linear EST 28-FEB-2002  
DEFINITION UI-E-CII-aft-a-17-0-UI.1 UI-E-CII Homo sapiens cDNA clone  
LOCUS BM707920  
ACCESSION UI-E-CII-aft-a-17-0-UI 5', mRNA sequence.  
VERSION BM707920.1 GI:19021178  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 506)  
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.regen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..506  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-CII-aft-a-17-0-UI"  
/tissue\_type="RPE and Choroid"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_id="UI-E-CII"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-E-CII is a normalized cDNA library containing the  
following tissue(s): RPE and Choroid. The library was  
constructed according to Ronaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is ACCTA.  
This library was created for the program, Gene Discovery  
(NEI)."

BASE COUNT 93 a 151 c 138 g 124 t

ORIGIN

Alignment Scores:

Pred. No.:	66.1	Length:	506
Score:	54.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	93.10%	Indels:	0
DB:	12	Gaps:	0

BS-09-214-836-2 (1-9) x BM707920 (1-506)

QY 1 LysValTTPGIYGINTYTTPGINVal 9

Db 63 AAGACCTGGGCGCAATGCGCAAGTT 89

RESULT 7  
LOCUS BE407844  
DEFINITION BE407844 515 bp mRNA linear EST 21-JUL-2000  
LOCUS BE407844  
ACCESSION BE407844.1 GI:9344294  
VERSION BE407844  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 515)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE NIH-MGC  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at: image.lln.gov  
Plate: LNCM31 row: d column: 22  
High quality sequence start: 2  
High quality sequence stop: 503.  
Location/Qualifiers  
1..515  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3635301"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_21"  
/note="Organ: placenta; Vector: pOT87; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the Laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 126 a 120 c 149 g 120 t

ORIGIN

Alignment Scores:

Pred. No.:	67.7	Length:	515
Score:	54.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	93.10%	Indels:	0
DB:	10	Gaps:	0

US-09-214-836-2 (1-9) x BE407844 (1-515)

QY 1 LysValTTPGIYGINTYTTPGINVal 9

Db 462 AAGACCTGGGCGCAATGCGCAAGTC 488

RESULT 8  
LOCUS BE276871  
DEFINITION BE276871 523 bp mRNA linear EST 13-JUN-2000  
LOCUS BE276871  
ACCESSION BE276871  
VERSION BE276871.1 GI:9151933

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 523)  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DRP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCM37 row: b column: 10  
High quality sequence stop: 523.  
Location/Qualifiers  
1. 523  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3050793"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 20"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 124 a 117 c 158 g 124 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 69.2 Length: 523  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 10 Gaps: 0  
US-09-214-836-2 (1-9) x BE276871 (1-523)  
QY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 454 AAGACCTGGGGCCAACTACTGCAAGTT 480  
RESULT 9  
BE280517 531 bp mRNA linear EST 13-JUL-2000  
LOCUS 601155392F1 NIH\_MGC\_21 Homo sapiens CDNA clone IMAGE:3138863 5',  
DEFINITION mRNA sequence.  
ACCESSION BE280517  
VERSION BE280517.1 GI:9155522  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCM104 row: g column: 24  
High quality sequence stop: 529.  
Location/Qualifiers  
1. 531  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3138863"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 21"  
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 102 a 170 c 143 g 116 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 70.7 Length: 531  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 10 Gaps: 0  
US-09-214-836-2 (1-9) x BE280517 (1-531)  
QY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
Db 8 AAGACCTGGGGCCAACTACTGCAAGTT 34  
RESULT 10  
BE408811 546 bp mRNA linear EST 21-JUL-2000  
LOCUS 60130333F1 NIH\_MGC\_21 Homo sapiens CDNA clone IMAGE:3637544 5',  
DEFINITION mRNA sequence.  
ACCESSION BE408811  
VERSION BE408811.1 GI:9345261  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCM37 row: b column: 09  
High quality sequence stop: 543.  
Location/Qualifiers  
1. 546  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3637544"  
/tissue\_type="choriocarcinoma"

/lab host="DH10B (phage-resistant)"  
/note="Organism: placenta; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGCAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 98 a 170 c 145 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 73.6 Length: 546  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 10 Gaps: 0

US-09-214-836-2 (1-9) x BE408811 (1-546)

OY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
DB 77 AAGACCTGGGGCCAACTACTGGCAAGTT 103

RESULT 11  
CA397722 577 bp mRNA linear EST 06-NOV-2002  
LOCUS cs94912.y1 Human Retinal pigment epithelium/choroid cDNA  
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs94912  
5' mRNA sequence.

ACCESSION CA397722.1 GI:24735291  
VERSION CA397722.1 GI:24735291  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 577)  
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Fariss,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NIH Bank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
JOURNAL MEDLINE 22103460  
PUBMED 12107410  
COMMENT Contact: Wistow, G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: gwaem@helix.nih.gov  
Plate: 94 row: 9 column: 12  
Seq primer: M13R1 reverse primer (ABI).  
Location/Qualifiers  
1..577  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="cs94912"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA

library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the Superscript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>. The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/Mui sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NSC)."

BASE COUNT 121 a 161 c 160 g 135 t  
ORIGIN

Alignment Scores:  
Pred. No.: 79.6 Length: 577  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x CA397722 (1-577)

OY 1 LysValTrpGlyGlnTyrTrpGlnVal 9  
DB 194 AAGACCTGGGGCCAACTACTGGCAAGTT 220

RESULT 12  
BE281030 585 bp mRNA linear EST 13-JUL-2000  
LOCUS 601156355F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3139788 5',  
DEFINITION mRNA sequence.  
ACCESSION BE281030  
VERSION BE281030.1 GI:9156043  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 585)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE Unpublished  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov  
Plate: LCM106 row: n column: 13.  
Location/Qualifiers  
1..585  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3139788"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_21"  
/note="Organ: placenta; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGCAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 144 a 137 c 171 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 81.1 Length: 585

Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 10 Gaps: 0

US-09-214-836-2 (1-9) x BE281030 (1-585)

Qy 1 LysValTPGlyGlnTyrTPGlnVal 9  
Db 470 AAGACCTGGGCCCAATCTGGCAAGTT 496

RESULT 13  
CA392552 587 bp mRNA linear EST 06-NOV-2002  
LOCUS cs26a07.Y1 Human Retinal pigment epithelium/choroid cDNA  
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs26a07  
5', mRNA sequence.

ACCESSION CA392552  
VERSION CA392552.1 GI:24725382  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 587)  
Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,  
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.

Expressed sequence tag analysis of human RPE/choroid for the  
NEBank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants

Mol. Vis. 8 (4), 205-220 (2002)  
22103460  
12107410

JOURNAL MEDLINE PUBMED

COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078

Email: graeme@helix.nih.gov  
Plate: 26 row: a column: 07  
Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers  
1..587

#### FEATURES

source

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="cs26a07"

/tissue\_type="RPE/choroid"

/dev\_stage="Adult"

/lab\_host="EMDH10B"

/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"

/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>". The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

BASE COUNT 145 a 135 c 173 g 134 t  
ORIGIN

Alignment Scores:  
Pred. No.: 81.5  
Score: 54.00

Length: 587  
Matches: 8

Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x CA392552 (1-587)

Qy 1 LysValTPGlyGlnTyrTPGlnVal 9  
Db 478 AAGACCTGGGCCCAATCTGGCAAGTT 504

RESULT 14  
CA396509 587 bp mRNA linear EST 06-NOV-2002  
LOCUS cs78g10.Y1 Human Retinal pigment epithelium/choroid cDNA  
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs78g10  
5', mRNA sequence.

ACCESSION CA396509  
VERSION CA396509.1 GI:24732961  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 587)  
Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,  
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.

Expressed sequence tag analysis of human RPE/choroid for the  
NEBank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants

Mol. Vis. 8 (4), 205-220 (2002)  
22103460  
12107410

JOURNAL MEDLINE PUBMED

COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078

Email: graeme@helix.nih.gov  
Plate: 78 row: g column: 10  
Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers  
1..587

#### FEATURES

source

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="cs78g10"

/tissue\_type="RPE/choroid"

/dev\_stage="Adult"

/lab\_host="EMDH10B"

/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"

/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>". The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

BASE COUNT 145 a 135 c 174 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 81.5  
Score: 54.00

Length: 587  
Matches: 8  
Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x CA396509 (1-587)

Qy 1 LysValTTPGlyGlnTyrTTPGlnVal 9  
DB 475 AAGACCTGGGGCAATCTGGCAAGTT 501

RESULT 15  
BG762070 594 bp mRNA linear EST 15-MAY-2001  
LOCUS 602718443P1 NIH\_MGC\_49 Homo sapiens CDNA clone IMAGE:4858379 5',  
DEFINITION mRNA sequence.  
ACCESSION BG762070  
VERSION BG762070.1 GI:14072723  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1CM1712 row: F column: 12  
High quality sequence stop: 590.  
Location/Qualifiers

FEATURES  
source 1..594  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4858379"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_49"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

BASE COUNT 145 a 141 c 175 g 133 t

ORIGIN

Alignment Scores:  
Pred. No.: 82.9 Length: 594  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 12 Gaps: 0

US-09-214-836-2 (1-9) x BG762070 (1-594)

Qy 1 LysValTTPGlyGlnTyrTTPGlnVal 9  
DB 470 AAGACCTGGGGCAATCTGGCAAGTT 496

RESULT 16

BE743315  
LOCUS BE743315 595 bp mRNA linear EST 15-SEP-2000  
DEFINITION 60157322P1 NIH\_MGC\_9 Homo sapiens CDNA clone IMAGE:3834247 5',  
mRNA sequence.  
ACCESSION BE743315  
VERSION BE743315.1 GI:10157307  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
Plate: L1CM514 row: F column: 08  
High quality sequence stop: 595.  
Location/Qualifiers

FEATURES  
source 1..595  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3834247"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_9"  
/note="Organ: ovary; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 142 a 140 c 177 g 136 t

ORIGIN

Alignment Scores:  
Pred. No.: 83.1 Length: 595  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 10 Gaps: 0

US-09-214-836-2 (1-9) x BE743315 (1-595)

Qy 1 LysValTTPGlyGlnTyrTTPGlnVal 9  
DB 461 AAGACCTGGGGCAATCTGGCAAGTT 487

RESULT 17  
BG767860 603 bp mRNA linear EST 15-MAY-2001  
LOCUS 60274135P1 NIH\_MGC\_49 Homo sapiens CDNA clone IMAGE:4870935 5',  
mRNA sequence.  
ACCESSION BG767860  
VERSION BG767860.1 GI:14078513  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
TITLE NIH-MGC http://mgc.nci.nih.gov/.

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DRP

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 Plate: LNCM1745 row: a column: 16  
 High quality sequence stop: 601.  
 Location/Qualifiers

**FEATURES**  
 source

1..603  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4870935"  
 /tissue\_type="melanotic melanoma, high MDR (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 49"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."  
**BASE COUNT** 140 a 155 c 172 g 136 t  
**ORIGIN**

**Alignment Scores:**

**Pred. No.:** 84.7 **Length:** 603  
**Score:** 54.00 **Matches:** 8  
**Percent Similarity:** 88.89% **Conservative:** 0  
**Best Local Similarity:** 88.89% **Mismatches:** 1  
**Query Match:** 93.10% **Indels:** 0  
**DB:** 12 **Gaps:** 0

US-09-214-836-2 (1-9) x BG767860 (1-603)

**Qy** 1 LysValTrpGlyGlnVal 9  
**Db** 391 AAGACCTGGGCGCAATCTGCAAGTT 417

**RESULT 18** BE384038 604 bp mRNA linear EST 21-JUN-2000  
**LOCUS** 60127829F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3613927 5',  
**DEFINITION** mRNA sequence.  
**ACCESSION** BE384038  
**VERSION** BE384038.1 GI:9329403  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 604)  
**REFERENCE** NIH-MGC <http://mgs.nci.nih.gov/>.  
**AUTHORS** National Institutes of Health, Mammalian Gene Collection (MGC)  
**TITLE** Unpublished  
**JOURNAL** Contact: Robert Strausberg, Ph.D.  
**COMMENT** Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DRP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 Plate: LNCM275 row: j column: 08

**FEATURES** High quality sequence stop: 599.  
 Location/Qualifiers  
 1..604  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3613927"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 20"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
**BASE COUNT** 140 a 147 c 176 g 141 t  
**ORIGIN**

**Alignment Scores:**

**Pred. No.:** 84.9 **Length:** 604  
**Score:** 54.00 **Matches:** 8  
**Percent Similarity:** 88.89% **Conservative:** 0  
**Best Local Similarity:** 88.89% **Mismatches:** 1  
**Query Match:** 93.10% **Indels:** 0  
**DB:** 10 **Gaps:** 0

US-09-214-836-2 (1-9) x BE384038 (1-604)

**Qy** 1 LysValTrpGlyGlnVal 9  
**Db** 454 AAGACCTGGGCGCAATCTGCAAGTT 480

**RESULT 19** BG761374 605 bp mRNA linear EST 15-MAY-2001  
**LOCUS** 60271825F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4858262 5',  
**DEFINITION** mRNA sequence.  
**ACCESSION** BG761374  
**VERSION** BG761374.1 GI:14072027  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 605)  
**REFERENCE** NIH-MGC <http://mgs.nci.nih.gov/>.  
**AUTHORS** National Institutes of Health, Mammalian Gene Collection (MGC)  
**TITLE** Unpublished  
**JOURNAL** Contact: Robert Strausberg, Ph.D.  
**COMMENT** Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DRP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 Plate: LNCM1712 row: a column: 15  
 High quality sequence stop: 605.  
 Location/Qualifiers

**FEATURES**  
 source

1..605  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4858262"  
 /tissue\_type="melanotic melanoma, high MDR (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 49"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH-MGC  
Library."

BASE COUNT 139 a 154 c 173 g 139 t  
ORIGIN

Alignment Scores:  
Pred. No.: 85.1 Length: 605  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 12 Gaps: 0

US-09-214-836-2 (1-9) x BG761374 (1-605)

OY 1 LysValTTPGlyGlnTTPGlnVal 9  
DB 412 AAGACCTGGGCGCAATCTGCAAGTT 438

RESULT 20  
CA397065 605 bp mRNA linear EST 06-NOV-2002  
LOCUS CA397065  
DEFINITION c885f10.y2 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs Homo sapiens cDNA clone c885f10  
5', mRNA sequence.  
VERSION CA397065  
KEYWORDS CA397065.1 GI:24734031  
SOURCE EST.  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE Wistow, G., Bernstein, S. L., Wylt, M. K., Farris, R. N., Behal, A.,  
Touchman, J. W., Bouffard, G., Smith, D. and Peterson, K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NEI-Bank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL  
MEDLINE 22103460  
PUBMED 12107410  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 85 row: F column: 10  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

FEATURES  
source

1..605  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="c885f10"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="BMD10B"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: PCWSPORTE6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the PCWSPORTE vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the Superscript

Plasmid System (Invitrogen Corp.  
<http://www.invitrogen.com>). The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/Mlu sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

BASE COUNT 122 a 188 c 162 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 85.1 Length: 605  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x CA397065 (1-605)

OY 1 LysValTTPGlyGlnTTPGlnVal 9  
DB 30 AAGACCTGGGCGCAATCTGCAAGTT 56

RESULT 21  
BM722309 606 bp mRNA linear EST 01-MAR-2002  
LOCUS BM722309  
DEFINITION UI-E-E00-ahx-c-18-0-UI.r1 UI-E-E00 Homo sapiens cDNA clone  
UI-E-E00-ahx-c-18-0-UI 5', mRNA sequence.  
VERSION BM722309  
KEYWORDS BM722309.1 GI:19042795  
SOURCE EST.  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE Bonaldo, M. F., Lennon, G. and Soares, M. B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

JOURNAL  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 Reverse.

FEATURES  
source

1..605  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-E00-ahx-c-18-0-UI"  
/tissue\_type="fetal eye"  
/dev\_stage="fetal"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-E00"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-E-E00 is a cDNA library containing the following  
tissue(s): fetal eye. The library was constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double



stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GPI)8 tail. The sequence tag for this library is GCGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 127 a 164 c 167 g 147 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 85.3 Length: 606  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 12 Gaps: 0

US-09-214-836-2 (1-9) x BM722309 (1-606)

Oy 1 LysValTPGlyGlnTYrTPGlnVal 9  
Db 288 AAGACCTGGGCGCAATCTGGCAAGTT 314

RESULT 22 CA397499 611 bp mRNA linear EST 06-NOV-2002  
CA397499  
LOCUS (c91h07.v1 Human Retinal pigment epithelium/choroid cDNA c91h07  
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone c91h07  
5', mRNA sequence.  
CA397499  
VERSION CA397499.1 GI:24734863  
KEYWORDS EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

1 (bases 1 to 611)  
Wistow,G., Bernstein,S.L., Walt,M.K., Paria,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NEI/Bank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
22103460  
12107410

Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 91 row: h column: 07  
Seq primer: M13RPI reverse primer (ABI).

FEATURES  
SOURCE  
Location/Qualifiers  
1..611  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="c91h07"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_idb="Human Retinal pigment epithelium/choroid cDNA  
/note="Organ: Eye; Vector: PCWVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the PCWVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),

essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>). The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/Mlu sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

BASE COUNT 144 a 146 c 178 g 143 t  
ORIGIN

Alignment Scores:  
Pred. No.: 86.3 Length: 611  
Score: 54.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 93.10% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x CA397499 (1-611)

Oy 1 LysValTPGlyGlnTYrTPGlnVal 9  
Db 464 AAGACCTGGGCGCAATCTGGCAAGTT 490

RESULT 23 BE389689 616 bp mRNA linear EST 21-JUL-2000  
BE389689  
LOCUS 601281927F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3603823 5',  
DEFINITION mRNA sequence.  
CA397499  
VERSION BE389689  
KEYWORDS BE389689.1 GI:9335054  
EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

1 (bases 1 to 616)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strauberg, Ph.D.  
Email: sgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM249 row: e column: 08  
High quality sequence stop: 560.  
Location/Qualifiers  
1..616  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3603823"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_idb="NIH MGC 44"  
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
SOURCE  
Location/Qualifiers  
1..616  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3603823"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_idb="NIH MGC 44"  
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 144 a 149 c 176 g 147 t  
ORIGIN

Alignment Scores:  
Pred. No.: 87.3 Length: 616  
Score: 54.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 10 Gaps: 0

US-09-214-836-2 (1-9) x BE389689 (1-616)

QY 1 LysValTPGlyGlnTyrTPGlnVal 9  
 DB 454 AAGACCTGGGGCCAACTGCGCAAGTT 480

## RESULT 24

CA396195 619 bp mRNA linear EST 06-NOV-2002  
 LOCUS CA396195  
 DEFINITION cs75b02.y1 Human Retinal pigment epithelium/choroid cDNA cs75b02  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs75b02  
 5', mRNA sequence.

ACCESSION CA396195  
 VERSION CA396195  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 619)  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.

TITLE Expressed sequence tag analysis of human RPE/choroid for the

NEBank Project: Over 6000 non-redundant transcripts, novel genes

and splice variants

Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL 22103460

MEDLINE 12107410

COMMENT Contact: Wiscow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 75 row: b column: 02  
 Seq primer: M13RP1 reverse primer (ABI).

FEATURES  
 source  
 1..619  
 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="cs75b02"

/tissue\_type="RPE/choroid"

/dev\_stage="Adult"

/lab\_host="EMD10B"

/clone\_lib="Human Retinal pigment epithelium/choroid cDNA

(Un-normalized, unamplified): cs"

/note="Organ: Eye; Vector: PCWVS/PCWVS6; Two different donor

eyes (75-80 years old) yielded approximately 600 mg of

dissected RPE/choroid tissue. This in turn yielded 340 ug

of total RNA and 7 ug of mRNA. A directionally cloned cDNA

library in the PCWVS/PCWVS6 vector was constructed at Life

Technologies (Rockville, MD; now part of Invitrogen Corp),

essentially following the protocols of the Superscript

Plasmid System (Invitrogen Corp).

<http://www.invitrogen.com/>. The library code

designation was cs. For this library, cDNA inserts were

cloned into the NotI/MluI sites of the vector. EST

analysis was performed on the unamplified library at the

NIH Intramural Sequencing Center (NISC)."

BASE COUNT 126 a 175 c 168 g 150 t

## ALIGNMENT SCORES:

Pred. No.: 87.9  
 Score: 54.00  
 Percent Similarity: 88.89%

Length: 619  
 Matches: 8  
 Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 93.10% Indels: 0  
 DB: 14 Gaps: 0

US-09-214-836-2 (1-9) x CA396195 (1-619)

QY 1 LysValTPGlyGlnTyrTPGlnVal 9  
 DB 218 AAGACCTGGGGCCAACTGCGCAAGTT 244

## RESULT 25

BE384085 622 bp mRNA linear EST 21-JUL-2000  
 LOCUS BE384085  
 DEFINITION 60127888F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3614085 5',  
 mRNA sequence.

ACCESSION BE384085  
 VERSION BE384085.1 GI:9329450  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 622)  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

Plate: LICM275 row: p column: 22

High quality sequence stop: 622.

FEATURES  
 source  
 1..622  
 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3614085"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAAGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 145 a 151 c 180 g 146 t

## ALIGNMENT SCORES:

Pred. No.: 88.5  
 Score: 54.00  
 Percent Similarity: 88.89%

Best Local Similarity: 88.89% Mismatches: 0  
 Query Match: 93.10% Indels: 0  
 DB: 10 Gaps: 0

US-09-214-836-2 (1-9) x BE384085 (1-622)

QY 1 LysValTPGlyGlnTyrTPGlnVal 9

DB 459 AAGACCTGGGGCCAACTGCGCAAGTT 485

Search completed: August 24, 2003, 03:57:11

Job time: 1898.5 secs

Mon Aug 25 09:47:43 2003

us-09-214-836-2.rst

---

Page 13



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:41 ; Search time 37 Seconds  
(without alignments)  
38.609 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KVMQYQV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:.\*  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	9	AAW45774	Melanoma associate
2	57	98.3	9	AAW4803	Modified MART-1 me
3	57	98.3	9	AAW45772	Melanoma associate
4	57	98.3	9	AAU28952	Modified gp100 G9-
5	55	94.8	9	AAW4802	Modified MART-1 me
6	55	94.8	9	AAW4801	Modified MART-1 me
7	55	94.8	9	AAW45773	Melanoma associate
8	55	94.8	9	AAW45782	Melan A/MART epito
9	55	94.8	9	AAU28950	Modified gp100 G9-

10	55	94.8	9	AAU28951	Modified gp100 G9-
11	54	93.1	9	AAW78644	Immunogenic peptide
12	54	93.1	9	AAW77119	gp100/Pmel17 synth
13	54	93.1	9	AAW78850	Pmel 17 (Gp100) pr
14	54	93.1	9	AAW70010	Melanoma-associate
15	54	93.1	9	AAW4598	Peptide 3 from gp
16	54	93.1	9	AAW42536	Gp 100 epitope (re
17	54	93.1	9	AAW45770	Melanoma associate
18	54	93.1	9	AAV49653	Tumour antigenic p
19	54	93.1	9	AAV53524	Human melanoma Pme
20	54	93.1	9	AAV47616	Immunogenic peptid
21	54	93.1	9	AAV33172	Human gp100-Pmel1
22	54	93.1	9	AAV40211	Amino acid sequenc
23	54	93.1	9	AAV26867	Melanoma-derived 1
24	54	93.1	9	AAV01753	Exemplary antigen
25	54	93.1	9	AAV00715	Tumour antigen booc
26	54	93.1	9	AAV10449	HLA Class I motif
27	54	93.1	9	AAW33662	MHC class I associ
28	54	93.1	9	AAW3679	Cytotoxic T lympho
29	54	93.1	9	AAW8654	Antigenic peptide
30	54	93.1	9	AAV71520	Human gp100 Pmel1
31	54	93.1	9	AAW82632	Tumour associated
32	54	93.1	9	AAV90803	Human leukocyte an
33	54	93.1	9	AAV92299	gp100-Pmel117 anti
34	54	93.1	9	AAV84236	Tumour associated
35	54	93.1	9	AAV82979	gp100 (Pmel117) tum
36	54	93.1	9	AAV56614	gp100-Pmel117 gen
37	54	93.1	9	AAU71993	gp100 melanoma ant
38	54	93.1	9	AAU28928	gp100 immunogenic
39	54	93.1	9	AAW6841	Human gp100-Pmel11
40	54	93.1	9	AAW3758	Human Pmel 17 (Gp1
41	54	93.1	9	AAW2661	Human melanoma gp1
42	54	93.1	9	AAW2111	gp100-Pmel1 17 hum
43	54	93.1	9	AAW5908	MHC class-I associ
44	54	93.1	9	AAW0451	Human melanoma gp1
45	54	93.1	9	AAW31354	Exemplary antigen

#### ALIGNMENTS

RESULT 1	
AAW45774	AAW45774 standard; peptide: 9 AA.
XX	
AC	AAW45774;
XX	
DT	22-JUN-1998 (first entry)
XX	
DE	Melanoma associated peptide analogue #5.
XX	
KW	Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;
KW	antigen; CTL; immunogenic; viral disease.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FN	W09802538-A1.
XX	
PD	22-JAN-1998.
XX	
PF	08-JUL-1997; 97WO-EP03712.
XX	
PR	11-JUL-1996; 96EP-0201945.
XX	
PA	(ALKU ) AKZO NOBEL NV.
XX	
PI	Adema GJ, Figdor CG;
XX	
DR	WPI; 1998-110586/10.
XX	
PT	Melanoma associated peptide analogues - useful in vaccines against
PT	melanoma

XX Claim 4; Figure 2; 47bp; English.  
PS  
XX This sequence represents a specifically claimed example of a novel  
CC peptide, which is immunogenic with lymphocytes directed against  
CC metastatic melanoma. It is characterised in that it comprises at least  
CC a part of the following sequence, where the amino acid at position 2 or 8  
CC is substituted: Lys-Thr-Tyr-Gly-Gln-Tyr-Trp-Gln-Val. Vaccines comprising  
CC the peptide, an epitope of the peptide, nucleotide sequence encoding the  
CC peptide, or an antigen presenting cell preloaded with the peptide or  
CC antibody as above, are useful for cancer, particularly melanoma,  
CC treatment. The peptides can also be used to generate antigen reactive  
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The  
CC peptides can be exploited to elicit native epitope-reactive CTL. Usage  
CC of the peptides with improved immunogenicity may contribute to the  
CC development of CTL-epitope based vaccines in viral disease and cancer.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 100.0%; Score 58; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KVMGQYMOV 9  
DB 1 KVMGQYMOV 9  
XX  
RESULT 2  
AAR84803  
ID AAR84803 standard; peptide; 9 AA.  
XX  
AC AAR84803;  
XX  
DT 25-APR-1996 (first entry)  
XX  
DE Modified MART-1 melanoma antigen immunogenic peptide G9-154-21.  
XX  
KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;  
KW metastatic melanoma; tumour-associated antigen;  
KW immunogenic peptide; diagnosis; prognosis; prophylaxis;  
KW therapy; vaccine.  
XX  
OS Synthetic.  
XX  
PN WO9529193-A2.  
XX  
PD 02-NOV-1995.  
XX  
PF 21-APR-1995; 95WO-US05063.  
XX  
PR 05-APR-1995; 95US-0417174.  
PR 22-APR-1994; 94US-0231565.  
XX  
PA (USSH ) US SEC DEPT HEALTH.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
DR WPI; 1995-382963/49.  
XX  
PT DNA encoding melanoma antigens recognised by T-lymphocytes - also  
PT vectors, host cells and antibodies, used to detect, treat and  
PT immunise animal against melanoma.  
XX  
PS Example 5; Page 106; 184pp; English.  
XX  
AAR84783-800 are G9-154 peptides modified to improve immunogenicity.  
CC G9-154 is an immunogenic peptide based on the melanoma antigen (MART-1)  
CC (see AAR84208). The peptides are used in medicaments for the treatment  
CC or prevention (by immunization) of melanoma. Antibodies against MART-1  
CC and its immunogenic peptides may be used in the detection and  
CC isolation of MART-1 from a sample, the detection of which is  
CC indicative of a disease state (melanoma or metastatic melanoma).

XX SQ Sequence 9 AA;  
XX  
Query Match 98.3%; Score 57; DB 16; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KVMGQYMOV 9  
DB 1 KVMGQYMOV 9  
XX  
RESULT 3  
AAM45772  
ID AAM45772 standard; peptide; 9 AA.  
XX  
AC AAM45772;  
XX  
DT 22-JUN-1998 (first entry)  
XX  
DE Melanoma associated peptide analogue #3.  
XX  
KW Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;  
KW antigen; CTL; immunogenic; viral disease.  
XX  
OS Synthetic.  
XX  
PN WO9802538-A1.  
XX  
PD 22-JAN-1998.  
XX  
PE 08-JUL-1997; 97WO-EP03712.  
XX  
PR 11-JUL-1996; 96EP-0201945.  
XX  
PA (ALKU ) AKZO NOBEL NV.  
XX  
PI Adema GJ, Figdor CG;  
XX  
DR WPI; 1998-110586/10.  
XX  
PT Melanoma associated peptide analogues - useful in vaccines against  
PT melanoma  
XX  
PS Claim 4; Figure 2; 47bp; English.  
XX  
CC This sequence represents a specifically claimed example of a novel  
CC peptide, which is immunogenic with lymphocytes directed against  
CC metastatic melanoma. It is characterised in that it comprises at least  
CC a part of the following sequence, where the amino acid at position 2 or 8  
CC is substituted: Lys-Thr-Tyr-Gly-Gln-Tyr-Trp-Gln-Val. Vaccines comprising  
CC the peptide, an epitope of the peptide, nucleotide sequence encoding the  
CC peptide, or an antigen presenting cell preloaded with the peptide or  
CC antibody as above, are useful for cancer, particularly melanoma,  
CC treatment. The peptides can also be used to generate antigen reactive  
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The  
CC peptides can be exploited to elicit native epitope-reactive CTL. Usage  
CC of the peptides with improved immunogenicity may contribute to the  
CC development of CTL-epitope based vaccines in viral disease and cancer.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 98.3%; Score 57; DB 19; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KVMGQYMOV 9  
DB 1 KVMGQYMOV 9  
XX  
RESULT 4

AAU28952  
ID AAU28952 standard; Peptide; 9 AA.  
XX  
AC AAU28952;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Modified gp100 G9-154 peptide #3.  
XX  
KW Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;  
KW diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;  
KW in vivo tumour rejection.  
XX  
OS Synthetic.  
XX  
FN US6270778-B1.  
XX  
PD 07-AUG-2001.  
XX  
PF 12-MAR-1999; 99US-0267439.  
XX  
PR 05-MAY-1998; 98US-0073138.  
PR 22-APR-1994; 94US-0231565.  
PR 05-APR-1995; 95US-0417174.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
DR WPI; 2001-595403/67.  
XX  
PT Immunogenic peptide useful in vaccines comprises specific amino acids  
PT of new melanoma antigen recognised by T lymphocytes -  
XX  
PS Example 5; Column 54; 73pp; English.  
XX  
CC The invention relates to a novel immunogenic peptide comprising 5-20  
CC contiguous amino acids of new melanoma antigen recognised by T  
CC lymphocytes (MART-1). The peptide sequence contains at least one amino  
CC acid modification of MART-1. The peptide is used in diagnostic and  
CC therapeutic methods as an immunogen or vaccine to prevent or treat  
CC melanoma, and for in vivo tumour recognition and rejection. AAU2888-  
CC AAU29008 represent MART-1 peptide amino acid sequences, and related  
CC sequences of the invention.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 98.3%; Score 57; DB 22; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVMGOYMOV 9  
DB 1 KVMGOYMOV 9  
XX  
RESULT 5  
AAR84802  
ID AAR84802 standard; Peptide; 9 AA.  
XX  
AC AAR84802;  
XX  
DT 25-APR-1996 (first entry)  
XX  
DE Modified MART-1 melanoma antigen immunogenic peptide G9-154-2M.  
XX  
KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;  
KW metastatic melanoma; tumour-associated antigen;  
KW immunogenic peptide; diagnosis; prognosis; prophylaxis;  
KW therapy; vaccine.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
OS Synthetic.  
XX

EN W09529193-A2.  
XX  
PD 02-NOV-1995.  
XX  
PE 21-APR-1995; 95WO-US05063.  
XX  
PR 05-APR-1995; 95US-0417174.  
PR 22-APR-1994; 94US-0231565.  
XX  
PA (USSH ) US SEC DEPT HEALTH.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
DR WPI; 1995-382963/49.  
XX  
PT DNA encoding melanoma antigens recognised by T-lymphocytes - also  
PT vectors, host cells and antibodies, used to detect, treat and  
PT immunise animal against melanoma.  
XX  
PS Example 5; Page 106; 184pp; English.  
XX  
CC AAR84783-800 are G9-154 peptides modified to improve immunogenicity.  
CC G9-154 is an immunogenic peptide based on the melanoma antigen (MART-1)  
CC (see AAR84208). The peptides are used in medicaments for the treatment  
CC or prevention (by immunization) of melanoma. Antibodies against MART-1  
CC and its immunogenic peptides may be used in the detection and  
CC isolation of MART-1 from a sample, the detection of which is  
CC indicative of a disease state (melanoma or metastatic melanoma).  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 94.8%; Score 55; DB 16; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KVMGOYMOV 9  
DB 1 KVMGOYMOV 9  
XX  
RESULT 6  
AAR84801  
ID AAR84801 standard; Peptide; 9 AA.  
XX  
AC AAR84801;  
XX  
DT 25-APR-1996 (first entry)  
XX  
DE Modified MART-1 melanoma antigen immunogenic peptide G9-154-2L.  
XX  
KW MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;  
KW metastatic melanoma; tumour-associated antigen;  
KW immunogenic peptide; diagnosis; prognosis; prophylaxis;  
KW therapy; vaccine.  
XX  
OS Synthetic.  
XX  
PN W09529193-A2.  
XX  
PD 02-NOV-1995.  
XX  
PE 21-APR-1995; 95WO-US05063.  
XX  
PR 05-APR-1995; 95US-0417174.  
PR 22-APR-1994; 94US-0231565.  
XX  
PA (USSH ) US SEC DEPT HEALTH.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
DR WPI; 1995-382963/49.  
XX  
PT DNA encoding melanoma antigens recognised by T-lymphocytes - also

PT vectors, host cells and antibodies, used to detect, treat and  
PT immunise animal against melanoma.  
XX  
PS Example 5; Page 106; 184pp; English.  
CC AAR84783-800 are G9-154 peptides modified to improve immunogenicity.  
CC G9-154 is an immunogenic peptide based on the melanoma antigen (MART-1)  
CC (see AAR84208). The peptides are used in medicaments for the treatment  
CC or prevention (by immunization) of melanoma. Antibodies against MART-1  
CC and its immunogenic peptides may be used in the detection and  
CC isolation of MART-1 from a sample, the detection of which is  
CC indicative of a disease state (melanoma or metastatic melanoma).  
XX  
SQ Sequence 9 AA;

Query Match 94.8%; Score 55; DB 16; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
|:|||||  
Db 1 KLMGQYMOV 9

RESULT 7  
AAM45773  
ID AAM45773 standard; peptide; 9 AA.  
AC AAM45773;  
XX  
DT 22-JUN-1998 (first entry)  
XX  
DE Melanoma associated peptide analogue #4.  
KM Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;  
KM antigen; CTL; immunogenic; viral disease.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FN WO9802538-A1.  
PD 22-JAN-1998.  
XX  
PF 08-JUL-1997; 97MO-EP03712.  
XX  
PR 11-JUL-1996; 96EP-0201945.  
XX  
PA (ALKU) AKZO NOBEL NV.  
XX  
PI Adema GJ, Figdor CG;  
XX  
WPI; 1998-110586/10.  
XX  
PT Melanoma associated peptide analogues - useful in vaccines against  
PT melanoma  
XX  
PS Claim 4; Figure 2; 47pp; English.  
XX  
CC This sequence represents a specifically claimed example of a novel  
CC peptide, which is immunogenic with lymphocytes directed against  
CC metastatic melanomas. It is characterised in that it comprises at least  
CC a part of the following sequence, where the amino acid at position 2 or 8  
CC is substituted: Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val. Vaccines comprising  
CC the peptide, an epitope of the peptide, nucleotide sequence encoding the  
CC peptide, or an antigen presenting cell preloaded with the peptide or  
CC antibody as above, are useful for cancer, particularly melanoma,  
CC treatment. The peptides can also be used to generate antigen reactive  
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The  
CC peptides can be exploited to elicit native epitope-reactive CTL. Usage  
CC of the peptides with improved immunogenicity may contribute to the  
CC development of CTL-epitope based vaccines in viral disease and cancer.  
XX

SQ Sequence 9 AA;

Query Match 94.8%; Score 55; DB 19; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
|:|||||  
Db 1 KLMGQYMOV 9

RESULT 8  
AAM45782  
ID AAM45782 standard; peptide; 9 AA.  
XX  
AC AAM45782;  
XX  
DT 22-JUN-1998 (first entry)  
XX  
DE Melan A/MART epitope (residues 27-35) analogue #14.  
XX  
KM Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;  
KM antigen; CTL; immunogenic; viral disease; GP 100; Melan A/MART-1.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FN WO9802538-A1.  
PD 22-JAN-1998.  
XX  
PF 08-JUL-1997; 97MO-EP03712.  
XX  
PR 11-JUL-1996; 96EP-0201945.  
XX  
PA (ALKU) AKZO NOBEL NV.  
XX  
PI Adema GJ, Figdor CG;  
XX  
WPI; 1998-110586/10.  
XX  
PT Melanoma associated peptide analogues - useful in vaccines against  
PT melanoma  
XX  
PS Example 2; Page 29; 47pp; English.  
XX

CC This sequence is shown in the specification. The invention relates to  
CC peptides, which are immunogenic with lymphocytes directed against  
CC metastatic melanomas. They are characterised in that they comprise at  
CC least a part of the following sequence, where the amino acid at position  
CC 2 or 8 is substituted: Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val. Vaccines  
CC comprising the peptide, an epitope of the peptide, nucleotide sequence  
CC encoding the peptide, or an antigen presenting cell preloaded with the  
CC peptide or antibody as above, are useful for cancer, particularly  
CC melanoma, treatment. The peptides can also be used to generate antigen  
CC reactive tumour infiltrating lymphocytes, which can also be used in  
CC vaccines. The peptides can be exploited to elicit native epitope-reactive  
CC CTL. Usage of the peptides with improved immunogenicity may contribute  
CC to the development of CTL-epitope based vaccines in viral disease and  
CC cancer.  
XX  
SQ Sequence 9 AA;

Query Match 94.8%; Score 55; DB 19; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
|:|||||  
Db 1 KLMGQYMOV 9

RESULT 9



AAU28950  
ID AAU28950 standard; Peptide; 9 AA.  
XX  
AC AAU28950;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Modified gp100 G9-154 peptide #1.  
XX  
KM Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;  
KM diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;  
XX in vivo tumour rejection.  
XX Synthetic.  
OS  
PN US6270778-B1.  
XX  
PF 07-AUG-2001.  
XX  
PF 12-MAR-1999; 99US-0267439.  
XX  
PR 05-MAY-1998; 98US-0073138.  
PR 22-APR-1994; 94US-0231565.  
PR 03-APR-1995; 95US-0417174.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
DR WPI; 2001-595403/67.  
XX  
PT Immunogenic peptide useful in vaccines comprises specific amino acids  
PT of new melanoma antigen recognised by T lymphocytes -  
XX  
PS Example 5; Column 54; 73pp; English.  
XX  
CC The invention relates to a novel immunogenic peptide comprising 5-20  
CC contiguous amino acids of new melanoma antigen recognised by T  
CC lymphocytes (MART-1). The peptide sequence contains at least one amino  
CC acid modification of MART-1. The peptide is used in diagnostic and  
CC therapeutic methods as an immunogen or vaccine to prevent or treat  
CC melanoma, and for in vivo tumour recognition and rejection. AAU28888-  
CC AAU29008 represent MART-1 peptide amino acid sequences, and related  
CC sequences of the invention.  
XX  
SQ Sequence 9 AA;  
XX  
QY Query Match 94.8%; Score 55; DB 22; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 1 KMWGQYQV 9  
1 KLMGQYQV 9  
XX  
RESULT 10  
AAU28951  
ID AAU28951 standard; Peptide; 9 AA.  
XX  
AC AAU28951;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Modified gp100 G9-154 peptide #2.  
XX  
KM Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;  
KM diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;  
XX in vivo tumour rejection.  
XX Synthetic.  
OS  
PN US6270778-B1.

XX  
PD 07-AUG-2001.  
XX  
PE 12-MAR-1999; 99US-0267439.  
XX  
PR 05-MAY-1998; 98US-0073138.  
PR 22-APR-1994; 94US-0231565.  
PR 05-APR-1995; 95US-0417174.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Kawakami Y, Rosenberg SA;  
XX  
DR WPI; 2001-595403/67.  
XX  
PT Immunogenic peptide useful in vaccines comprises specific amino acids  
PT of new melanoma antigen recognised by T lymphocytes -  
XX  
PS Example 5; Column 54; 73pp; English.  
XX  
CC The invention relates to a novel immunogenic peptide comprising 5-20  
CC contiguous amino acids of new melanoma antigen recognised by T  
CC lymphocytes (MART-1). The peptide sequence contains at least one amino  
CC acid modification of MART-1. The peptide is used in diagnostic and  
CC therapeutic methods as an immunogen or vaccine to prevent or treat  
CC melanoma, and for in vivo tumour recognition and rejection. AAU28888-  
CC AAU29008 represent MART-1 peptide amino acid sequences, and related  
CC sequences of the invention.  
XX  
SQ Sequence 9 AA;  
XX  
QY Query Match 94.8%; Score 55; DB 22; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 1 KMWGQYQV 9  
1 KLMGQYQV 9  
XX  
RESULT 11  
AAR78644  
ID AAR78644 standard; Protein; 9 AA.  
XX  
AC AAR78644;  
XX  
DT 22-JAN-1996 (first entry)  
XX  
DE Immunogenic peptide of melanoma associated antigen gp100.  
XX  
KM Melanoma; antigen; vaccine; immunogen; primer; probe; detection;  
KM identification; tumour; gp100.  
XX  
OS Homo sapiens.  
XX  
PN EP668350-A1.  
XX  
PD 23-AUG-1995.  
XX  
PF 14-FEB-1995; 95EP-0200348.  
XX  
PR 21-DEC-1994; 94EP-0203709.  
PR 16-FEB-1994; 94EP-0200337.  
XX  
PA (ALKU ) AKZO NOBEL NV.  
XX  
PI Adema GJ, Figdor CG;  
XX  
DR WPI; 1995-284790/38.  
DR N-PSDB; AAQ96055.  
XX  
PT Melanoma associated antigen gp100 - used in vaccines and for the  
PT detection of tumours

XX Claim 5; Page 31; 40pp; English.  
 PS  
 XX  
 CC Immunogenic peptides derived from the melanoma associated antigen  
 CC (See AAW78639-45) may be used in the production of vaccines.  
 CC Nucleotide sequences encoding the immunogenic peptides may be used  
 CC as primers and probes in the detection of melanoma cells. Tumour  
 CC infiltrating lymphocytes capable of binding to the melanoma  
 CC associated antigen can be cultured ex vivo and returned to melanoma  
 CC particles, and when radiolabelled, they may be used to identify  
 CC tumour deposits.  
 CC  
 XX  
 SQ Sequence 9 AA;  
 Query Match 93.1%; Score 54; DB 16; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMQV 9  
 DB 1 KTMGQYMQV 9

RESULT 12  
 AAW77119  
 ID AAW77119 standard; peptide; 9 AA.  
 AC AAW77119;  
 XX  
 DT 16-NOV-1998 (first entry)  
 XX  
 DE SP100/Pmel17 synthetic peptide epitope 1.  
 XX  
 KM Tyrosinase; tyrosinase cytotoxic lymphocyte response;  
 KM cytotoxic T lymphocyte; cysteine-depleted; melanoma.  
 XX  
 OS Synthetic.  
 PN WO9833810-A2.  
 PD 06-AUG-1998.  
 PF 29-JAN-1998; 98WO-US01592.  
 PR 30-JAN-1997; 97US-0037781.  
 PA (UUYI-) UNIV VIRGINIA PATENT FOUND.  
 PI Engelhard VH, Hunt DF, Kittlesen D, Slingluff CL;  
 DR WPI; 1998-437388/37.  
 XX  
 PT Disease specific immunogen - comprises disease specific cytotoxic T  
 PT lymphocyte epitope used to elicit melanoma specific CTL response  
 PS  
 XX Disclosure; Page 27; 93pp; English.  
 CC The peptide epitope AAW77119-W77138 were created for human  
 CC tumour-specific cytotoxic T lymphocyte response. These peptides are  
 CC cysteine-depleted mutants of a native disease-specific CTL epitope. The  
 CC cysteine-depleted CTL epitopes elicit a stronger or more specific CTL  
 CC response than the native epitope. The epitopes can be used in a  
 CC disease-specific immunogen to protect a mammal against disease in  
 CC particular melanomas. The peptides may also be used to screen a sample  
 CC for the presence of an antigen with the same epitope, or with a different  
 CC cross-reactive epitope.  
 CC  
 XX  
 SQ Sequence 9 AA;  
 Query Match 93.1%; Score 54; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMQV 9  
 DB 1 KTMGQYMQV 9

RESULT 13  
 AAW78850  
 ID AAW78850 standard; peptide; 9 AA.  
 AC AAW78850;  
 XX  
 DT 17-NOV-1998 (first entry)  
 XX  
 DE PMEL 17 (GP100) protein fragment 154-162.  
 XX  
 KM Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;  
 KM class II associated peptide; pathogen; gene therapy; genetic disease;  
 KM infection; downregulation; immune response.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO9831398-A1.  
 PD 23-JUL-1998.  
 PF 22-JAN-1998; 98WO-US01499.  
 PR 06-JAN-1998; 98US-0003253.  
 PR 22-JAN-1997; 97US-0787547.  
 PA (PANG-) PANGAEA PHARM INC.  
 PI Curley JM, Hedley ML, Langer RS, Lunsford LB;  
 DR WPI; 1998-427556/36.  
 XX  
 PT New preparations of microparticles - comprising a synthetic polymer  
 PT matrix and nucleic acid comprising an expression vector for use in  
 PT gene therapy  
 PS  
 XX Disclosure; Page 10; 101pp; English.  
 CC A microparticle preparation (MP) has been developed, consisting of  
 CC microparticles having a diameter of less than 100 nm. The MP  
 CC comprises: (a) a polymeric matrix (PM) consisting of one or more  
 CC synthetic polymers having a solubility in water of less than 1 mg/l; and  
 CC (b) an expression vector selected from RNA molecules (at least 50% of  
 CC which are closed circles) or circular plasmid DNA (at least 50% of which  
 CC are supercoiled). Also described is a MP of at most 20 microns in  
 CC diameter, comprising: (a) a PM; and (b) a NAM comprising an expression  
 CC control sequence operatively linked to a coding sequence, where the  
 CC coding sequence encodes an expression product selected from: (1) a  
 CC polypeptide at least 7 amino acids in length, having a sequence identical  
 CC to the sequence of: (i) a fragment of a naturally-occurring mammalian  
 CC protein; or (ii) a fragment of a naturally-occurring protein from an  
 CC infectious agent which infects a mammal; (2) a peptide having a length  
 CC and sequence which permits it to bind to an MHC class I or II molecule;  
 CC and (3) the polypeptide or the peptide linked to a trafficking sequence.  
 CC AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for  
 CC use in the present invention. The MPs are highly effective vehicles for  
 CC the delivery of polynucleotides into phagocytic cells. They can be used  
 CC for gene therapy, e.g. for treating genetic diseases, infections or  
 CC tumours or for downregulating an immune response.  
 CC  
 XX  
 SQ Sequence 9 AA;  
 Query Match 93.1%; Score 54; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMQV 9  
 DB 1 KTMGQYMQV 9

DB 1 KTWGQYMOV 9

RESULT 14  
AAW70010  
ID AAW70010 standard; peptide; 9 AA.

XX  
AC AAW70010;  
XX  
DT 22-OCT-1998 (first entry)  
XX  
DE Melanoma-associated antigen gp100 derived HLA-A2.1 binding peptide 1.

XX  
XX Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
XX human leukocyte antigen; HLA; tumour associated antigen; cancer;  
XX antigen presenting cell; APC; immunogenic peptide; immune disorder;  
XX viral infection; AIDS; hepatitis; bacterial infection; malaria;  
XX fungal infection; tuberculosis; melanoma; gp100.

XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX W09833888-A1.  
XX  
XX 06-AUG-1998.  
XX  
XX 30-JAN-1998; 98WO-US01959.  
XX  
XX 31-JAN-1997; 97US-0036696.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Cells B, Sette A, Sidney J, Southwood S, Teal V;  
XX  
XX WPI; 1998-437445/37.

DR  
XX  
XX Production of antigen-specific cytotoxic T cells - by incubating  
PT immunogenic peptide(s) from antigen that binds class I major  
PT histocompatibility complex molecules with pre-treated antigen  
PT presenting cells  
XX  
XX  
XX Example 4; Page 62; 104pp; English.

XX  
XX Sequences shown in AAW70010 to AAW70026 represent peptides derived from  
CC melanoma-associated antigen gp100 that can bind to a human leukocyte  
CC antigen (HLA), HLA-A2.1. The peptides are used to exemplify the method  
CC of invention of producing antigen-specific cytotoxic T cells (CTLs) in  
CC vitro. The method comprises contacting immunogenic peptides from an  
CC antigen that binds class I major histocompatibility complex (MHC)  
CC molecules with antigen presenting cells (APCs) pretreated with  
CC pretreatment growth factors, and incubating the APCs with purified CD8  
CC cells in the presence of at least 2 incubation growth factors, thereby  
CC producing antigen-specific CTLs. A method for specifically killing  
CC target cells in a human patient is also provided which comprises  
CC obtaining a fluid sample containing CTLs from a patient, contacting the  
CC cytotoxic T cells with APCs pretreated with pre-treatment growth  
CC factors, where the APCs comprise class I MHC molecules. The pretreated  
CC APCs are incubated with the cytotoxic growth factors, thereby producing  
CC activated CTLs which are contacted with a carrier to form a composition.  
CC The composition can then be administered to the patient. The activated  
CC CTLs can be used for treating cancers, immune disorders, viral  
CC infections, AIDS, hepatitis, bacterial infection, fungal infection,  
CC malaria or tuberculosis.

XX  
XX  
SQ Sequence 9 AA;

Query Match 93.1%; Score 54; DB 19; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9  
DB 1 KTWGQYMOV 9

RESULT 15  
AAW54598  
ID AAW54598 standard; peptide; 9 AA.

XX  
AC AAW54598;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Peptide 3 from gp 100/Pmel-17.

XX  
XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
XX vaccine; treatment.  
XX  
OS Synthetic.  
XX  
XX W09813378-A1.  
XX  
XX  
XX 02-APR-1998.  
XX  
XX 25-SEP-1997; 97WO-NL00536.  
XX  
XX 26-SEP-1996; 96EP-0202701.  
XX  
XX (VYLE-) RIJCKSUNIV LEIDEN.  
XX  
XX Drifhout JW, Konig F;  
XX  
XX WPI; 1998-230631/20.

DR  
XX  
XX Increasing uptake and presentation of antigen(s) - by adding mannose  
PT residue(s) to antigen for increasing T cell response, useful in,  
PT e.g. vaccines against viral infection(s)  
XX  
XX  
XX Disclosure; Page 24; 47pp; English.

XX  
XX The peptides AAW54598-W54809 are examples of peptides to which at least  
CC 1 (preferably 2) mannose can be attached to increase their uptake as  
CC antigens by antigen-presenting cells. Uptake of agonist mannosylated  
CC peptides will increase the T cell response, whereas uptake of antagonist  
CC peptides blocks the T cell response. Blocking binding of immunogenic  
CC autoantigens can be used in treatment of type I diabetes, rheumatoid  
CC arthritis, graft rejection etc., also to induce T-cell non-  
CC responsiveness. Vaccines containing mannosylated antigen are used to  
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths  
CC and parasites.

XX  
XX  
SQ Sequence 9 AA;

Query Match 93.1%; Score 54; DB 19; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMOV 9  
DB 1 KTWGQYMOV 9

RESULT 16  
AAW42536  
ID AAW42536 standard; peptide; 9 AA.

XX  
AC AAW42536;  
XX  
XX  
XX 22-JUN-1998 (first entry)  
XX  
DE Gp 100 epitope (residues 154-162) analogue #2.

XX  
XX Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;  
XX antigen; CTL; immunogenic; viral disease; gp 100; Melan A/MART-1.  
XX  
XX Synthetic.

OS Homo sapiens.  
 XX WO9802538-A1.  
 XX 22-JAN-1998.  
 PD 08-JUL-1997; 97WO-EP03712.  
 XX 11-JUL-1996; 96EP-0201945.  
 XX (ALKU) AKZO NOBEL NV.  
 PA Adema GJ, Figdor CG;  
 XX WPI, 1998-110586/10.  
 DR Melanoma associated peptide analogues - useful in vaccines against  
 XX melanoma  
 PT Example 1; Page 28; 47pp; English.  
 PS This sequence is shown in the specification. The invention relates to  
 CC peptides, which are immunogenic with lymphocytes directed against  
 CC metastatic melanomas. They are characterised in that they comprise at  
 CC least a part of the following sequence, where the amino acid at position  
 CC 2 or 8 is substituted: Lys-Thr-Tyr-Gly-Gln-Tyr-Tyr-Gln-Val. Vaccines  
 CC comprising the peptide, an epitope of the peptide, nucleotide sequence  
 CC encoding the peptide, or an antigen presenting cell preloaded with the  
 CC peptide or antibody as above, are useful for cancer, particularly  
 CC melanoma, treatment. The peptides can also be used to generate antigen  
 CC reactive tumour infiltrating lymphocytes, which can also be used in  
 CC vaccines. The peptides can be exploited to elicit native epitope-reactive  
 CC CTL. Usage of the peptides with improved immunogenicity may contribute  
 CC to the development of CTL-epitope based vaccines in viral disease and  
 CC cancer.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 93.1%; Score 54; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KVMGQYMOV 9  
 | | | | | | | |  
 1 KAMGQYMOV 9  
 DB  
 RESULT 17  
 AAM45770  
 ID AAM45770 standard; peptide; 9 AA.  
 XX  
 AC AAM45770;  
 XX  
 DT 22-JUN-1998 (first entry)  
 XX  
 DE Melanoma associated peptide analogue #1.  
 XX  
 KW Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;  
 KW antigen; CTL; immunogenic; viral disease.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9802538-A1.  
 XX  
 PD 22-JAN-1998.  
 XX  
 PF 08-JUL-1997; 97WO-EP03712.  
 XX  
 PR 11-JUL-1996; 96EP-0201945.  
 XX  
 PA (ALKU) AKZO NOBEL NV.  
 XX

PI Adema GJ, Figdor CG;  
 XX WPI, 1998-110586/10.  
 DR Melanoma associated peptide analogues - useful in vaccines against  
 PT melanoma  
 XX  
 PS Claim 1; Figure 1; 47pp; English.  
 CC This sequence represents a specifically claimed example of a novel  
 CC peptide, which is immunogenic with lymphocytes directed against  
 CC metastatic melanomas. It is characterised in that it comprises at least  
 CC a part of the following sequence, where the amino acid at position 2 or 8  
 CC is substituted: Lys-Thr-Tyr-Gly-Gln-Tyr-Tyr-Gln-Val. Vaccines comprising  
 CC the peptide, an epitope of the peptide, nucleotide sequence encoding the  
 CC peptide, or an antigen presenting cell preloaded with the peptide or  
 CC antibody as above, are useful for cancer, particularly melanoma,  
 CC treatment. The peptides can also be used to generate antigen reactive  
 CC tumour infiltrating lymphocytes, which can also be used in vaccines. The  
 CC peptides can be exploited to elicit native epitope-reactive CTL. Usage  
 CC of the peptides with improved immunogenicity may contribute to the  
 CC development of CTL-epitope based vaccines in viral disease and cancer.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 93.1%; Score 54; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KVMGQYMOV 9  
 | | | | | | | |  
 1 KTWGQYMOV 9  
 DB  
 RESULT 18  
 AAY49663  
 ID AAY49663 standard; peptide; 9 AA.  
 XX  
 AC AAY49663;  
 XX  
 DT 14-JAN-2000 (first entry)  
 XX  
 DE Tumour antigenic peptide SEQ ID NO:30.  
 XX  
 KW Human; sdp3.10; SAGE; sdp3.8; HAGE; sdp3.5; TRAP; sarcoma;  
 KW tumour rejection antigen precursor; tumour associated nucleic acid;  
 KW carcinoma; cancer; immune response; diagnosis.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9953061-A2.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 14-APR-1999; 99WO-US08163.  
 XX  
 PR 15-APR-1998; 98US-0060706.  
 PR 27-JUL-1998; 98US-01222989.  
 PR 30-OCT-1998; 98US-0183706.  
 PR 30-OCT-1998; 98US-0183789.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Martelange V, De Smet C, Boon-Falleur T;  
 XX  
 DR WPI, 1999-620430/53.  
 XX  
 PF New nucleic acid encoding sarcoma-associated gene products, useful for  
 PT diagnosing, e.g. treating and preventing cancer  
 XX  
 PS Disclosure; Page 25; 93pp; English.  
 XX  
 CC The present invention describes sarcoma-associated gene products (I).

CC Agents, specifically sarcoma associated nucleic acids (II) or their  
CC expression products that are tumour rejection antigens (TRA), that  
CC selectively increase formation of HLA (human leucocyte antigen)/(I)  
CC complexes are used for treating cancer, especially sarcoma and  
CC carcinoma, in humans and other animals. Compositions containing  
CC autologous cytolytic T cells (CTL), specific for the HLA(I) complex,  
CC are similarly useful, also transformed cells that stimulate such CTL  
CC in vivo. (II) are also used: (i) as source of therapeutic antisense  
CC sequences that reduce expression of (II); (ii) for recombinant  
CC production of (i); (iii) particularly its fragments, as primers and  
CC probes in usual hybridisation and amplification assays, for diagnosis,  
CC prognosis and monitoring of tumours, or for measuring binding  
CC specificity of HLA molecules or CTL clones; (iv) to identify related  
CC sequences; and (v) for generating transgenic animals, e.g. for studying  
CC cancer and immune responses to it. (I) are used to raise specific  
CC antibodies (Ab) and therapeutically. Ab are used to diagnose tumours in  
CC immunosays, also for delivering drugs, toxins, imaging agents etc. to  
CC (I)-expressing cells. AAY49637 to AAY49670 represent exemplary tumour  
CC antigenic peptides given in the present invention.

CC Sequence 9 AA;

Query Match 93.1%; Score 54; DB 20; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYQOV 9  
| | | | |  
Db 1 KTMGQYQOV 9

RESULT 19  
AAY3524  
ID AAY3524 standard; Protein; 9 AA.

AAV5324;

18-JAN-2000 (first entry)

Human melanoma Pmel17 (gp100) (aa 154-162) binds HLA-A2.

Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;  
electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;  
human immunodeficiency virus; hepatitis B virus; papilloma virus;  
melanoma; malaria; parasite.

Synthetic.  
Homo sapiens.

FR276926-A1.

08-OCT-1999.

07-APR-1998; 98FR-0004323.

07-APR-1998; 98FR-0004323.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

(CNRS) CNRS CENT NAT RECH SCI.

(INSP) INST PASTEUR LILLE.

Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;

WPI; 1999-563113/50.

New lipopeptide containing lipid regions and two epitopes, all  
separated by peptide spacers that impart hydrophilicity, useful in-

Dis disclosure; Page 24; 35pp; French.

The invention relates to the generation of a lipopeptide comprising at  
least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)

CC epitope and at least one lipid residue with (i) the epitopes and lipid  
CC portion and (ii) the epitopes, being separated independently by peptide  
CC spacers. These spacers comprise sequences of amino acids which carry an  
CC overall electrical charge in neutral media to ensure that the  
CC lipopeptide is hydrophilic. The peptides AAY3301-Y3359 represents  
CC examples of peptide epitopes used to generate the lipopeptides. These are  
CC used in therapeutic or prophylactic compositions and vaccines to induce  
CC specific immune responses against human immunodeficiency, hepatitis B or  
CC papilloma viruses; p53 of melanoma or the malaria parasite.

CC Sequence 9 AA;

Query Match 93.1%; Score 54; DB 20; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYQOV 9  
| | | | |  
Db 1 KTMGQYQOV 9

RESULT 20

AAY47616  
ID AAY47616 standard; Peptide; 9 AA.

AAV47616;

01-DEC-1999 (first entry)

Immunogenic peptide having a human leukocyte antigen binding motif #2227.

Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
immune response; T cell activation; major histocompatibility complex;  
cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
vaccine; immunisation.

Synthetic.

Homo sapiens.

WO9945954-A1.

16-SEP-1999.

13-MAR-1998; 98WO-US05039.

13-MAR-1998; 98WO-US05039.

(EPIM-) EPIMUNE INC.

Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

WPI; 1999-551214/46.

New immunogenic peptides with HLA binding motif, useful in treatment  
and diagnosis of cancers and viral diseases -

Claim 1; Page 116; 150pp; English.

AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
having a human major histocompatibility complex (MHC) Class I (also  
known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
normally induced by an antigen in the form of a peptide fragment bound  
to a HLA molecule, rather than the intact foreign antigen itself, and  
are particularly important in tumour rejection and in fighting viral  
infections. The peptides are therefore useful therapeutically to treat  
or prevent viral infections and cancers in mammals (especially humans)  
e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
They can be administered as vaccines to elicit an immune response in

CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.

CC Sequence 9 AA;

Query Match 93.1%; Score 54; DB 20; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
 Db 1 KTMGQYMOV 9

RESULT 21

AAV33172  
 ID AAY33172 standard; peptide; 9 AA.

AC AAY33172;

DT 17-NOV-1999 (first entry)

DE Human gp100-Pmel17 peptide #1.

KM Human; protein delivery; Yersinia sp.; effector gene; mutant; antigen;  
 KM immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;  
 KM pathological disorder; gp100-Pmel17.

OS Homo sapiens.

XX WO945098-A2.

PD 10-SEP-1999.

PE 03-MAR-1999; 99WO-1B00587.

PR 06-MAR-1998; 98US-0036582.

PA (VBRU/) VAN DER BRUGGEN P B.

PA (CORN/) CORNELIS G R.

PA (BOLA/) BOLAND A M.

PA (BOON/) BOON-FALLEUR T R.

PI Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Falleur TR;

DR WPI; 1999-540840/45.

XX New mutant Yersinia strains useful for treating a pathological disorder

PS Example 1; Page 71; 80pp; English.

CC This invention describes a novel mutant Yersinia (Y1) strain, comprising  
 CC mutation(s) in effector-encoding gene(s) and deficient in the production  
 CC of functional effector protein(s). The invention describes (1) a  
 CC quintuple mutant Yersinia strain, having the designation Yersinia  
 CC enterocolitica yopEHOMP or Yersinia pseudotuberculosis yopEHOMJ; (2) an  
 CC expression vector (EV1) for delivering a heterologous protein into a  
 CC eukaryotic cell, comprising in the 5'-3' direction: (3) a Yersinia or  
 CC mutant Yersinia strain for delivering a heterologous protein into a  
 CC eukaryotic cell, comprising contacting the cell with a Y1 transformed  
 CC with the above vector (Y1-EV1); (4) a method for delivering a  
 CC heterologous protein into a eukaryotic cell, comprising contacting the  
 CC cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method  
 CC for inducing an immune response specific for a heterologous protein; (6)  
 CC a method for inducing a cytotoxic T-lymphocyte (CTL) response specific  
 CC for a heterologous protein; (7) a method for determining the efficacy of  
 CC an antigen vaccination regimen in a subject. Y1 is used to treat a  
 CC pathological disorder, by providing recombinant Yersinia for the safe

CC delivery of proteins into eukaryotic cells. AAY33147-Y33178 are  
 CC human-derived peptides used to illustrate the method of the invention.

CC Sequence 9 AA;

Query Match 93.1%; Score 54; DB 20; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
 Db 1 KTMGQYMOV 9

RESULT 22

AAV40211  
 ID AAY40211 standard; Peptide; 9 AA.

AC AAY40211;

DT 19-NOV-1999 (first entry)

DE Amino acid sequence of a human melanoma epitope.

KM Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;  
 KM CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
 KM vaccine; tumor; infection; immune response; cytokine profile;  
 KM acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
 KM autoimmune disease.

OS Homo sapiens.

XX FR274687-A1.

PD 13-AUG-1999.

PE 06-FEB-1998; 98FR-0001439.

PR 06-FEB-1998; 98FR-0001439.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP ) INST PASTEUR LITTE.

PI Thiam K, Guillet JG, Ver Maerde C, Auriault C, Gras MH, Loing E;

DR WPI; 1999-510734/43.

XX New lipopeptide comprising C-terminal interferon-gamma fragment with

PT attached lipophilic groups, used as interferon mimic, e.g. for treating

PT cancer or virus infection

XX Disclosure; Page 35; 53pp; French.

CC AAY40123-Y40379 represent epitopes that are able to activate cytotoxic  
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or  
 CC B epitopes recognized by corresponding antibodies. The epitopes may be  
 CC used in the composition of the invention. The specification describes a  
 CC lipopeptide that has a peptide part derived from mammalian interferon  
 CC gamma (IFN $\gamma$ ) and one or more lipophilic parts comprising a linear or  
 CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The  
 CC lipopeptide mimics the activity of IFN $\gamma$ . Compositions comprising the  
 CC lipopeptide are used to treat or prevent any condition that responds  
 CC to IFN $\gamma$ , and as adjuvant for vaccines (particularly those directed  
 CC against tumors, viral or parasitic infections), to stimulate or  
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.  
 CC Particular applications are treatment of infections (particularly  
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and  
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers  
 CC (particularly of kidney, cutaneous T cells or ovary, chronic  
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune  
 CC diseases.  
 CC Sequence 9 AA;

Query Match 93.1%; Score 54; DB 20; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYQV 9  
 DB 1 KTMGQYQV 9

## RESULT 23

AA026867 standard; peptide; 9 AA.

XX AAY26867;

DT 14-SEP-1999 (first entry)

XX Melanoma-derived lipopeptide epitope #8 for mixed micelles.

XX Micelle; microaggregate; induction; immune response; lipopeptide; CTL;

KM cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;

KM tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;

XX melanoma; Plasmodium falciparum; malaria.

XX Synthetic.

OS Homo sapiens.

XX FR2771640-A1.

XX 04-JUN-1999.

XX 03-DEC-1997; 97FR-0015246.

XX 03-DEC-1997; 97FR-0015246.

XX (CNRS ) CNRS CENT NAT RECH SCI.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PI (INSP ) INST PASTEUR LILLE.

XX Bousus M, Bourgaud VT, Gras-Masse H, Guillet JG, Lippens G;

XX Tatar A, Wierszkecki JM;

XX WPI; 1999-349509/30.

XX Immunogenic lipopeptide micelles - comprising lipopeptides

PT containing cytotoxic and helper T-lymphocyte epitopes

XX Disclosure; Page 37; 60pp; French.

XX The invention relates to the generation of mixed micelles or

CC microaggregates for inducing an immune response comprising: (a) a first

CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope

CC and at least one lipid unit; and (b) a second lipopeptide comprising at

CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit

CC different from that of the first lipopeptide. This peptide represents

CC an example of a lipopeptide epitope used in the invention and is derived

CC from a human melanoma protein. The immunogenic lipopeptide micelles

CC are used in vaccines, especially against HIV, hepatitis B virus (HBV),

CC papilloma viruses, p53, melanoma or Plasmodium falciparum malaria.

XX Sequence 9 AA;

XX Query Match 93.1%; Score 54; DB 20; Length 9;

XX Best Local Similarity 88.9%; Pred. No. 9.3e+05;

XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYQV 9

DB 1 KTMGQYQV 9

## RESULT 24

AA01753 standard; peptide; 9 AA.

XX AAY01753;

DT 25-JUN-1999 (first entry)

XX Exemplary antigenic peptide derived from gp100(Pmel117).

KM MAGE-3; tumour associated gene; human leucocyte antigen Class II;

KM autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;

XX osteosarcoma; leukemia; carcinoma.

XX Homo sapiens.

XX WO9914326-A1.

XX 25-MAR-1999.

XX 04-SEP-1998; 98WO-US18601.

XX 12-SEP-1997; 97US-0928615.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYVR-) UNIV VIRIE BRUSSEL.

XX Boon-Falleur T, Chau P, Corthals J, Heiman C;

XX Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;

XX WPI; 1999-244031/20.

XX Isolated peptides that bind to human leucocyte antigen class II

XX molecules

XX Disclosure; Page 29; 86pp; English.

XX The present sequence represents an exemplary tumour associated peptide

CC antigen. The specification describes a MAGE-3 tumour associated gene.

CC Peptides (AA01721-25) that bind human leucocyte antigen (HLA) Class II

CC molecules can be derived from the MAGE-3 protein. These peptides and

CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide

CC and HLA Class II, are used to treat MAGE-3 related diseases,

CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and

CC various forms of carcinoma). The peptides are also used to produce

CC specific antibodies. Detection of of the peptides, e.g. in binding

CC assays, particularly with antibodies, is used for diagnosis of such

XX diseases.

XX Sequence 9 AA;

XX Query Match 93.1%; Score 54; DB 20; Length 9;

XX Best Local Similarity 88.9%; Pred. No. 9.3e+05;

XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYQV 9

DB 1 KTMGQYQV 9

RESULT 25  
 AA00715 standard; peptide; 9 AA.

XX AAY00715;

DT 12-MAY-1999 (first entry)

XX Tumour antigen booster peptide gp100Pmel117 HLA-A2 #1.

XX Tumour antigen, booster peptide; immune response modulation; allergy;

KM immune response enhancer; tumour cell; tumour rejection antigen;

KM leukocyte antigen-presenting molecule; autoimmune disease;

XX allograft rejection.

```

XX Homo sapiens.
OS
XX WO9858956-A2.
XX
XX 30-DEC-1998.
XX
XX 19-JUN-1998; 98WO-US12894.
XX
XX 23-JUN-1997; 97US-0880979.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon-Falleur T, Uytendhove C, Warnier G;
XX
XX WPI: 1999-105612/09.
XX
XX Immunization methods using viruses expressing antigen for priming
XX and booster immunizations - useful for modulating immune responses
XX against antigen, e.g. enhancing immune response against tumour cells
XX expressing tumour rejection antigens
XX
XX Disclosure: Page 10; 33pp; English.
XX
XX This sequence represents a tumour antigen booster peptide that can be
XX used in the method of the invention. The method is for for modulating an
XX immune response in a mammal against an antigen, and comprises:
XX (A) inducing an immune response by: (i) administering a virus containing
XX a nucleic acid molecule encoding the antigen or its precursor to generate
XX an immune response; and (ii) administering at least one booster dose
XX comprising a peptide including the antigen, in an adjuvant, in a combined
XX amount effective to enhance the initial immune response; or
XX (B) reducing an immune response as defined for (A) but using a
XX non-adjuvant with the peptide which includes the antigen in an amount
XX effective to reduce the initial immune response. Method (A) is used to
XX enhance the immune response against tumour cells expressing tumour
XX rejection antigens, and against pathogens in subjects having human
XX leukocyte antigen-presenting molecules. Method (B) is used to reduce the
XX immune response in allergy, autoimmune disease, and allograft rejection.
XX Method (A) provides an immunisation method which, unlike prior art, is
XX not limited by the host immune response against viral vectors.
XX
XX Sequence 9 AA;
XX
XX Query Match 93.1%; Score 54; DB 20; Length 9;
XX Best Local Similarity 88.9%; Pred No. 9.3e+05;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 KVMGQYMOV 9
XX | | | | |
XX 1 KTMGQYMOV 9

```

Search completed: August 14, 2003, 09:11:30  
 Job time : 37 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 20.5 seconds  
(without alignments)  
18.575 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KVMGQYQV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database :

1: Issued Patents\_Aa.\*  
2: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	98.3	9	2	US-08-417-174-70
2	57	98.3	9	3	US-09-267-439-70
3	57	98.3	9	4	US-09-073-138-70
4	55	94.8	9	2	US-08-417-174-68
5	55	94.8	9	2	US-08-417-174-69
6	55	94.8	9	3	US-09-267-439-68
7	55	94.8	9	3	US-09-267-439-69
8	55	94.8	9	4	US-09-073-138-68
9	55	94.8	9	4	US-09-073-138-69
10	54	93.1	9	1	US-08-787-547-61
11	54	93.1	9	2	US-08-417-174-46
12	54	93.1	9	2	US-08-902-516-29
13	54	93.1	9	2	US-09-036-582-26
14	54	93.1	9	3	US-09-183-706-30
15	54	93.1	9	3	US-09-267-439-46
16	54	93.1	9	3	US-09-166-448-71
17	54	93.1	9	4	US-09-567-995-30
18	54	93.1	9	4	US-09-165-863-26
19	54	93.1	9	4	US-09-697-884-71
20	54	93.1	9	4	US-09-847-185-29
21	54	93.1	9	4	US-08-388-8528-22
22	54	93.1	9	4	US-09-289-350-26
23	54	93.1	9	4	US-09-073-138-46
24	54	93.1	9	4	US-09-574-749B-27
25	54	93.1	9	4	US-09-341-962-82
26	54	93.1	10	2	US-08-417-174-47
27	54	93.1	10	3	US-09-267-439-47

28	54	93.1	10	4	US-08-388-8528-21	Sequence 21, App1
29	54	93.1	10	4	US-09-073-138-47	Sequence 47, App1
30	54	93.1	11	4	US-08-388-8528-20	Sequence 20, App1
31	54	93.1	12	4	US-08-388-8528-10	Sequence 10, App1
32	54	93.1	661	2	US-08-417-174-121	Sequence 121, App
33	54	93.1	661	3	US-09-267-439-121	Sequence 121, App
34	54	93.1	661	4	US-08-388-8528-2	Sequence 2, App1
35	54	93.1	661	4	US-09-073-138-121	Sequence 121, App
36	54	93.1	668	4	US-07-891-942G-6	Sequence 6, App1
37	50	86.2	9	2	US-08-417-174-78	Sequence 78, App1
38	50	86.2	9	2	US-08-417-174-79	Sequence 79, App1
39	50	86.2	9	2	US-08-417-174-80	Sequence 80, App1
40	50	86.2	9	2	US-08-417-174-81	Sequence 81, App1
41	50	86.2	9	2	US-08-417-174-82	Sequence 82, App1
42	50	86.2	9	3	US-09-267-439-78	Sequence 78, App1
43	50	86.2	9	3	US-09-267-439-79	Sequence 79, App1
44	50	86.2	9	3	US-09-267-439-80	Sequence 80, App1
45	50	86.2	9	3	US-09-267-439-81	Sequence 81, App1

## ALIGNMENTS

RESULT 1  
US-08-417-174-70  
Sequence 70, Application US/08417174  
Patent No. 5844075  
GENERAL INFORMATION:  
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/417.174  
FILING DATE: 05-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/231.565  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPE  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-08-417-174-70  
Query Match 98.3%; Score 57; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

Oy 1 KVMGYMOV 9  
|:|||||  
Db 1 KIMGYMOV 9

## RESULT 2

US-09-267-439-70  
; Sequence 70, Application US/09267439  
; Patent No. 6270778

## GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439  
FILING DATE:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994

## ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341

## REFERENCE/DOCKET NUMBER: 2026-4124US1

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

TELEX: 421792

## INFORMATION FOR SEQ ID NO: 70:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-09-267-439-70

Query Match 98.3%; Score 57; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;

Matches .8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVMGYMOV 9  
|:|||||  
Db 1 KIMGYMOV 9

## RESULT 3

US-09-073-138-70

; Sequence 70, Application US/09073138  
; Patent No. 6537560

## GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,138  
FILING DATE:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

TELEX: 421792

## INFORMATION FOR SEQ ID NO: 70:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-09-073-138-70

Query Match 98.3%; Score 57; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVMGYMOV 9  
|:|||||  
Db 1 KIMGYMOV 9

## RESULT 4

US-08-417-174-68

; Sequence 68, Application US/08417174  
; Patent No. 5844075

## GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

US-08-417-174-68

; Sequence 68, Application US/08417174  
; Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-08-417-174-68

Query Match 94.8%; Score 55; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWMGQYQV 9  
|:|||||  
Db 1 KLMGQYQV 9

RESULT 5  
US-08-417-174-69  
Sequence 69, Application US/08417174  
Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide  
US-08-417-174-69

Query Match 94.8%; Score 55; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWMGQYQV 9  
|:|||||  
Db 1 KLMGQYQV 9

RESULT 6  
US-09-267-439-68

Sequence 68, Application US/09267439  
Patent No. 6270778

GENERAL INFORMATION:

APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & PINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439  
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-09-267-439-68

Query Match 94.8%; Score 55; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWMGQYQV 9  
|:|||||  
Db 1 KLMGQYQV 9

RESULT 7  
US-09-267-439-69

Sequence 69, Application US/09267439  
Patent No. 6270778

GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-09-267-439-69

Query Match 94.8%; Score 55; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVMGQYQV 9  
Db 1 KVMGQYQV 9

RESULT 8  
US-09-073-138-68  
Sequence 68, Application US/09073138  
Patent No. 6537560  
GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,138  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-09-073-138-68

Query Match 94.8%; Score 55; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVMGQYQV 9  
Db 1 KVMGQYQV 9

RESULT 9  
US-09-073-138-69  
Sequence 69, Application US/09073138  
Patent No. 6537560  
GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,138  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

TELEX: 421792  
INFORMATION FOR SEQ ID NO: 69;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-09-073-138-69

Query Match 94.8%; Score 55; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWMGQYMOV 9  
Db 1 KWMGQYMOV 9

RESULT 10  
US-08-787-547-61  
Sequence 61, Application US/08787547  
Patent No. 5783567  
GENERAL INFORMATION:  
APPLICANT: Hedley, Mary Lynne  
APPLICANT: Curley, Joanne M.  
APPLICANT: Langer, Robert S.  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY  
TITLE OF INVENTION: OF NUCLEIC ACID  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/787,547  
FILING DATE: 22-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraiser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-787-547-61

Query Match 93.1%; Score 54; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWMGQYMOV 9  
Db 1 KWMGQYMOV 9

RESULT 11  
US-08-417-174-46  
Sequence 46, Application US/08417174  
Patent No. 5844075  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-08-417-174-46

Query Match 93.1%; Score 54; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWMGQYMOV 9  
Db 1 KWMGQYMOV 9

RESULT 12  
US-08-902-516-29  
Sequence 29, Application US/08902516  
Patent No. 5891432  
GENERAL INFORMATION:  
APPLICANT: Soo Hoo, William  
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
TITLE OF INVENTION: COMBINING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
TITLE OF INVENTION: RESPONSE USING SAME  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States

ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,516  
FILING DATE: 29-JUL-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-1M 2442  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-902-516-29

Query Match 93.1%; Score 54; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | |  
| | | | |  
Db 1 KTMGQYMOV 9

RESULT 13  
US-09-036-582-26  
Sequence 26, Application US/09036582A  
Patent No. 5965381  
GENERAL INFORMATION:  
APPLICANT: van der Bruggen, Pierre  
TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
TITLE OF INVENTION: WITH RECOMBINANT YERSINIA  
FILE REFERENCE: 11154  
CURRENT APPLICATION NUMBER: US/09/036,582A  
CURRENT FILING DATE: 1998-03-06  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 26  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Human gp100fme1117 peptide  
US-09-036-582-26

Query Match 93.1%; Score 54; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | |  
| | | | |  
Db 1 KTMGQYMOV 9

RESULT 14  
US-09-183-706-30  
Sequence 30, Application US/09183706  
Patent No. 6245525  
GENERAL INFORMATION:  
APPLICANT: Martelange, Valrie  
APPLICANT: De Smet, Charles  
APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
FILE REFERENCE: L0461/7054

CURRENT APPLICATION NUMBER: US/09/183,706  
CURRENT FILING DATE: 1998-10-30  
EARLIER APPLICATION NUMBER: 09/122,989  
EARLIER FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 43  
SEQ ID NO 30  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-183-706-30

Query Match 93.1%; Score 54; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | |  
| | | | |  
Db 1 KTMGQYMOV 9

RESULT 15  
US-09-267-439-46  
Sequence 46, Application US/09267439  
Patent No. 6270778  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPT  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-267-439-46

Query Match 93.1%; Score 54; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | |  
| | | | |  
Db 1 KTMGQYMOV 9

Db 1 KTWGQYMOV 9

RESULT 16  
US-09-166-448-71

; Sequence 71, Application US/09166448  
; Patent No. 6291430  
; GENERAL INFORMATION:  
; APPLICANT: Chaux, Pascal  
; APPLICANT: Vantomme, Valerie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Cortbals, Jurgen  
; TITLE OF INVENTION: MAG-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/09/166,448  
; CURRENT FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 71  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-166-448-71

Query Match 93.1%; Score 54; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9

RESULT 17  
US-09-567-995-30

; Sequence 30, Application US/09567995  
; Patent No. 6303756  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val,rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/567,995  
; CURRENT FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 30  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-567-995-30

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9

RESULT 18  
US-09-165-863-26

; Sequence 26, Application US/09165863  
; Patent No. 6407063  
; GENERAL INFORMATION:  
; APPLICANT: Lutten, Rosalie

; APPLICANT: Duffour, Marie-Therese  
; APPLICANT: Demotte, Nathalie  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Cornelis, Guy  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Lurquin, Christophe  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: Chaux, Pascal  
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
; FILE REFERENCE: 11727  
; CURRENT APPLICATION NUMBER: US/09/165,863  
; CURRENT FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human gp100Pmel117 peptide  
US-09-165-863-26

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9

RESULT 19  
US-09-697-884-71

; Sequence 71, Application US/09697884  
; Patent No. 6426217  
; GENERAL INFORMATION:  
; APPLICANT: Chaux, Pascal  
; APPLICANT: Vantomme, Val,rie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Cortbals, Jurgen  
; TITLE OF INVENTION: MAG-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L0461/7052  
; CURRENT APPLICATION NUMBER: US/09/697,884  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: 09/166,448  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 71  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-697-884-71

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMOV 9

RESULT 20  
US-09-847-185-29

; Sequence 29, Application US/09847185  
; Patent No. 6482407  
; GENERAL INFORMATION:  
; APPLICANT: Soo Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE

RESPONSE USING SAME

NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92121

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/847,185  
FILING DATE: 01-May-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/201,931  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-1M 2442

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-847-185-29

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | | | | | | |  
Db 1 KTMGQYMOV 9

RESULT 21  
US-08-388-852B-22  
Sequence 22, Application US/08388852B  
Patent No. 6500919

GENERAL INFORMATION:  
APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.  
TITLE OF INVENTION: Melanoma associated antigenic polypeptide,  
TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav  
STREET: Philips van Leydenlaan 25  
CITY: Nijmegen  
STATE: Brabant  
COUNTRY: the Netherlands  
ZIP: 6525 EX

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388 852B  
FILING DATE: February 15, 1995  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-08-388-852B-22

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | | | | | | |  
Db 1 KTMGQYMOV 9

RESULT 22  
US-09-289-350-26  
Sequence 26, Application US/09289350  
Patent No. 6531451

GENERAL INFORMATION:  
APPLICANT: Chaux, Pascal  
APPLICANT: Luiten, Rosalie  
APPLICANT: Demotte, Nathalie  
APPLICANT: Deffour, Marie-Therese  
APPLICANT: Lurquin, Christophe  
APPLICANT: Traversari, Catia  
APPLICANT: Stroobant, Vincent  
APPLICANT: Cornelis, Guy R.  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: Van Der Bruggen, Pierre

TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
TITLE OF INVENTION: PROCEDURE  
FILE REFERENCE: 117272  
CURRENT APPLICATION NUMBER: US/09/289,350  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 09/165,863  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Human gp100Pmel117 peptide  
US-09-289-350-26

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | | | | | | |  
Db 1 KTMGQYMOV 9

RESULT 23  
US-09-073-138-46  
Sequence 46, Application US/09073138  
Patent No. 6537560

GENERAL INFORMATION:  
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA



ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,138  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-09-073-138-46

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMWGQYQWV 9  
DB 1 KTWGQYQWV 9

RESULT 24  
US-09-574-749B-27  
Sequence 27, Application US/09574749B  
Patent No. 6548299  
GENERAL INFORMATION:  
APPLICANT: ROSENZWEIG, Michael  
APPLICANT: PYKEIT, Mark J.  
APPLICANT: SCADDEN, David T.  
APPLICANT: POZNANSKY, Mark C.  
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
FILE REFERENCE: C1005/7012/KA/ERG  
CURRENT APPLICATION NUMBER: US/09/574,749B  
CURRENT FILING DATE: 2002-05-31  
PRIOR APPLICATION NUMBER: US 60/107,972  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: PCT/US99/26795  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 09/524,749  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 27  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Homo Sapiens source  
US-09-574-749B-27

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMWGQYQWV 9  
DB 1 KTWGQYQWV 9

RESULT 25  
US-09-341-982-82  
Sequence 82, Application US/09341982  
Patent No. 6558671  
GENERAL INFORMATION:  
APPLICANT: SLINGLUFF, Craig L.  
APPLICANT: HUNT, Donald P.  
APPLICANT: ENGELHARD, Victor H.  
APPLICANT: KITLISEN, David  
TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
FILE REFERENCE: SLINGLUFF=3B  
CURRENT APPLICATION NUMBER: US/09/341,982  
CURRENT FILING DATE: 1999-09-20  
EARLIER APPLICATION NUMBER: PCT/US98/01592  
EARLIER FILING DATE: 1998-01-29  
EARLIER APPLICATION NUMBER: 60/037,781  
EARLIER FILING DATE: 1997-01-31  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 82  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
US-09-341-982-82

Query Match 93.1%; Score 54; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMWGQYQWV 9  
DB 1 KTWGQYQWV 9

Search completed: August 14, 2003, 09:08:01  
Job time : 21.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:07:19 ; Search time 153 Seconds  
(without alignments)  
7,706 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KWMQYQV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues  
Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCF\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/PCFUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	98.3	9	12	US-09-898-860-70 Sequence 70, Appl
2	55	94.8	9	12	US-09-898-860-68 Sequence 68, Appl
3	55	94.8	9	12	US-09-898-860-69 Sequence 69, Appl
4	54	93.1	9	9	US-09-847-185-29 Sequence 29, Appl
5	54	93.1	9	10	US-09-923-831-30 Sequence 30, Appl
6	54	93.1	9	10	US-09-766-889A-42 Sequence 42, Appl
7	54	93.1	9	10	US-09-909-860-61 Sequence 61, Appl
8	54	93.1	9	12	US-09-898-860-46 Sequence 46, Appl
9	54	93.1	9	14	US-10-106-487-2 Sequence 2, Appl
10	54	93.1	9	14	US-10-047-539-5 Sequence 5, Appl
11	54	93.1	9	15	US-10-080-013-5 Sequence 5, Appl
12	54	93.1	9	15	US-10-161-097-27 Sequence 27, Appl
13	54	93.1	9	15	US-10-224-286-29 Sequence 29, Appl
14	54	93.1	10	12	US-09-898-860-47 Sequence 47, Appl
15	54	93.1	92	14	US-10-106-487-24 Sequence 24, Appl

16	54	93.1	661	9	US-09-862-260A-2 Sequence 2, Appl
17	54	93.1	661	10	US-09-812-238B-2 Sequence 2, Appl
18	54	93.1	661	12	US-09-898-860-121 Sequence 121, Appl
19	54	93.1	661	15	US-10-207-655-77 Sequence 77, Appl
20	54	93.1	668	14	US-10-047-539-4 Sequence 4, Appl
21	50	86.2	9	12	US-09-898-860-78 Sequence 78, Appl
22	50	86.2	9	12	US-09-898-860-79 Sequence 79, Appl
23	50	86.2	9	12	US-09-898-860-80 Sequence 80, Appl
24	50	86.2	9	12	US-09-898-860-81 Sequence 81, Appl
25	50	86.2	9	12	US-09-898-860-82 Sequence 82, Appl
26	50	86.2	9	14	US-10-047-539-8 Sequence 8, Appl
27	50	86.2	626	14	US-10-047-539-2 Sequence 2, Appl
28	50	86.2	661	12	US-09-898-860-27 Sequence 27, Appl
29	49	84.5	9	12	US-09-898-860-71 Sequence 71, Appl
30	49	84.5	9	12	US-09-898-860-72 Sequence 72, Appl
31	49	84.5	9	12	US-09-898-860-73 Sequence 73, Appl
32	49	84.5	9	12	US-09-898-860-74 Sequence 74, Appl
33	49	84.5	9	12	US-09-898-860-75 Sequence 75, Appl
34	45	77.6	9	12	US-09-898-860-76 Sequence 76, Appl
35	44	75.9	9	12	US-09-898-860-77 Sequence 77, Appl
36	41	70.7	267	15	US-10-106-698-4732 Sequence 4732, Ap
37	41	70.7	756	9	US-09-796-872-15 Sequence 15, Appl
38	41	70.7	756	10	US-09-771-161A-232 Sequence 232, App
39	41	70.7	756	10	US-09-844-908-9 Sequence 9, Appl
40	41	70.7	756	10	US-09-844-988-9 Sequence 9, Appl
41	41	70.7	756	15	US-10-243-408-2 Sequence 2, Appl
42	41	70.7	756	15	US-10-338-462-9 Sequence 9, Appl
43	40	69.0	136	9	US-09-864-761-39224 Sequence 39224, A
44	39	67.2	165	15	US-10-156-761-12033 Sequence 12033, A
45	38	65.5	45	11	US-09-776-724A-257 Sequence 257, App

#### ALIGNMENTS

RESULT 1  
US-09-898-860-70  
Sequence 70, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA, ROSENBERG,  
STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898, 860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267, 439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417, 174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231, 565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPEI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-09-898-860-70

Query Match 98.3%; Score 57; DB 12; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
|:|||||  
Db 1 KVMGQYMOV 9

RESULT 2  
US-09-898-860-68  
; Sequence 68, Application US/09898860  
; Publication No. US2003014482A1  
; GENERAL INFORMATION:  
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
; STEVEN A.  
; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS  
; NUMBER OF SEQUENCES: 126  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & PINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994

## ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341

## REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792

## INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-898-860-68

Query Match 94.8%; Score 55; DB 12; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
|:|||||  
Db 1 KVMGQYMOV 9

RESULT 3  
US-09-898-860-69  
; Sequence 69, Application US/09898860  
; Publication No. US2003014482A1  
; GENERAL INFORMATION:  
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
; STEVEN A.  
; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS  
; NUMBER OF SEQUENCES: 126  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & PINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994

## ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341

## REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792

## INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-898-860-69

Query Match 94.8%; Score 55; DB 12; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
|:|||||  
Db 1 KVMGQYMOV 9

RESULT 4  
US-09-847-185-29  
; Sequence 29, Application US/09847185  
; Patent No. US20020076392A1

GENERAL INFORMATION:  
APPLICANT: Soo Hoo, William  
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
RESPONSE USING SAME  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/847,185  
FILING DATE: 01-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/201,931  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-1M 2442  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-847-185-29

Query Match 93.1%; Score 54; DB 9; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 KVMGQYMOV 9  
Db 1 KTMGQYMOV 9

RESULT 5  
US-09-923-831-30  
Sequence 30, Application US/09923831  
Patent No. US20020115142A1  
GENERAL INFORMATION:  
APPLICANT: Martelange, Val, tie  
APPLICANT: De Smet, Charles  
APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
FILE REFERENCE: L0461/7054  
CURRENT APPLICATION NUMBER: US/09/923,831  
CURRENT FILING DATE: 2001-08-07  
PRIOR APPLICATION NUMBER: 09/183,706  
PRIOR FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 43  
SEQ ID NO 30  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-923-831-30

Query Match 93.1%; Score 54; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 KVMGQYMOV 9  
Db 1 KTMGQYMOV 9

RESULT 6  
US-09-766-889A-42  
Sequence 42, Application US/09766889A  
Patent No. US2002016454A1  
GENERAL INFORMATION:  
APPLICANT: Luiten, Rosalie  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Stroobant, Vincent  
APPLICANT: Demotte, Nathalie  
APPLICANT: Schultze, Erwin  
TITLE OF INVENTION: WAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
FILE REFERENCE: L0461/7104  
CURRENT APPLICATION NUMBER: US/09/766,889A  
CURRENT FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 60/177,242  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: US 60/243,212  
PRIOR FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 42  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-766-889A-42

Query Match 93.1%; Score 54; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 KVMGQYMOV 9  
Db 1 KTMGQYMOV 9

RESULT 7  
US-09-909-460-61  
Sequence 61, Application US/09909460  
Publication No. US20020182258A1  
GENERAL INFORMATION:  
APPLICANT: Lunsford, Lynn B.  
APPLICANT: Putnam, David  
APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC  
FILE REFERENCE: 08191/014001  
CURRENT APPLICATION NUMBER: US/09/909,460  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-909-460-61

Query Match 93.1%; Score 54; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 KVMGQYMOV 9  
Db 1 KTMGQYMOV 9

RESULT 8  
US-09-898-860-46  
Sequence 46, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-898-860-46  
Query Match 93.1%; Score 54; DB 12; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | | | | | | |  
Db 1 KTMGQYMOV 9

RESULT 9  
US-10-106-487-2  
Sequence 2, Application US/10106487  
Publication No. US20020164721A1  
GENERAL INFORMATION:  
APPLICANT: FIRAT, HUSEYIN  
APPLICANT: LEMONNIER, FRANCOIS  
APPLICANT: LANGLADE-DEMOYEN, PIERRE  
APPLICANT: MICHEL, MARIE-LOUISE  
TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION  
TITLE OF INVENTION: OF

TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING  
TITLE OF INVENTION: HHD MICE  
FILE REFERENCE: 03495.0196 SEQUENCE LISTING  
CURRENT APPLICATION NUMBER: US/10/106,487  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: 09/675,673  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/158,356  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-106-487-2  
Query Match 93.1%; Score 54; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | | | | | | |  
Db 1 KTMGQYMOV 9

RESULT 10  
US-10-047-539-5  
Sequence 5, Application US/10047539  
Publication No. US20020177547A1  
GENERAL INFORMATION:  
APPLICANT: MOLLING, KARIN  
APPLICANT: PAVLOVIC, JOVAN  
APPLICANT: NARRATH, MICHAEL  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING  
TITLE OF INVENTION: CANCER  
FILE REFERENCE: VOS-27  
CURRENT APPLICATION NUMBER: US/10/047,539  
CURRENT FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
PRIOR FILING DATE: 2001-01-16  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-047-539-5  
Query Match 93.1%; Score 54; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | | | | | | |  
Db 1 KTMGQYMOV 9

RESULT 11  
US-10-080-013-5  
Sequence 5, Application US/10080013  
Publication No. US20030077248A1  
GENERAL INFORMATION:  
APPLICANT: Moriarty, Ann  
APPLICANT: Leturcq, Didier  
APPLICANT: Degraw, Juli  
APPLICANT: Heiskala, Marja  
APPLICANT: Peterson, Per  
APPLICANT: Jackson, Michael  
TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS  
FILE REFERENCE: ORT-1557  
CURRENT APPLICATION NUMBER: US/10/080,013  
CURRENT FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 5  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-080-013-5

Query Match 93.1%; Score 54; DB 15; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWMGQYQV 9  
 Db 1 KTMGQYQV 9

RESULT 12  
 US-10-161-097-27  
 Sequence 27, Application US/10161097  
 Publication No. US20030096404A1  
 GENERAL INFORMATION:  
 APPLICANT: ROSENZWEIG, Michael  
 APPLICANT: PYRETT, Mark J.  
 APPLICANT: SCADDEN, David T.  
 APPLICANT: POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 TITLE OF INVENTION: DEVICES  
 FILE REFERENCE: C1005/7012/Ka/ERG  
 CURRENT APPLICATION NUMBER: US/10/161,097  
 CURRENT FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US/09/574,749  
 PRIOR FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US 60/107,972  
 PRIOR FILING DATE: 1998-11-12  
 PRIOR APPLICATION NUMBER: PCT/US99/26795  
 PRIOR FILING DATE: 1999-11-12  
 PRIOR APPLICATION NUMBER: US 09/524,749  
 PRIOR FILING DATE: 2000-05-18  
 NUMBER OF SEQ ID NOS: 58  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO: 27  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Homo Sapiens source  
 US-10-161-097-27

Query Match 93.1%; Score 54; DB 15; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWMGQYQV 9  
 Db 1 KTMGQYQV 9

RESULT 13  
 US-10-224-286-29  
 Sequence 29, Application US/10224286  
 Publication No. US20030108517A1  
 GENERAL INFORMATION:  
 APPLICANT: Soo Hoo, William  
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 RESPONSE USING SAME  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego

STATE: California  
 COUNTRY: United States  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/224,286  
 FILING DATE: 19-Aug-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/902,516  
 FILING DATE: 29-JUL-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-1M 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)535-9001  
 TELEFAX: (619)535-8949  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
 US-10-224-286-29

Query Match 93.1%; Score 54; DB 15; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWMGQYQV 9  
 Db 1 KTMGQYQV 9

RESULT 14  
 US-09-898-860-47  
 Sequence 47, Application US/09898860  
 Publication No. US2003014482A1  
 GENERAL INFORMATION:  
 APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG, STEVEN A.  
 TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS  
 NUMBER OF SEQUENCES: 126  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/898,860  
 FILING DATE: 03-JUL-2001  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/267,439  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US/08/417,174  
 FILING DATE: 05-APR-1995  
 APPLICATION NUMBER: US/08/231,565  
 FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPE  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
US-09-898-860-47

Query Match 93.1%; Score 54; DB 12; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.064;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVMGQYQWV 9  
Db 1 KTWGQYQWV 9

RESULT 15  
US-10-106-487-24  
Sequence 24, Application US/10106487  
Publication No. US20020164721A1  
GENERAL INFORMATION:  
APPLICANT: FIRAT, HUSEYIN  
APPLICANT: LEMONNIER, FRANCOIS  
APPLICANT: LANGLADE-DEMOYEN, PIERRE  
APPLICANT: MICHEL, MARIE-LOUISE  
TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION  
TITLE OF INVENTION: OF  
TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING  
TITLE OF INVENTION: HHD MICE  
FILE REFERENCE: 03495.0196 SEQUENCE LISTING  
CURRENT APPLICATION NUMBER: US/10/106,487  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: 09/675,673  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/158,356  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-106-487-24

Query Match 93.1%; Score 54; DB 14; Length 92;  
Best Local Similarity 88.9%; Pred. No. 0.43;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVMGQYQWV 9  
Db 38 KTWGQYQWV 46

RESULT 16  
US-09-862-260A-2  
Sequence 2, Application US/09862260A  
Patent No. US20020082217A1  
GENERAL INFORMATION:  
APPLICANT: NICOLETTE, Charles A.  
TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
FILE REFERENCE: 126881210200  
CURRENT APPLICATION NUMBER: US/09/862,260A

CURRENT FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/208,955  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/267,877  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 661  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-862-260A-2

Query Match 93.1%; Score 54; DB 9; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVMGQYQWV 9  
Db 154 KTWGQYQWV 162

RESULT 17  
US-09-812-238B-2  
Sequence 2, Application US/09812238B  
Patent No. US20020169132A1  
GENERAL INFORMATION:  
APPLICANT: NICOLETTE, Charles  
TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
FILE REFERENCE: G2 2094.00  
CURRENT APPLICATION NUMBER: US/09/812,238B  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 661  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-812-238B-2

Query Match 93.1%; Score 54; DB 10; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVMGQYQWV 9  
Db 154 KTWGQYQWV 162

RESULT 18  
US-09-898-860-121  
Sequence 121, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/09/898, 860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267, 439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417, 174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231, 565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPT  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 661  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 121:  
US-09-898-860-121

Query Match 93.1% Score 54; DB 12; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | |  
Db 154 KTMGQYMOV 162

RESULT 19  
US-10-207-655-77  
Sequence 77, Application US/10207655  
Publication No. US20030118592A1  
GENERAL INFORMATION:  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Hayden-Ledbetter, Martha S.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390069, 401C1  
CURRENT APPLICATION NUMBER: US/10/207, 655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 77  
LENGTH: 661  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-207-655-77

Query Match 93.1% Score 54; DB 15; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | |  
Db 154 KTMGQYMOV 162

RESULT 20  
US-10-047-539-4  
Sequence 4, Application US/10047539  
Publication No. US20020177547A1  
GENERAL INFORMATION:  
APPLICANT: MOLLING, KARIN  
APPLICANT: PAYLOVIC, JOVAN  
APPLICANT: NAVRATH, MICHAEL  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING

TITLE OF INVENTION: CANCER  
FILE REFERENCE: VOS-27  
CURRENT APPLICATION NUMBER: US/10/047, 539  
CURRENT FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
PRIOR FILING DATE: 2001-01-16  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 668  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-047-539-4

Query Match 93.1% Score 54; DB 14; Length 668;  
Best Local Similarity 88.9%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMOV 9  
| | | | |  
Db 154 KTMGQYMOV 162

RESULT 21  
US-09-898-860-78  
Sequence 78, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG, STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCIT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898, 860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267, 439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417, 174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231, 565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPT  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 78:  
US-09-898-860-78

Query Match 86.2%; Score 50; DB 12; Length 9;  
Best Local Similarity 87.5%; Pred. No. 4.4e+05;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VWGQYQV 9  
:|||||  
Db 2 LMGQYQV 9

RESULT 22

US-09-898-860-79

; Sequence 79, Application US/09898860  
; Publication No. US20030144482A1

; GENERAL INFORMATION:

; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

; STEVEN A.

; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS

; NUMBER OF SEQUENCES: 126

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/898,860

; FILING DATE: 03-Jul-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/267,439

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/08/417,174

; FILING DATE: 05-APR-1995

; APPLICATION NUMBER: US/08/231,565

; FILING DATE: 22-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: CAROL M. GRUPPI

; REGISTRATION NUMBER: 37,341

; REFERENCE/DOCKET NUMBER: 2026-4124US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 79:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9

; TYPE: amino acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; MOLECULE TYPE: Peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Query Match 86.2%; Score 50; DB 12; Length 9;

Best Local Similarity 87.5%; Pred. No. 4.4e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VWGQYQV 9  
:|||||  
Db 2 LMGQYQV 9

RESULT 23

US-09-898-860-80

; Sequence 80, Application US/09898860

; Publication No. US20030144482A1

; GENERAL INFORMATION:

; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

; STEVEN A.

; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS

; NUMBER OF SEQUENCES: 126

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/898,860

; FILING DATE: 03-Jul-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/267,439

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/08/417,174

; FILING DATE: 05-APR-1995

; APPLICATION NUMBER: US/08/231,565

; FILING DATE: 22-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: CAROL M. GRUPPI

; REGISTRATION NUMBER: 37,341

; REFERENCE/DOCKET NUMBER: 2026-4124US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 80:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9

; TYPE: amino acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; MOLECULE TYPE: Peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Query Match 86.2%; Score 50; DB 12; Length 9;

Best Local Similarity 87.5%; Pred. No. 4.4e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VWGQYQV 9  
:|||||  
Db 2 LMGQYQV 9

RESULT 24

US-09-898-860-81

; Sequence 81, Application US/09898860

; Publication No. US20030144482A1

; GENERAL INFORMATION:

; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

; STEVEN A.

; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS

; NUMBER OF SEQUENCES: 126

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPT  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 81:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 81:  
US-09-898-860-81

Query Match 86.2%; Score 50; DB 12; Length 9;  
Best Local Similarity 87.5%; Pred. No. 4.4e+05;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMGQYMOV 9  
:|||||  
Db 2 LMGQYMOV 9

RESULT 25  
US-09-898-860-82  
Sequence 82, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPT  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 82:  
US-09-898-860-82

Query Match 86.2%; Score 50; DB 12; Length 9;  
Best Local Similarity 87.5%; Pred. No. 4.4e+05;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMGQYMOV 9  
:|||||  
Db 2 LMGQYMOV 9

Search completed: August 14, 2003, 09:25:45  
Job time : 153 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 24 Seconds  
(without alignments)  
36.063 Million cell updates/sec

Title: US-09-214-836-2

Perfect score: 58

Sequence: 1 KWMGQYQWV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	93.1	662	2	138400 melanoma-associated
2	54	93.1	662	2	A41234 melanocyte-specific
3	50	86.2	626	2	S53871 Pmel 17 protein -
4	49	84.5	264	2	F91017 hypothetical prote
5	49	84.5	264	2	H85861 hypothetical prote
6	49	84.5	549	2	H64992 hypothetical prote
7	43	74.1	305	1	S52775 hypothetical prote
8	42	72.4	281	2	A82104 conserved hypotnet
9	40	69.0	277	1	QRECS7 sulfate/thiosulfat
10	40	69.0	277	2	G91040 sulfate transport
11	40	69.0	277	2	AF0366 sulfate transport
12	40	69.0	277	2	B85885 sulfate transport
13	40	69.0	313	2	AG0018 hypothetical prote
14	40	69.0	335	1	A39862 hypothetical prote
15	40	69.0	400	2	S76446 D-ribulokinase (EC
16	40	69.0	525	2	A36183 ribitol kinase (im
17	40	69.0	537	2	B96681 protein FIE22.4 [i
18	40	69.0	580	2	AH2138 ABC transporter AT
19	40	69.0	807	2	F64844 ycds protein precu
20	40	69.0	807	2	F90787 probable outer mem
21	40	69.0	807	2	F85647 probable outer mem
22	40	69.0	1870	2	D84866 protein F20H1.2 [
23	40	67.2	114	2	B87339 conserved hypotnet
24	39	67.2	145	2	T13342 conserved hypotnet
25	39	67.2	145	2	H71341 conserved hypotnet
26	39	67.2	537	2	G84283 TRK potassium upca
27	39	67.2	537	2	G84283 amino acid transpo
28	39	67.2	602	1	S38111 hypothetical prote
29	38	65.5	209	2	S75029

30	38	65.5	259	2	AF1847 hypothetical prote
31	38	65.5	277	2	AH0811 sulphate transport
32	38	65.5	396	2	AF1903 hypothetical prote
33	38	65.5	545	2	A84432 probable peptide/a
34	38	65.5	568	2	E96648 hypothetical prote
35	38	65.5	585	2	C84432 histidine transpor
36	38	65.5	586	2	D91013 probable ATP-depen
37	38	65.5	586	2	F85857 probable ATP-depen
38	38	65.5	586	2	yeH protein - Bsc
39	38	65.5	586	2	AH0785 probable helicase
40	38	65.5	586	2	S46236 histidine transpor
41	38	65.5	656	2	S30483 pol polypeptide -
42	38	65.5	656	2	S30484 pol polypeptide -
43	38	65.5	1008	2	T49470 phosphatidic acid-
44	38	65.5	1009	2	C64483 hypothetical prote
45	38	65.5	1039	2	S46347 pol polypeptide -

#### ALIGNMENTS

RESULT 1  
138400 melanoma-associated ME20 antigen (me20m) - human  
N:Alternate names: melanoma antigen 25  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence revision 01-Nov-1996 #text\_change 01-Dec-2000  
C:Accession: 138400; A53668; A55753  
R:Marsh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.; Ma,  
DNA Cell Biol. 13, 87-95, 1994  
A:Title: Cloning and expression of the gene for the Melanoma-Associated ME20 Antigen.  
A:Reference number: 138400; MUID:94235155; PMID:8179825  
A:Accession: 138400  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-662 <RES>  
A:Cross-references: EMBL:U01874; NID:9494939; PIDN:AA18479.1; PID:9494940  
J:Adams, G.J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.  
J. Biol. Chem. 269, 20126-20133, 1994  
A:Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.  
A:Reference number: A53668; MUID:94327568; PMID:7519602  
A:Accession: A53668  
A:Molecule type: mRNA  
A:Residues: 1-592, 594-662 <ADE>  
A:Cross-references: GB:S73003; NID:9639589; PIDN:AA060634.1; PID:9639590  
R:Kawakami, Y.; Eliyahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E.; Yr,  
Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994  
A:Title: Identification of a human melanoma antigen recognized by tumor-infiltrating lymph  
A:Reference number: A55753; MUID:94294401; PMID:8022805  
A:Accession: A55753  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-161, 163-592, 594-662 <KAW>  
C:Keywords: glycoprotein

Query Match 93.1%; Score 54; DB 2; Length 662;  
Best Local Similarity 88.9%; Pred. No. 0.67;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KWMGQYQWV 9  
DB 154 KWMGQYQWV 162

RESULT 2  
A41234 melanocyte-specific protein Pmel-17 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 30-Sep-1993  
C:Accession: A41234  
R:Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.;  
Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991  
A:Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on mc

A:Reference number: A41234; MUID:92021023; PMID:1924386  
A:Accession: A41234  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-668 <KMO>  
A:Cross-references: GB:M77348

Query Match 93.1%; Score 54; DB 2; Length 668;  
Best Local Similarity 88.9%; Pred. No. 0.68;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMQV 9  
|||||  
Db 154 KTMGQYMQV 162

RESULT 3  
S53871  
Pmel 17 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S53871  
R:Kwon, B.S.; Halaban, R.; Ponnazhagan, S.; Kim, K.; Chintamani, C.; Bennett, D.; Pick  
Nucleic Acids Res. 23, 154-158, 1995  
A>Title: Mouse silver mutation is caused by a single base insertion in the putative cyt  
A:Reference number: S53871; MUID:95175358; PMID:7870580  
A:Accession: S53871  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-626 <KMO>  
A:Cross-references: GB:U14133; NID:9887940; PIDN:AAA69538.1; PID:9887941

Query Match 86.2%; Score 50; DB 2; Length 626;  
Best Local Similarity 77.8%; Pred. No. 2.6;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYMQV 9  
|||||  
Db 154 KTMGQYMQV 162

RESULT 4  
F91017  
hypotheoretical protein Ecs3110 [imported] - Escherichia coli (strain O157:H7, substrain RI  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: F91017  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: F91017  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BAR36533.1; PID:G13362579; GSPDB:GN00154  
C:Genetics:  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
A:Gene: Ecs3110

Query Match 84.5%; Score 49; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMGQYMQ 8  
|||||  
Db 124 VMGQYMQ 130

RESULT 5  
H85861  
hypotheoretical protein Z3480 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: H85861  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobeck, E.O.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potlowski, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: H85861  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <STO>  
A:Cross-references: GB:AE005174; NID:G12516559; PIDN:AA657356.1; GSPDB:GN00145; UMGW:Z34  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z3480

Query Match 84.5%; Score 49; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMGQYMQ 8  
|||||  
Db 124 VMGQYMQ 130

RESULT 6  
HE4992  
hypotheoretical protein b2226 - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: HE4992  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A>Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: HE4992  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-549 <BLAT>  
A:Cross-references: GB:AE000312; GB:U00096; NID:G1788555; PIDN:AACT5286.1; PID:G1788557;  
A:Experimental source: strain K-12, substrain MG1655  
C:Superfamily: Escherichia coli hypotheoretical protein b2226

Query Match 84.5%; Score 49; DB 2; Length 549;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMGQYMQ 8  
|||||  
Db 124 VMGQYMQ 130

RESULT 7  
S52775  
hypotheoretical protein 2 - Chloroflexus aurantiacus  
C:Species: Chloroflexus aurantiacus  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: S52775  
R:Niedermeyer, G.; Shiozawa, J.A.; Lotzpeich, F.; Feick, R.G.  
FEMS Lett. 342, 61-65, 1994  
A>Title: The primary structure of two chlorosome proteins from Chloroflexus aurantiacus.  
A:Reference number: S43678; MUID:94192803; PMID:7511541  
A:Accession: S52775  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-305 <NIE>  
A:Cross-references: EMBL:Z34000; NID:9496485; PIDN:CAA83969.1; PID:9496488  
A>Note: only a part of the coding sequence is given in this paper  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994  
C:Superfamily: Methanococcus jannaschii conserved hypotheoretical protein M00279

Query Match 74.1%; Score 43; DB 1; Length 305;  
Best Local Similarity 83.3%; Pred. No. 15;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VMGOYV 7  
Db 245 IMGOYV 250

RESULT 8  
A82104  
conserved hypothetical protein VC2229 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C/Species: Vibrio cholerae  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C/Accession: A82104  
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chaudhry, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, H.; R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A/Reference number: A82035; MUID:20406833; PMID:10952301  
A/Accession: A82104  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-281 <HEI>  
A/Cross-references: GB:AE004294; GB:AE003852; NID:g9656774; PIDN:AAF95373.1; GSPDB:GN001  
A/Experimental source: serogroup O1, strain N16961, biotype El Tor  
C/Genetics:  
A/Gene: VC2229  
A/Map position: 1  
C/Superfamily: hypothetical protein H11037

Query Match 72.4%; Score 42; DB 2; Length 281;  
Best Local Similarity 71.4%; Pred. No. 20;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVMGOYV 7  
Db 97 ELWGOYV 103

RESULT 9  
QRECS7  
sulfate/thiosulfate transport protein cyrT - Escherichia coli (strain K-12)

N/Alternate names: sulfate transport system permease protein cyrT  
C/Species: Escherichia coli  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 01-Mar-2002  
C/Accession: A35402; G65016; E35403  
R/Sirko, A.; Hryniewicz, M.; Hulanicka, D.; Boeck, A.  
J. Bacteriol. 172, 3351-3357, 1990  
A/Title: Sulfate and thiosulfate transport in Escherichia coli K-12: nucleotide sequence  
A/Reference number: A35402; MUID:90264334; PMID:2188958  
A/Accession: A35402  
A/Molecule type: DNA  
A/Residues: 1-277 <SIR>  
A/Cross-references: GB:M32101; GB:M38050; NID:g145657; PIDN:AAA23637.1; PID:g145659  
A/Experimental source: strain K12  
R/Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.  
A.; Rose, D.V.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of Escherichia coli K-12.  
A/Reference number: A64720; MUID:97426617; PMID:9278503  
A/Accession: G65016  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-277 <BAT>  
A/Cross-references: GB:AE000330; GB:U00096; NID:g1788763; PIDN:AACT5477.1; PID:g1788764;  
A/Experimental source: strain K-12, substrain MG1655  
R/Hryniewicz, M.; Sirko, A.; Palucha, A.; Boeck, A.; Hulanicka, D.  
J. Bacteriol. 172, 3358-3366, 1990  
A/Title: Sulfate and thiosulfate transport in Escherichia coli K-12: identification of a  
A/Reference number: A35403; MUID:90264335; PMID:2188959  
A/Accession: B35403

A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-126, 'F', 128-133 <HRY>  
C/Comment: This is one of the membrane-associated components of the binding protein-depe  
C/Genetics:  
A/Gene: cyrT  
A/Map position: 52 min  
C/Superfamily: maltose transport protein malG  
C/Keywords: binding protein-dependent transport system; inner membrane; membrane protein

Query Match 69.0%; Score 40; DB 1; Length 277;  
Best Local Similarity 71.4%; Pred. No. 41;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WGOYV 9  
Db 44 WQYMEV 50

RESULT 10  
G91040  
sulfate transport system permease T protein EC83295 [imported] - Escherichia coli (strain K-12)

C/Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C/Accession: G91040  
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom  
A/Reference number: A9629; MUID:21156231; PMID:11258796  
A/Accession: G91040  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-277 <HAY>  
A/Cross-references: GB:BA000007; PIDN:BA36718.1; PID:g13362765; GSPDB:GN00154  
A/Experimental source: strain O157:H7, substrain RIMD 0509952  
C/Genetics:  
A/Gene: EC83295  
C/Superfamily: maltose transport protein malG

Query Match 69.0%; Score 40; DB 2; Length 277;  
Best Local Similarity 71.4%; Pred. No. 41;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WGOYV 9  
Db 44 WQYMEV 50

RESULT 11  
AF0366  
sulfate transport system permease protein CyST cyst [imported] - Yersinia pestis (strain K/10)

C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C/Accession: AF0366  
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F.  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AF0366  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-277 <GR>  
A/Cross-references: GB:AL590842; PIDN:CMC92257.1; PID:g15980968; GSPDB:GN00175  
C/Genetics:  
A/Gene: cyrT  
C/Superfamily: maltose transport protein malG

Query Match 69.0%; Score 40; DB 2; Length 277;  
Best Local Similarity 71.4%; Pred. No. 41;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYMOV 9  
| | | | |  
DB 44 WAQYMEV 50

## RESULT 12

B85885  
sulfate transport system permease T protein Ecs3295 [imported] - *Escherichia coli* (strain  
C)Species: *Escherichia coli*  
C)Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 27-Nov-2001  
C)Accession: B85885  
R)Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Natter, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A)Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A)Reference number: A85480; MUID:21074935; PMID:11206551  
A)Accession: B85885  
A)Status: preliminary  
A)Molecule type: DNA  
A)Residues: 1-277 <STO>  
A)Cross-references: GB:AB005174; NID:g12516799; PIDN:AA657542.1; GSPDB:GN00145; UMGPR:Z36  
A)Experimental source: strain O157:H7, substrain EDJ933  
C)Genetics:  
A)Gene: *cysU*  
C)Superfamily: maltose transport protein malG

Query Match 69.0%; Score 40; DB 2; Length 277;  
Best Local Similarity 71.4%; Pred. No. 41;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYMOV 9  
| | | | |  
DB 44 WAQYMEV 50

## RESULT 13

AG0018  
hypothetical protein YP00146 [imported] - *Yersinia pestis* (strain CO92)  
C)Species: *Yersinia pestis*  
C)Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C)Accession: AG0018  
R)Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.  
dano-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;  
M., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,  
Nature 413, 523-527, 2001  
A)Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A)Reference number: AB0001; MUID:21470413; PMID:11586360  
A)Accession: AG0018  
A)Status: preliminary  
A)Molecule type: DNA  
A)Residues: 1-313 <KUN>  
A)Cross-references: GB:AL590842; PIDN:CA089009.1; PID:g15978251; GSPDB:GN00175  
C)Genetics:  
A)Gene: YP00146

Query Match 69.0%; Score 40; DB 2; Length 313;  
Best Local Similarity 66.7%; Pred. No. 46;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
| | | | |  
DB 15 KMYSQYMOV 23

## RESULT 14

A39862  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - yeast (*Saccharomyces ce*  
N)Alternate names: protein DO815; protein YDL230W  
C)Species: *Saccharomyces cerevisiae*  
C)Date: 30-Dec-1991 #sequence\_revision 08-Mar-1996 #text\_change 21-Jul-2000  
C)Accession: A39862; S67793  
R)Guan, K.; Deschenes, R.J.; Qiu, H.; Dixon, J.E.

J. Biol. Chem. 266, 12964-12970, 1991  
A)Title: Cloning and expression of a yeast protein tyrosine phosphatase.  
A)Reference number: A39862; MUID:91302312; PMID:1649172  
A)Accession: A39862

A)Molecule type: DNA  
A)Residues: 1-335 <GUA>  
A)Cross-references: GB:M64062; NID:g172295; PIDN:AAA34923.1; PID:g172296  
R)Raamussen, S.W.  
submitted to the Protein Sequence Database, July 1996  
A)Reference number: S67778  
A)Accession: S67793  
A)Molecule type: DNA  
A)Residues: 1-335 <RAS>  
A)Cross-references: EMBL:Z74278; NID:g1431387; PIDN:CAA98809.1; PID:g1431388; GSPDB:GN00C  
A)Experimental source: strain S286C  
C)Genetics:  
A)Gene: SGD:PTP1; MIPS:YDL230W  
A)Cross-references: SGD:S0002389; MIPS:YDL230W  
A)Map position: 4L  
C)Superfamily: *Saccharomyces* protein-tyrosine-phosphatase, nonreceptor type 1; protein-ty

C)Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase;  
F)52/307/Domains: protein-tyrosine-phosphatase homology <PTP>  
F)252/Active site: Cys (phosphocysteine intermediate) #status predicted  
F)258/Binding site: substrate phosphate (Arg) #status predicted

Query Match 69.0%; Score 40; DB 1; Length 335;  
Best Local Similarity 55.6%; Pred. No. 49;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
| | | | |  
DB 108 KTWQDFWQM 116

## RESULT 15

S76446  
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)  
C)Species: *Synechocystis* sp.  
A)Variety: PCC 6803  
C)Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
C)Accession: S76446  
R)Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,  
DNA Res. 3, 109-136, 1996  
A)Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
S.  
A)Reference number: S74322; MUID:97061201; PMID:8905231  
A)Accession: S76446  
A)Status: preliminary  
A)Molecule type: DNA  
A)Residues: 1-400 <KAN>  
A)Cross-references: EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BA18575.1; PID:d1019306  
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 69.0%; Score 40; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGOYMOV 7  
| | | | |  
DB 335 WGOYMOV 339

## RESULT 16

A96183  
D-ribulokinase (EC 2.7.1.47) [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)  
C)Species: *Agrobacterium tumefaciens*  
C)Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
C)Accession: A96183  
R)Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A)Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*



A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: A96183  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-525 <KUR>  
A:Cross-references: GB:AE007870; PIDN:AAK8987.1; PID:gl5158771; GSPDB:GN00170  
C:Genetics:  
A:Gene: AGR\_L\_826  
A:Map position: linear chromosome  
C:Keywords: phosphotransferase

Query Match 69.0%; Score 40; DB 2; Length 525;  
Best Local Similarity 71.4%; Pred. No. 76;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VMGOYMQ 8  
Db 298 LMGPYMQ 304

RESULT 17  
A13103  
ribitol kinase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: A13103  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moe, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayarin, T.; Levy, R.; Li, M.; McClell  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: A13103  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-525 <KUR>  
A:Cross-references: GB:AE008689; PIDN:AAL45247.1; PID:gl7742931; GSPDB:GN00187  
C:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu4453  
A:Map position: linear chromosome

Query Match 69.0%; Score 40; DB 2; Length 525;  
Best Local Similarity 71.4%; Pred. No. 76;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VMGOYMQ 8  
Db 298 LMGPYMQ 304

RESULT 18  
E96681  
proteins F1E22.4 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: E96681  
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hutzlar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: E96681  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-537 <STO>  
A:Cross-references: GB:AE005173; NID:G6686410; PIDN:AAF23844.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F1E22.4  
A:Map position: 1

Query Match 69.0%; Score 40; DB 2; Length 537;  
Best Local Similarity 71.4%; Pred. No. 78;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VMGOYMQ 8  
Db 404 VMGSYWK 410

RESULT 19  
AH2138  
ABC transporter ATP-binding protein alr2663 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AH2138  
R:Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriuchi  
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB18077; MUID:21595285; PMID:11759840  
A:Accession: AH2138  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-580 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BAH74362.1; PID:gl7131756; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr2663

Query Match 69.0%; Score 40; DB 2; Length 580;  
Best Local Similarity 44.4%; Pred. No. 84;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGOYMQV 9  
Db 7 QIMOOQFWOI 15

RESULT 20  
F64844  
ycds protein precursor - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: F64844  
R:Bletner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.D.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: F64844  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-807 <BLAT>  
A:Cross-references: GB:AE00204; GB:U00096; NID:gl787256; PIDN:AACT4109.1; PID:gl787261;  
A:Experimental source: strain K-12, substrain M01655  
C:Genetics:  
A:Gene: ycds  
C:Superfamily: Escherichia coli ycds protein  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-807/Product: ycds protein #status predicted <MAT>

Query Match 69.0%; Score 40; DB 2; Length 807;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VMGOYMQ 7

Db 314 WGOYW 318  
|||||  
RESULT 21  
F90787  
Probable outer membrane protein ECs1270 [imported] - Escherichia coli (strain O157:H7, S  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C:Accession: F90787  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gasaawa, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A96629; MUID:21156231; PMID:11258796  
A:Accession: F90787  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-807 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA834693.1; PID:G13360730; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: ECs1270  
C:Superfamily: Escherichia coli ycds protein  
Query Match 69.0%; Score 40; DB 2; Length 807;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 3 WGOYW 7  
|||||  
Db 314 WGOYW 318  
RESULT 22  
F85647  
Probable outer membrane protein ycds [imported] - Escherichia coli (strain O157:H7, sub  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: F85647  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: F85647  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-807 <STO>  
A:Cross-references: GB:AE005174; NID:G12514389; PIDN:AGS5642.1; GSPDB:GN00145; UWGP:Z15  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: ycds  
C:Superfamily: Escherichia coli ycds protein  
Query Match 69.0%; Score 40; DB 2; Length 807;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 3 WGOYW 7  
|||||  
Db 314 WGOYW 318  
RESULT 23  
D88466  
Protein F20H11.2 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: D88466  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: D88466  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-1870 <STO>  
A:Cross-references: GB:chr\_III; PIDN:AAB53984.1; PID:G2076895; GSPDB:GN00021; CESP:F20H1  
C:Genetics:  
A:Gene: F20H11.2  
A:Map position: 3  
Query Match 69.0%; Score 40; DB 2; Length 1870;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 2 WGOYW 7  
|||||  
Db 990 WGOYW 995  
RESULT 24  
B87339  
Conserved hypothetical protein CC0725 [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C:Accession: B87339  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.O.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Brnolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: B87339  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <STO>  
A:Cross-references: GB:AE005673; NID:G13421952; PIDN:AAK22710.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC0725  
C:Superfamily: Synectocystis hypothetical protein s111442  
Query Match 67.2%; Score 39; DB 2; Length 114;  
Best Local Similarity 71.4%; Pred. No. 24;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 3 WGOYW 9  
|||||  
Db 70 WGOYW 76  
RESULT 25  
T13342  
Hypothetical protein 53 - Streptococcus phage phi-O1205  
C:Species: Streptococcus phage phi-O1205  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 05-May-2000  
C:Accession: T13342  
R:Stanley, E.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.  
Microbiology 143, 3417-3429, 1997  
A:Title: Sequence analysis and characterization of phi O1205, a temperate bacteriophage  
A:Reference number: Z17654; MUID:98048466; PMID:9387220  
A:Accession: T13342  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-145 <STO>  
A:Cross-references: EMBL:U88974; NID:G2444080; PID:G2444131; PIDN:AACT9567.1  
A:Experimental source: host Streptococcus thermophilus strain CNR2105  
C:Superfamily: Streptococcus phage phi-O1205 hypothetical protein 53  
Query Match 67.2%; Score 39; DB 2; Length 145;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy	1	KVWGQYMOV	9
		:   :	
Db	41	KVYGLYWEV	49

Search completed: August 14, 2003, 09:07:15  
Job time : 26 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 13.5 seconds  
(without alignments)  
31.351 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KVMGQYQV 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	93.1	661	PM17_HUMAN	P40967 homo sapien
2	50	86.2	626	PM17_MOUSE	Q60696 mus musculu
3	49	84.5	549	YFAQ_ECOLI	P76463 escherichia
4	45	77.6	762	P115_CHICK	O98917 gallus galli
5	41	70.7	756	IKKB_HUMAN	O14920 homo sapien
6	41	70.7	757	IKKB_MOUSE	O88351 mus musculu
7	41	70.7	757	IKKB_RAT	O99778 ratu
8	40	69.0	277	CYST_ECOLI	P16701 escherichia
9	40	69.0	335	PRPI_YEAST	P25044 sacharomyc
10	40	69.0	807	YCDS_ECOLI	P75907 escherichia
11	39	67.2	515	COAT_TBSV	O88894 tobaco rin
12	39	67.2	602	GAP1_YEAST	P19145 sacharomyc
13	38	65.5	100	POL_SIV3	P12501 simian immu
14	38	65.5	277	CYST_SALTY	P41032 salmonella
15	38	65.5	394	LIP3_DROME	O46108 drosophila
16	38	65.5	585	PT2B_ARATH	P46032 arabidopsis
17	38	65.5	586	YERH_ECOLI	P33919 escherichia
18	38	65.5	880	GNM4_THERU	P26221 thermomonos
19	38	65.5	1009	Y668_METUA	Q88863 methanococ
20	38	65.5	1045	GNB_CELFI	P26225 cellulomona
21	38	65.5	1046	POL_SIVG	P27980 simian immu
22	38	65.5	1047	POL_SIVAI	P27973 simian immu
23	38	65.5	1061	POL_SIVAT	P05895 simian immu
24	37	63.8	256	RM09_MOUSE	O99894 mus musculu
25	37	63.8	263	CCMC_BRAVA	P10962 bradyrhizob
26	37	63.8	267	RM09_HUMAN	O99894 mus musculu
27	37	63.8	290	UBIA_ECOLI	O99894 mus musculu
28	37	63.8	305	SL2B_BACSU	P56601 bacillus su
29	37	63.8	1034	POL_HV2CA	P24107 human immu
30	37	63.8	1035	POL_HV2CA	O74120 human immu
31	37	63.8	1035	POL_HV2NZ	P05962 human immu
32	37	63.8	1035	POL_HV2SB	P12451 human immu
33	37	63.8	1036	POL_HV2RO	P04584 human immu

34	37	63.8	1049	POL_HV2G1	P18042 human immu
35	37	63.8	1055	POL_HV2ST	P20876 human immu
36	37	63.8	1073	POL_HV2D1	P17577 human immu
37	37	63.8	1142	POL_HV2BE	P18096 human immu
38	37	63.8	2211	FA5_BOVIN	O28107 bos tauru
39	37	63.8	2224	FA5_HUMAN	P12259 homo sapien
40	37	63.8	2258	FA5_PIG	O99151 sus scrofa
41	37	63.8	248	EX15_ARATH	O80622 arabidopsis
42	36	62.1	249	EX10_ARATH	O91475 arabidopsis
43	36	62.1	250	EXPI_ARATH	O9554 arabidopsis
44	36	62.1	251	VG37_BPM1	P08231 bacterioph
45	36	62.1	251	VG37_BPOX2	P08232 bacterioph

## ALIGNMENTS

RESULT 1

PM17\_HUMAN STANDARD; PRT; 661 AA.

AC P40967; Q12763; Q14448; Q14817; Q16565;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanocyte protein Pmel 17 precursor (Melanocyte lineage-specific antigen GP100) (Melanoma-associated ME20 antigen) (ME20W/ME20S) (ME20-W/ME20-S) (95 kDa melanocyte-specific secreted glycoprotein).  
GN SILV OR PMEL17 OR D12533E.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
[2]  
[3]  
[4]  
[5]  
[6]

SEQUENCE FROM N.A.  
MEDLINE=92021023; PubMed=1924386;  
Kwon B.S., Chintamaneni C., Kozak C.A., Copeland N.G., Gilbert D.J., Jenkins N.A., Barton D., Francke U., Kobayashi Y., Kim K.-K.;  
"A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on mouse chromosome 10 and is in a syntenic region on human chromosome 12.";  
Proc. Natl. Acad. Sci. U.S.A. 88:9228-9232(1991).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=94327568; PubMed=7519602;  
Adema G.J., de Boer A.J., Vogel A.M., Loenen W.A., Figdor C.G.;  
"Molecular characterization of the melanocyte lineage-specific antigen gp100.";  
J. Biol. Chem. 269:20126-20133(1994).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=96154052; PubMed=8592076;  
Ballin T., Lee S.T., Spritz R.A.;  
"Genomic organization and sequence of D12S53E (Pmel 17), the human homologue of the mouse silver (si) locus.";  
J. Invest. Dermatol. 106:24-27(1996).  
[4]  
SEQUENCE FROM N.A. AND SEQUENCE OF 25-53.  
MEDLINE=94235165; PubMed=8179825;  
Marresh G.A., Marken J.S., Neubauer M., Aruffo A., Hellstrom I., Hellstrom K.E., Marguardt H.;  
"Cloning and expression of the gene for the melanoma-associated ME20 antigen.";  
DNA Cell Biol. 13:87-95(1994).  
[5]  
SEQUENCE FROM N.A.  
Kwon B.S., Kim K., Heng H.H., Shi X.M., Teui L., Lee Z.H., Young B., Pickard R.T.;  
Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
[6]  
SEQUENCE FROM N.A.  
Vogel A.;  
Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COULD BE A MELANOGENIC ENZYME. COULD REPRESENT AN  
CC ONCOFETAL SELF-ANTIGEN THAT IS NORMALLY EXPRESSED AT LOW LEVELS IN  
CC QUIESCENT ADULT MELANOCYTES BUT OVEREXPRESSED BY PROLIFERATING  
CC NEONATAL MELANOCYTES AND DURING TUMOR GROWTH. RELEASE OF THE  
CC SOLUBLE FORM, ME20-S, COULD PROTECT TUMOR CELLS FROM ANTIBODY  
CC MEDIATED IMMUNITY.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL). THERE  
CC IS ALSO A SECRETED SOLUBLE FORM, ME20-S, PROBABLY PRODUCT OF  
CC PROTEOLYTIC CLEAVAGE.  
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN MELANOMAS. SOME  
CC TISSUES NOR IN CARCINOMAS.  
CC -1- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.  
CC -1- SIMILARITY: Contains 1 PKD domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: M77348; AAC60121.1; -  
CC EMBL: S73003; AAC60634.1; -  
CC EMBL: U31799; AAB00386.1; -  
CC EMBL: U31808; AAB00386.1; JOINED.  
CC EMBL: U31807; AAB00386.1; JOINED.  
CC EMBL: U31797; AAB00386.1; JOINED.  
CC EMBL: U31798; AAB00386.1; JOINED.  
CC EMBL: U20093; AAB19181.1; -  
CC EMBL: U19491; AAB19181.1; JOINED.  
CC EMBL: M32295; AAB35930.1; ALT\_INIT.  
CC PIR: I38400; I38400.  
CC GeneW: HGNC:10880; SILV.  
CC MIM: 155550; -  
CC GO: GO:0005886; C:Plasma membrane; TAS.  
CC InterPro: IPR000601; PKD\_domain.  
CC Pfam: PF00801; PKD\_1.  
CC SMART: SM00089; PKD; 1.  
CC Transmembrane; Glycoprotein; signal; Melanin biosynthesis; Repeat;  
CC Antigen.  
CC SIGNAL. 1 24  
CC CHAIN 25 661  
CC DOMAIN 25 595  
CC TRANSMEM 596 616  
CC DOMAIN 617 661  
CC DOMAIN 255 292  
CC DOMAIN 315 444  
CC REPEAT 315 327  
CC REPEAT 328 340  
CC REPEAT 341 353  
CC REPEAT 354 366  
CC REPEAT 367 379  
CC REPEAT 380 392  
CC REPEAT 393 405  
CC REPEAT 406 418  
CC REPEAT 419 431  
CC REPEAT 432 444  
CC REPEAT 445 457  
CC CARBOHYD 81 81  
CC CARBOHYD 106 106  
CC CARBOHYD 111 111  
CC CARBOHYD 321 321  
CC CARBOHYD 321 321  
CC CARBOHYD 568 568  
CC CARBOHYD 274 274  
CC CONFLICT 587 587  
CC CONFLICT 592 592  
CC CONFLICT 597 597  
CC CONFLICT 642 661  
CC SEQUENCE 661 AA; 70255 MW; 8A304FAB16715653 CRC64;

Query Match 93.1%; Score 54; DB 1; Length 661;  
Best Local Similarity 88.9%; Pred. No. 0.24;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 KVMGQYQV 9  
DB 154 KTMGQYQV 162  
RESULT 2  
ID PM17\_MOUSE STANDARD; PRT; 626 AA.  
AC Q60696;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Melanocyte protein Pmel 17 precursor (Silver locus protein).  
GN SILV OR PMEL17 OR D10H12553E OR SI.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Skin;  
RX MEDLINE=95175358; PubMed=7870580;  
RA Kwon B.S., Halaban R., Ponnazhagan S., Kim K., Chintamani C.,  
RA Bennett D., Fickard R.T.;  
RT "Mouse silver mutation is caused by a single base insertion in the  
RT putative cytoplasmic domain of Pmel 17.";  
RL Nucleic Acids Res. 23:154-158(1995).  
CC -1- FUNCTION: COULD BE A MELANOGENIC ENZYME.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).  
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN MELANOCYTES.  
CC -1- DISEASE: DEFECTS IN SILV ARE THE CAUSE OF THE SILVER COAT COLOR  
CC WHICH SEEMS TO BE DUE TO PREMATURE DEATH OF PIGMENT CELLS DURING  
CC THE HAIR CYCLE.  
CC -1- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.  
CC -1- SIMILARITY: Contains 1 PKD domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U14133; AAA69538.1; -  
CC PIR: S53871; S53871.  
CC MCD: MGI:98301; Si.  
CC InterPro: IPR000601; PKD\_domain.  
CC Pfam: PF00801; PKD; 1.  
CC SMART: SM00089; PKD; 1.  
CC PROSITE: PS50093; PKD; 1.  
CC Transmembrane; Glycoprotein; signal; Melanin biosynthesis; Repeat;  
CC Disease mutation.  
CC SIGNAL. 1 24  
CC CHAIN 25 626  
CC DOMAIN 25 562  
CC TRANSMEM 563 583  
CC DOMAIN 584 626  
CC DOMAIN 255 292  
CC DOMAIN 315 411  
CC REPEAT 315 327  
CC REPEAT 328 340  
CC REPEAT 341 353  
CC REPEAT 354 366  
CC REPEAT 367 379  
CC REPEAT 380 392  
CC REPEAT 393 411  
CC CARBOHYD 81 81  
CC SEQUENCE 81 AA; 70255 MW; 8A304FAB16715653 CRC64;

FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 170 170 S -> L (IN SILVER).  
 FT VARIANT 175 175 R -> G (IN SILVER).  
 FT VARIANT 373 373 D -> N (IN SILVER).  
 FT VARIANT 471 471 F -> S (IN SILVER).  
 FT VARIANT 603 626 AAPASGLARGLGENSPILSGOQV -> SSASLRSSRRPW  
 RKPAPQWTLGLTIILKAPWISMG (IN SILVER).  
 SQ SEQUENCE 626 AA; 65980 MM; 7AB941D2E3FBI044 CRC64;

Query Match 86.2%; Score 50; DB 1; Length 626;  
 Best Local Similarity 77.8%; Pred. No. 0.94;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYMOV 9  
 DB 154 KVMGQYMOV 162

## RESULT 3

YFAO\_ECOLI STANDARD; PRT; 549 AA.  
 ID YFAO\_ECOLI  
 AC P76463;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein yfaQ precursor.  
 GN YFAO OR B2226.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=9742617; PubMed=9278503;  
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----  
 DR EMBL; AE000312; AAC75286.1; -;  
 DR PIR; H64992; H64992.  
 DR Ecogene; EG14079; YfaQ.  
 KW Hypothetical protein; Signal; Complete proteome.  
 FT SIGNAL 19  
 FT CHAIN 1  
 FT SEQUENCE 549 AA; 61475 MM; 72C26716D953C9D1 CRC64;

Query Match 84.5%; Score 49; DB 1; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VMGQYMO 8  
 DB 124 VMGQYMO 130

RESULT 4  
 P115\_CHICK STANDARD; PRT; 762 AA.  
 ID P115\_CHICK  
 AC Q98917;

DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 115 kDa melanosomal matrix protein precursor.  
 GN MPM15.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn; TISSUE=Retinal pigment epithelium;  
 RX MEDLINE=9202067; PubMed=1924173;  
 RA Mochii M., Agata K., Kobayashi H., Yamamoto T.S., Eguchi G.;  
 RT "Complete sequence and expression of a cDNA encoding a chicken  
 RT 115-kDa melanosomal matrix protein.";  
 RL Pigment Cell Res. 4:41-47(1991).  
 RN [2]

RP CHARACTERIZATION.  
 RC STRAIN=White Leghorn; TISSUE=Retinal pigment epithelium;  
 RX MEDLINE=88311098; PubMed=3409326;  
 RA Mochii M., Agata K., Kobayashi H., Yamamoto T.S., Eguchi G.;  
 RT "Expression of gene coding for a melanosomal matrix protein  
 RT transcriptionally regulated in the transdifferentiation of chick  
 RT embryo pigmented epithelial cells.";  
 RL Cell Differ. 24:67-74(1988).  
 CC -1- FUNCTION: MIGHT BE REQUIRED FOR POLYMERIZATION OF MELANIN ONTO THE  
 CC CORE STRUCTURE OF MELANOSOMES WITH ENZYMIC FUNCTION OF TYROSINASE.

CC -1- SUBCELLULAR LOCATION: ON THE FIBROUS MATRIX STRUCTURE OF THE  
 CC PREMELANOSOME.  
 CC -1- TISSUE SPECIFICITY: SPECIFIC TO PIGMENTED EPITHELIAL CELLS AND  
 CC MELANOCYTES. NOT EXPRESSED IN LENS, NEURAL RETINA, BRAIN, HEART,  
 CC GIZZARD OR LIVER.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE REDIFFERENTIATION OF  
 CC PIGMENTED EPITHELIAL CELLS (PEC).  
 CC -1- PTM: GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.  
 CC -1- SIMILARITY: Contains 1 PKD domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----  
 DR EMBL; D88348; BA13589.1; -;  
 DR InterPro; IPR000601; PKD\_domain.  
 DR Pfam; PF00801; PKD\_1.  
 DR SMART; SMO0089; PKD\_1.  
 DR PROSITE; PS50093; PKD; 1.  
 DR SIGNAL 19  
 DR CHAIN 1  
 DR DOMAIN 20 762  
 FT SIGNAL 19  
 FT CHAIN 1  
 FT DOMAIN 20 762  
 FT REPEAT 441 532  
 FT REPEAT 441 464  
 FT REPEAT 465 488  
 FT REPEAT 489 508  
 FT REPEAT 509 532  
 FT REPEAT 511 532  
 FT CARBOHYD 111 111  
 FT CARBOHYD 115 115  
 FT CARBOHYD 346 346  
 FT CARBOHYD 651 651  
 FT CARBOHYD 659 659  
 FT SEQUENCE 762 AA; 77356 MM; 172C8DB4FDC7C6 CRC64;

Query Match 77.6%; Score 45; DB 1; Length 762;  
 Best Local Similarity 85.7%; Pred. No. 6.9;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 P115\_CHICK STANDARD; PRT; 762 AA.  
 ID P115\_CHICK  
 AC Q98917;

OY 3 MGQWQV 9  
 ID 162 MGRWQV 168  
 DB 162 MGRWQV 168  
 RESULT 5  
 ID IKKB\_HUMAN STANDARD; PRT; 756 AA.  
 AC 014920; 075327;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).  
 GN IKKB OR IKKB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.  
 RC TISSUE=Cervical carcinoma;  
 RX MEDLINE=98008813; PubMed=9346484;  
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RT "IKK-1 and IKK-2: cytokine-activated Ikkappa kinases essential for  
 RT NF-kappaB activation.";  
 RT Science 278:860-866(1997).  
 [2]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RX MEDLINE=98008814; PubMed=9346485;  
 RA Woronicz J.D., Gao X., Cao Z., Roche M., Goeddel D.V.;  
 RT "Ikkappa kinase-beta: NF-kappaB activation and complex formation with  
 RT Ikkappa kinase-alpha and NIK.";  
 RT Science 278:866-869(1997).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=99032998; PubMed=9813230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RT "IkkappaB kinase-alpha and -beta genes are coexpressed in adult and  
 RT embryonic tissues but localized to different human chromosomes.";  
 RT Gene 222:31-40(1998).  
 [4]  
 RP SEQUENCE FROM N.A., AND GENE MAPPING.  
 RX MEDLINE=98438415; PubMed=9763654;  
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;  
 RT "Assignment of IkkappaB kinase beta (IKKB) to human chromosome band  
 RT 8p12--p11 by in situ hybridization.";  
 RT Cytogenet. Cell Genet. 82:32-33(1998).  
 [5]  
 RP SEQUENCE OF 1-256 FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buerger K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rahn S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalón D.K., Wuzny D.M., Sodergren B.U., Lu X., Gibbs R.A.,  
 RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield J.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [6]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 [7]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 [8]  
 RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKB.  
 RX MEDLINE=11968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 RT activity by I kappa B kinase.";  
 RL Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3 (By similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 CC peripheral blood.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL; AF029684; AAC51860.1; -;  
 DR EMBL; AF080158; AAD08957.1; -;  
 DR EMBL; AF031416; AAC64675.1; -;  
 DR EMBL; BC006231; AAH06231.1; -;  
 DR HSSP; O63450; 1A06.  
 DR GenSeq; HGNC:5960; IKKB.  
 DR MIM; 603258; -;  
 DR GO; GO:0005737; C:cytoplasm; NAS.  
 DR GO; GO:0005524; F:ATP binding activity; NAS.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.  
 DR GO; GO:0016563; F:transcriptional activator activity; NAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;



KT	Phosphorylation.	15	300	PROTEIN KINASE.
FT	DOMAIN	458	479	LEUCINE_ZIPPER (POTENTIAL).
FT	DOMAIN	737	742	NEMO-BINDING.
FT	NP_BIND	21	29	ATP (BY SIMILARITY).
FT	BINDING	44	44	ATP (BY SIMILARITY).
FT	ACT_SITE	145	145	BY SIMILARITY.
FT	MOD_RES	23	23	PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES	177	177	PHOSPHORYLATION.
FT	MOD_RES	181	181	PHOSPHORYLATION.
FT	MUTAGEN	44	44	K-2A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
FT	MUTAGEN	177	177	S-2A: DECREASE OF ACTIVITY.
FT	MUTAGEN	181	181	S-2B: FULL ACTIVATION.
FT	MUTAGEN	181	181	S-2E: DECREASE OF ACTIVITY.
FT	CONFLICT	231	255	S-2E: FULL ACTIVATION.
FT	CONFLICT	425	425	WHSKVKQSEVDIVSEEDNGTVKF -> CYRMPGTVAAH
FT	CONFLICT	756 AA;	86563 MW;	CONSTGSGRGM (IN REF. 5).
FT	SEQUENCE	756 AA;	86563 MW;	0 -> H (IN REF. 5).
FT	SEQUENCE	756 AA;	86563 MW;	P9CADF671AE9E14E CRC64;
Qy	1 KWGCQY 7	70.7%;	Score 41; DB 1; Length 756;	
Db	428 KWGCQY 434	6; Conservative	0; Mismatches	1; Indels 0; Gaps
RESULT 6				
IKKB_MOUSE	STANDARD;	PRT;	757 AA.	
ID	IKKB_MOUSE			
AC	O88351; O9RL6;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Inhibitor of nuclear factor kappa B kinase subunit (EC 2.7.1.-)			
DE	(I-kappa-B kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIBX)			
GN	IKKB OR IKK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEK1.			
RC	STEAIN-C57BL/6; TISSUE=Splice;			
RX	MEDLINE=96186238; PubMed=9520401;			
RA	Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,			
RA	Okumura K.;			
RT	"differential regulation of IkappaB kinase alpha and beta by two			
RT	upstream kinases, NF-kappaB-inducing kinase and mitogen-activated			
RT	protein kinase/ERK kinase kinase-1."			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542 (1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;			
RT	"Murine IKB kinase-B, a developmentally regulated protein kinase that			
RT	constitutively phosphorylates serine residues of IKB."			
RL	Submitted (AUG-1998) for the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	DEVELOPMENTAL STAGE.			
RX	MEDLINE=9945528; PubMed=10523828;			
RA	Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;			
RT	"Hematopoietic progenitor kinase-1 (HPK1) stress response signaling			
RT	pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a			
RT	developmentally regulated protein kinase."			
RL	Oncogene 18:5514-5524 (1999).			
RN	[4]			
RP	IKK PHOSPHORYLATION.			
RX	MEDLINE=99038238; PubMed=9819420;			
RA	Nemoto S., Didonato J.A., Lin A.;			

RT	"Coordinate regulation of Ikkapab kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappa-B-inducing kinase.";
RL	Mol. Cell. Biol. 18:7336-7343 (1998).
RN	(5).
RP	REVIEW.
RX	MEDLINE=20176139; PubMed=10712233;
RA	Jobin C., Sartor R.B.
RT	"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection."
RL	Am. J. Physiol. 278:C451-C462(2000).
CC	-I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.
CC	-I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MEKK1, MAP3K4/NIK, IKAP and IKB-ALPHA-P65-p50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBG and CREBBP (by similarity).
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic.
CC	-I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC	-I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout the mouse embryo, at E9.5 day its expression begins to be localized to the brain, neural ganglia, neural tube, and in liver at E12.5 day. At E15.5 day, the expression is further restricted to specific tissues of the embryo.
CC	-I- PTM: Phosphorylated by MEKK1 and probably also by MAP3K4/NIK. Weakly autophosphorylated.
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.
-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi.ac.uk/announcement/">http://www.ebi.ac.uk/announcement/</a> or send an email to <a href="mailto:license@ebi-eib.ch">license@ebi-eib.ch</a> ).
CC	
DR	EMBL; AF083524; AAC33557.1; -
DR	EMBL; AF088910; AAD52095.1; -
DR	HSSB; Q63450; LA06.
DR	MGP; MGI:1338071; Ikbb.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR002290; Ser_Thr_pkinase.
DR	InterPro; IPR001245; Tyr_pkinase.
DR	Pfam; PF00069; Pkinase; 1.
DR	PRINTS; PR00109; TYRKINASE.
DR	Prodom; PD000001; Prot_kinase; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW	Transferrase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
FT	DOMAIN 15 300
FT	DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT	DOMAIN 737 742 NEMO-BINDING.
FT	NP_BIND 21 29 ATP (BY SIMILARITY).
FT	BINDING 44 44 ATP (BY SIMILARITY).
FT	ACT_SITE 145 145 BY SIMILARITY.
FT	MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
FT	CONFLICT 56 56 N -> D (IN REF. 2).
FT	CONFLICT 343 343 N -> D (IN REF. 2).
FT	CONFLICT 356 356 K -> E (IN REF. 2).
FT	CONFLICT 390 390 L -> F (IN REF. 2).
FT	CONFLICT 406 406 P -> Q (IN REF. 2).
FT	CONFLICT 573 573 K -> R (IN REF. 2).
FT	CONFLICT 736 757 TLDSWTLMQDEDCSLDQACD -> VTA (IN REF. 2).

SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;  
 Query Match 70.7%; Score 41; DB 1; Length 757;  
 Best Local Similarity 85.7%; Pred. No. 29;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYV 7  
 |||||  
 428 KVMGQVW 434

DB 428 KVMGQVW 434

RESULT 7  
 IKKB RAT STANDARD; PRT; 757 AA.  
 AC 090Y78;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear kappa B kinase beta subunit (EC 2.7.1.1-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIB).  
 CN IKKB OR IKKB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Ravid K.  
 RT "IKK beta in megakaryocyte differentiation.";  
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of I-kappa-B kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappa-B-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Uobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKX, IKKKG  
 CC and CREBBP (by similarity).  
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -I- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; AF115282; AAF21978.1; -;  
 DR HSSP; Q63450; 1A06.  
 DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_kinase..  
 DR InterPro; IPR001245; Tyr\_kinase..  
 DR Pfam; PF00069; pkinase.1..  
 DR PRINTS; PR00109; TYRKINASE..  
 DR PRODOM; PD000001; Prot\_kinase.1..  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1..  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1..  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW phosphorylation..  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA; 86866 MW; 3AF646A7DF91F9C CRC64;

Query Match 70.7%; Score 41; DB 1; Length 757;  
 Best Local Similarity 85.7%; Pred. No. 29;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGQYV 7  
 |||||  
 428 KVMGQVW 434

DB 428 KVMGQVW 434

RESULT 8  
 CYST\_ECOLI STANDARD; PRT; 277 AA.  
 AC P16701;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Sulfate transport system permease protein cyst.  
 GN CYSU OR CYST OR B2424.  
 GN Escherichia coli.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=K12;  
 RX MEDLINE=90264334; PubMed=2188958;  
 RA Sliko A., Hryniewicz W.M., Hulanicka D.M., Boeck A.;  
 RT "Sulfate and thiosulfate transport in Escherichia coli K-12;  
 RT nucleotide sequence and expression of the cystWAM gene cluster.";  
 RL J. Bacteriol. 172:3351-3357(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=K12;  
 RX MEDLINE=97349980; PubMed=9205837;  
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,  
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
 RA Mitsuhashi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,  
 RA Oshima T., Oyama S., Saito N., Sempel G., Saich Y., Sivasubraman S.,  
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uenara K., Wada C.,  
 RA Yamagata S., Horiiuchi T.;  
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli  
 RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and

```

RT  analysis of its sequence features.";
RL  DNA Res. 4:91-113(1997).
CC  -1- FUNCTION: Part of the ABC transporter complex CysAMP (TC
CC  3.A.1.6.1) involved in sulfate/chiosulfate import. Probably
CC  responsible for the translocation of the substrate across the
CC  membrane.
CC  -1- SUBUNIT: The complex is composed of two ATP-binding proteins
CC  (CysA), two transmembrane proteins (CysT and CysW) and a solute-
CC  binding protein (CysP) (Probable).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC  (Probable).
CC  -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC  SYSTEM PERMEASE FAMILY. CysTW SUBFAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M32101; AAA23637.1; -.
DR  EMBL; AE000330; AAC75477.1; -.
DR  EMBL; D90871; BAA16298.1; -.
DR  EMBL; D90872; BAA16307.1; -.
DR  PIR; A35402; ORECSST.
DR  EcoGene; EG10197; CysU.
DR  InterPro; IPR000515; BPD_transp.
DR  InterPro; IPR005677; Sulph_transpct2.
DR  Pfam; PF00528; BPD_transp; 1.
DR  TIGRFAMs; TIGR00969; 3a0106s02; 1.
DR  PROSITE; PS00402; BPD_TRANS_P_NN_MEMBR; 1.
KW  Transport, Sulfate transport, Membrane, Inner membrane, Transmembrane;
KM  Complete proteome.
FT  TRANSMEM 17 37 POTENTIAL.
FT  TRANSMEM 64 84 POTENTIAL.
FT  TRANSMEM 99 119 POTENTIAL.
FT  TRANSMEM 136 156 POTENTIAL.
FT  TRANSMEM 185 205 POTENTIAL.
FT  TRANSMEM 215 235 POTENTIAL.
FT  TRANSMEM 243 263 POTENTIAL.
SQ  SEQUENCE 277 AA; 30291 MM; 1392821B0DE24459 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 277;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGYQYQV 9
Db 44 WAQYMEV 50

RESULT 9
PTPL_YEAST STANDARD; PRT; 335 AA.
ID PTPL_YEAST
AC P25044;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protein-tyrosine phosphatase 1 (EC 3.1.3.48) (PTPase 1).
GN PTPL OR YDL230W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91302312; PubMed=1649172;
RX Guan K., Deschenes R.J., Qiu H., Dixon J.E.;
RT "Cloning and expression of a yeast protein tyrosine phosphatase.";
RL J. Biol. Chem. 266:12964-12970(1991).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RA Rasmussen S.W.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IS NOT REQUIRED FOR VEGETATIVE GROWTH.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR  EMBL; M64062; AAA34923.1; -.
DR  EMBL; Z74278; CAA98809.1; -.
DR  PIR; A39862; A39862.
DR  HSP; P29350; 1GMZ.
DR  SGD; S0002389; PTP1.
DR  GO; GO:0006470; P:Protein amino acid dephosphorylation; IDA.
DR  InterPro; IPR000387; TYR_phosphatase.
DR  InterPro; IPR00242; TYR_PP.
DR  Pfam; PF00102; Y_phosphatase; 1.
DR  PRINTS; PR00700; PRTYPPHASE.
DR  SMART; SM00194; PTPC; 1.
DR  PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR  PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR  PROSITE; PS50055; TYR_PHOSPHATASE_PP; 1.
KW Hydrolase.
FT ACT SITE 252 252 BY SIMILARITY.
SQ SEQUENCE 335 AA; 38868 MM; 15F71E50694B562 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 335;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVMGYQYQV 9
Db 108 KTWQYQVQW 116

RESULT 10
YCD5_ECOLI STANDARD; PRT; 807 AA.
ID YCD5_ECOLI
AC P75907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ycd5 precursor.
GN YCD5 OR B1024 OR 21526 OR ECS1270.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Berra N.T., Burland V.,
RA Riley M., Collado-VIDE J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;

```

RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano M., Horikuchi T.,  
 RT "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome  
 RT corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocasts K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.,  
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7";  
 RL Nature 409:529-533(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Iehi K., Yokoyama K.,  
 RA Han C.-G., Ohnishi E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasekawa C., Ogasawara N., Yasunaga T.,  
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.,  
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*  
 RT O157:H7 and genomic comparison with a laboratory strain K-12";  
 RL DNA Res. 8:11-22(2001).  
 CC -1- SUBCELLULAR LOCATION: Outer membrane (Potential).  
 CC -1- SIMILARITY: STRONG, TO Y.PESTIS HEMIN-BINDING PROTEIN HNSH.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AE000204; AAC74109.1; -;  
 DR EMBL; D90739; BAA35806.1; -;  
 DR EMBL; D90740; BAA35808.1; -;  
 DR EMBL; AE005302; AAG55642.1; -;  
 DR EMBL; AP002554; BAB34693.1; -;  
 DR PIR; F64844; F64844.  
 DR PIR; F90787; F90787.  
 DR Ecogene; EG13865; ycds.  
 DR InterPro; IPR001440; TPR.  
 DR Pfam; PF00515; TPR; 1.  
 DR Hypothetical protein; Outer membrane; Signal; Complete proteome.  
 FT SIGNAL 1 26  
 FT CHAIN 27 807  
 FT SEQUENCE 807 AA; 92207 MW; B20067C3D41723FD CR64;  
 SQ  
 Query Match 69.0%; Score 40; DB 1; Length 807;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 WGOYW 7  
 DB 314 WGOYW 318  
 RESULT 11  
 ID COAT TRSV STANDARD; PRT; 515 AA.  
 AC Q88894;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Coat protein precursor (Capsid protein).  
 OS Tobacco ringspot virus (Tobry) (TRSV).  
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
 CC Nepoviruses.  
 CC NCBI\_TaxID=12282;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=94152161; PubMed=8109164;  
 RA Buckley B., Silva S., Singh S.,  
 RT "Nucleotide sequence and in vitro expression of the capsid protein  
 RT gene of tobacco ringspot virus";  
 RL Virus Res. 30:335-349(1993).  
 RN [2]  
 RP ERRATUM.  
 RX MEDLINE=95274284; PubMed=7754671;  
 RA Buckley B., Silva S., Singh S.,  
 RA Virus Res. 35:111-111(1995).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).  
 RX MEDLINE=98179933; PubMed=9519407;  
 RA Chandrasekar V., Johnson J.E.,  
 RT "The structure of tobacco ringspot virus: a link in the evolution of  
 RT icosahedral capsids in the picornavirus superfamily";  
 RL Structure 6:157-171(1998).  
 CC -1- SUBUNIT: THE VIRUS COAT IS FORMED OF 60 COPIES OF THE COAT  
 CC PROTEIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L09205; AAA74963.1; -;  
 DR PDB; 1A6C; 15-JUL-98.  
 DR InterPro; IPR005054; Nepo\_coat.  
 DR InterPro; IPR005305; Nepo\_coat\_C.  
 DR InterPro; IPR005306; Nepo\_coat\_N.  
 DR Pfam; PF03391; Nepo\_coat; 1.  
 DR Pfam; PF03689; Nepo\_coat\_C; 1.  
 DR Pfam; PF03689; Nepo\_coat\_N; 1.  
 DR Coat protein; 3D-structure.  
 KW PROPEP 1 2  
 FT CHAIN 3 515 COAT PROTEIN.  
 FT TURN 10 11  
 FT TURN 12 19  
 FT TURN 22 23  
 FT TURN 26 27  
 FT TURN 29 34  
 FT TURN 35 41  
 FT TURN 44 53  
 FT TURN 55 56  
 FT TURN 59 65  
 FT TURN 70 71  
 FT TURN 75 81  
 FT TURN 87 90  
 FT TURN 96 99  
 FT TURN 100 100  
 FT TURN 105 107  
 FT TURN 117 121  
 FT TURN 122 126  
 FT TURN 130 131  
 FT TURN 141 146  
 FT TURN 159 165  
 FT TURN 171 171  
 FT TURN 181 182  
 FT TURN 191 202  
 FT TURN 210 212  
 FT TURN 221 222  
 FT TURN 227 230

FT HELIX 231 236  
 FT TURN 237 238  
 FT STRAND 239 239  
 FT STRAND 241 242  
 FT STRAND 244 252  
 FT TURN 256 257  
 FT STRAND 259 267  
 FT HELIX 275 280  
 FT STRAND 284 286  
 FT STRAND 290 295  
 FT TURN 299 300  
 FT STRAND 303 304  
 FT STRAND 312 322  
 FT TURN 325 326  
 FT STRAND 331 342  
 FT STRAND 349 349  
 FT STRAND 357 363  
 FT TURN 369 371  
 FT STRAND 374 374  
 FT STRAND 378 378  
 FT STRAND 391 394  
 FT HELIX 398 404  
 FT TURN 405 405  
 FT STRAND 406 418  
 FT STRAND 421 421  
 FT TURN 425 427  
 FT STRAND 432 436  
 FT TURN 440 441  
 FT STRAND 447 450  
 FT STRAND 455 460  
 FT TURN 470 471  
 FT STRAND 480 484  
 FT TURN 489 491  
 FT STRAND 492 492  
 FT TURN 493 493  
 FT STRAND 494 510  
 FT STRAND 512 515  
 SQ SEQUENCE 515 AA; 57168 MW; 22084021BA349E96 CRC64;

Query March 67.2%; Score 39; DB 1; Length 515;  
 Best Local Similarity 83.3%; Pred. No. 41;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WGOYWO 8  
 Db 441 WGAATWQ 446

RESULT 12  
 ID\_GAP1\_YEAST STANDARD; PRT; 602 AA.  
 AC P19145;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE General amino-acid permease GAP1.  
 OS GAP1 OR YMR039W.  
 OC Saccharomycetes cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90306009; PubMed=2194797;  
 RA Jauniaux J.-C., Gremson M.;  
 RT "GAP1, the general amino acid permease gene of Saccharomycetes  
 RT cerevisiae. Nucleotide sequence, protein similarity with the other  
 RT bakers yeast amino acid permeases, and nitrogen catabolite  
 RT repression.";  
 RL Eur. J. Biochem. 190:39-44(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Urrastarazu L.A., Jauniaux J.-C.;

RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN FUNCTION IN L-CYSTEINE UPTAKE.  
 RX PubMed=10467005;  
 RA During-Olsen L., Regenberg B., Gjermansen C., Kielland-Brandt M.C.,  
 RA Hansen J.;  
 RT "Cysteine uptake by Saccharomycetes cerevisiae is accomplished by  
 RT multiple permeases.";  
 RL Curr. Genet. 35:609-617(1999).  
 CC -I- FUNCTION: Permease for various amino acids as well as for GABA.  
 CC Can also transport L-cysteine.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- SIMILARITY: Belongs to the amino acid permease family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announce/>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

DR EMBL; X52633; CA36858.1; -;  
 DR EMBL; Z28264; CA82113.1; -;  
 DR PIR; S38111; S38111.  
 DR SCD; S0001747; GAP1.  
 DR GO; GO:0005887; C: integral to plasma membrane; IDA.  
 DR GO; GO:0005281; F: general amino acid permease activity; IMP.  
 DR GO; GO:0006865; P: amino acid transport; IMP.  
 DR InterPro; IPR002293; AA/rel\_permease1.  
 DR InterPro; IPR004840; AAC\_permease.  
 DR InterPro; IPR004841; Permease.  
 DR InterPro; IPR004762; Yeast AA.perm.  
 DR Pfam; PF00324; aa\_permeases; 1.  
 DR TIGRfam; TIGR00913; 2A0310; 1.  
 DR PROSITE; PS00218; AMINO\_ACID\_PERMEASE\_1; 1.  
 DR KX Transport; Amino-acid transport; Transmembrane.  
 FT TRANSMEM 96 116 POTENTIAL.  
 FT TRANSMEM 122 142 POTENTIAL.  
 FT TRANSMEM 166 185 POTENTIAL.  
 FT TRANSMEM 205 224 POTENTIAL.  
 FT TRANSMEM 238 256 POTENTIAL.  
 FT TRANSMEM 281 298 POTENTIAL.  
 FT TRANSMEM 322 342 POTENTIAL.  
 FT TRANSMEM 377 396 POTENTIAL.  
 FT TRANSMEM 422 442 POTENTIAL.  
 FT TRANSMEM 452 472 POTENTIAL.  
 FT TRANSMEM 492 510 POTENTIAL.  
 FT TRANSMEM 530 548 POTENTIAL.  
 FT CONFLICT 122 122 MISSING (IN REF. 1).  
 FT CONFLICT 189 189 I -> A (IN REF. 1).  
 FT CONFLICT 338 338 I -> V (IN REF. 1).  
 FT CONFLICT 518 518 V -> L (IN REF. 1).  
 SQ SEQUENCE 602 AA; 65655 MW; 5363616447907458 CRC64;

Query March 67.2%; Score 39; DB 1; Length 602;  
 Best Local Similarity 83.3%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 WVGQYW 7  
 Db 496 WVGQYW 501

RESULT 13  
 ID\_POL\_SIV3 STANDARD; PRT; 100 AA.  
 AC P12501;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE POL polypeptide [Contains: Protease (Retropepsin) (EC 3.4.23.-);  
 DE Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)]

```

DE (Fragment).
GN POL.
OS Simian immunodeficiency virus (AGM385 isolate) (SIV-AGM).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OK NCBI_TaxId=11729;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89012184; PubMed=3172340;
RA Daniel M.D., Li Y., Naidu Y.M., Durda P.J., Schmidt D.K.,
RA Troup C.D., Silva D.P., Mackey J.J., Kestler H.W., Sehgal P.K.,
RA King N.W., Ohta Y., Hayami M., Desrosiers R.C.;
RT "Simian immunodeficiency virus from African green monkeys.";
RL J. Virol. 62:4123-4128(1988).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA)(N).
CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M21311; AAA47583.1; -.
CC DR HIV; M21311; POLSAGM38.
CC DR MEROPS: A02.0P; -.
CC DR InterPro: IPR001969; Asprotease_site.
CC DR InterPro: IPR002156; RNaseH.
CC DR Pfam: PF00075; rnaseh; 1.
CC DR PROSITE: PS00141; ASP_PROTEASE; PARTIAL.
CC DR AIBS: Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
CC KW Nuclease; Transferase; RNA-directed DNA polymerase.
CC FT NON TER 1 100
CC FT NON TER 1 100
CC SQ SEQUENCE 100 AA; 12023 MW; FC11C6792D37E3F CRC64;
Query Match 65.5%; Score 38; DB 1; Length 100;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 WGYWQV 9
Db 26 WADYQV 32

```

```

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RT Nature 413:852-856(2001).
RN (2)
RN SEQUENCE OF 1-15 FROM N.A.
RP STRAIN=LT2;
RX MEDLINE=91358382; PubMed=1909324;
RA Hryniewicz M.M., Kredich N.M.;
RT "The cysB promoter of Salmonella typhimurium: characterization of two
RT binding sites for CysB protein, studies of in vivo transcription
RT initiation, and demonstration of the anti-inducer effects of
RT thiosulfate.";
RL J. Bacteriol. 173:5876-5886(1991).
CC -1- FUNCTION: Part of the ABC transporter complex CysAMP (TC
CC 3.A.1.6.1) involved in sulfate/thiosulfate import. Probably
CC responsible for the translocation of the substrate across the
CC membrane (By similarity).
CC -1- SUBUNIT: The complex is composed of two ATP-binding proteins
CC (cysA), two transmembrane proteins (cysT and cysW) and a solute-
CC binding protein (cysP) (Probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (potential).
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF008810; AAU21337.1; -.
CC DR StyGene; SG10520; cysU.
CC DR InterPro: IPR000515; BPD_transp.
CC DR InterPro: IPR005667; BpLph_transpct2.
CC DR Pfam: PF00528; BPD_transp; 1.
CC DR TIGRFAMs: TIGR00965; 3a0106s02; 1.
CC DR PROSITE: PS00402; BPD_TRANSP_INN_MEMBER; 1.
CC KW Transport; Sulfate transport; Membrane; Inner membrane; Transmembrane;
CC Complete proteome.
CC FT TRANSMEM 17 37
CC FT TRANSMEM 64 84
CC FT TRANSMEM 99 119
CC FT TRANSMEM 136 156
CC FT TRANSMEM 188 205
CC FT TRANSMEM 215 235
CC FT TRANSMEM 243 263
CC FT TRANSMEM 277 301
CC SQ SEQUENCE 277 AA; 30182 MW; 8C22531C99E50748 CRC64;
Query Match 65.5%; Score 38; DB 1; Length 277;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 WGYWQV 9
Db 44 WADYQV 50

```

```

RESULT 15
LIP3 DROME STANDARD; PRT; 394 AA.
AC 046108;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lipase 3 precursor (EC 3.1.1.-) (DmLip3).
GN LIP3 OR CG8823.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

```

ON NCBI\_TaxID=7227;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Canton-S;  
 RX MEDLINE=98227315; PubMed=9566193;  
 RA Picotillo D., Manzi A., Tino A., Pilo Boyl P., Graziani F., Malva C.;  
 RT "The *Drosophila melanogaster* lipase homologs: a gene family with  
 RL tissue and developmental specific expression.";  
 RN J. Mol. Biol. 276:877-885(1998).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Butts K.C., Buxam D.A., Butler H., Cadenau E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.U., Wei M.-H., Ibeagwa C.,  
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Liao X., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Plittman G.S., Pan S., Pollard J.C., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -1- TISSUE SPECIFICITY: FAT BODY.  
 CC -1- DEVELOPMENTAL STAGE: ONLY AT LARVAL STAGES.  
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,  
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO  
 CC LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.  
 CC  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC  
 CC EMBL: Y14367, CAA74737.1; -.  
 CC EMBL: AE003699, AAF54935.1; -.  
 CC EMBL: FBgn0023495, Lip3.  
 CC InterPro: IPR000073; A/B hydrolase.  
 CC InterPro: IPR000734; Lipase.  
 CC InterPro: IPR000379; Ser esterase site.  
 CC Pfam: PF04083; abhydrolase\_1.  
 CC Pfam: PF00561; abhydrolase\_1.

```

CC PROSITE PS00120: LIPASE. SER: 1.
CC KM Hydrolyase; lipid degradation; Signal; Glycoprotein.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT CHAIN 1 394 LIPASE 3.
CC FT ACT_SITE 164 164 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 369 369 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 394 AA; 44901 MW; A719BD1743673802 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 394;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 KTWGQYWOV 9
Db 120 KWPPTWQOI 128

RESULT 16
PT2B ARATH STANDARD; PRT; 585 AA.
ID PT2B ARATH
AC P46032;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DN Peptide transporter PTR2-B (Histidine transporting protein).
GN PTR2-B OR NTRI OR AT2G02040 OR F14H20.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN NM
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RC Song W., Steiner H.-Y., Zhang L., Naider F., Stacey G.,
RA Becker U.M.;
RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
RN NM
RP SEQUENCE FROM N.A.
RC STRAIN=cv. C24;
RC MEDLINE=94307379; PubMed=8033999;
RX RA Frommer W.B., Hummel S., Rentsch D.;
RT "Cloning of an Arabidopsis histidine transporting protein related to
RT nitrate and peptide transporters.";
RN NM
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RX RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Ko H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Taiton L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
RA Niernm J.C., White O., Eissen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

```

CC -----
DR EMBL: U00008; AAA16381.1; ALT_FRAME.
DR EMBL: AE000308; AAC75245.1; -.
DR PIR: G64987; G64987.
DR EcoGene; EGI2045; YeJH.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR01650; Helicase_C.
DR Pfam; PF00270; DEAD_1.
DR Pfam; PF00271; Helicase_C_1.
DR SMART; SM00487; DEXDC_1.
DR SMART; SM00490; HELIC_C_1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 586 AA; 66413 MW; 2D173250F8333DF CRC64;

Query Match 65.5%; Score 38; DB 1; Length 586;
Best Local Similarity 57.1%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GQYMOV 9
DB 562 GQYMOV 567

RESULT 18
GN4_THERFU STANDARD; PRT; 880 AA.
AC P26221; Q08167;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Endoglucanase E-4 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase E-4)
GN CE1D.
OS Thermomonospora fusca.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptopodangineae; Nocardiopsaceae; Thermobifida.
OX NCBI_TaxID=2021;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=YX;
RX MEDLINE=94028932; PubMed=8215374;
RA Jung E.D., Lao G., Irwin D., Barr B.K., Benjamin A., Wilson D.B.;
RT "DNA sequences and expression in Streptomyces lividans of an
exoglucanase gene and an endoglucanase gene from Thermomonospora
fusca.";
RL Appl. Environ. Microbiol. 59:3032-3043(1993).
[2]
RP REVISIONS.
RA Wilson D.B.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP PARTIAL SEQUENCE FROM N.A.
RC STRAIN=YX;
RX MEDLINE=91258320; PubMed=1904434;
RA Lao G., Chanas G.S., Jung E.D., Wilson D.B.;
RT "DNA sequences of three beta-1,4-endoglucanase genes from
Thermomonospora fusca.";
RL J. Bacteriol. 173:3397-3407(1991).
[4]
RP SEQUENCE OF 47-67.
RA Wilson D.B.;
RL "Cellulases of Thermomonospora fusca.";
RL Mech. Enzymol. 160:314-323(1988).
[5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 47-651.
RX MEDLINE=97475222; PubMed=9334746;
RA Sakon J., Irwin D., Wilson D.B., Karplus P.A.;
RT "Structure and mechanism of endo/exocellulase E4 from Thermomonospora
fusca.";
RL Nat. Struct. Biol. 4:810-818(1997).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic

```

```

CC -----
DR EMBL: U00008; AAA16381.1; ALT_FRAME.
DR EMBL: AE000308; AAC75245.1; -.
DR PIR: G64987; G64987.
DR EcoGene; EGI2045; YeJH.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR01650; Helicase_C.
DR Pfam; PF00270; DEAD_1.
DR Pfam; PF00271; Helicase_C_1.
DR SMART; SM00487; DEXDC_1.
DR SMART; SM00490; HELIC_C_1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 586 AA; 66413 MW; 2D173250F8333DF CRC64;

Query Match 65.5%; Score 38; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GQYMOV 9
DB 562 GQYMOV 567

RESULT 17
YEJH_ECOLI STANDARD; PRT; 586 AA.
AC P33919; P36926; P36927; P76449;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yeJH.
GN YEJH OR B2184.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=X12 / BHB2600;
RA Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
RL Church G.M.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=X12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plundt G., Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
-i- SIMILARITY: SOME SIMILARITY TO A PHAGE PROTEIN AND RESTRICTION-
MODIFICATION SYSTEMS.
-i- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
THAT PRODUCE THREE SEPARATE ORFS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial

```



CC linkages in cellulose, lichenin and cereal beta-D-glucans.  
 CC -1- PATHWAY: Cellulose degradation.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY E (FAMILY 9 OF GLYCOSYL  
 CC HYDROLASES).  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by, and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L20093; AAB2155.1; -;  
 DR EMBL; M73322; AAB2397.1; ALT\_SEQ.  
 DR PDB; 1US4; 17-SEP-97.  
 DR PDB; 1TF4; 04-SEP-97.  
 DR PDB; 1TF4; 04-SEP-97.  
 DR PDB; 4TF4; 04-SEP-97.  
 DR InterPro; IPR001919; Bac\_celose-bind.  
 DR InterPro; IPR001956; CBD\_3.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR001701; Glyco\_hydro\_9.  
 DR Pfam; PF00553; CBM\_2; 1.  
 DR Pfam; PF00942; CBM\_3; 1.  
 DR Pfam; PF00041; fn3\_1.  
 DR Pfam; PF00759; Glyco\_hydro\_9; 1.  
 DR SMART; SM00637; CBD\_I1; 1.  
 DR SMART; SM00650; FN3; 1.  
 DR PROSITE; PS00561; CBD\_BACTERIAL; 1.  
 DR PROSITE; PS00592; GLYCOSYL\_HYDROL\_F9\_1; 1.  
 DR PROSITE; PS00698; GLYCOSYL\_HYDROL\_F9\_2; 1.  
 KM Cellulose degradation; Hydrolase; Glycosidase; Signal; 3D-structure.  
 FT SIGNAL 1 46  
 FT CHAIN 47 880  
 FT DOMAIN 675 766  
 FT ACT\_SITE 427 427  
 FT ACT\_SITE 461 461  
 FT ACT\_SITE 470 470  
 FT ACT\_SITE 52 65  
 FT HELIX 66 66  
 FT TURN 67 67  
 FT STRAND 69 69  
 FT TURN 73 73  
 FT TURN 78 78  
 FT STRAND 83 83  
 FT TURN 85 88  
 FT HELIX 89 91  
 FT TURN 92 92  
 FT STRAND 99 99  
 FT STRAND 107 108  
 FT HELIX 109 125  
 FT HELIX 127 132  
 FT TURN 133 134  
 FT TURN 136 152  
 FT HELIX 153 153  
 FT STRAND 156 156  
 FT TURN 157 158  
 FT STRAND 159 164  
 FT STRAND 167 171  
 FT TURN 172 172  
 FT HELIX 177 179  
 FT STRAND 186 190  
 FT TURN 191 192  
 FT STRAND 193 193  
 FT HELIX 196 213  
 FT TURN 214 216  
 FT HELIX 218 237  
 FT HELIX 242 244  
 FT TURN 245 245

FT TURN 247 248  
 FT HELIX 249 252  
 FT HELIX 259 273  
 FT HELIX 276 285  
 FT HELIX 286 288  
 FT STRAND 291 291  
 FT TURN 293 294  
 FT STRAND 298 298  
 FT HELIX 310 321  
 FT HELIX 324 336  
 FT TURN 337 339  
 FT STRAND 341 341  
 FT TURN 342 343  
 FT STRAND 344 344  
 FT STRAND 348 348  
 FT TURN 350 351  
 FT STRAND 354 354  
 FT TURN 359 360  
 FT HELIX 361 378  
 FT HELIX 382 400  
 FT TURN 401 401  
 FT TURN 404 405  
 FT STRAND 410 410  
 FT TURN 411 412  
 FT HELIX 424 427  
 FT TURN 428 428  
 FT TURN 434 435  
 FT TURN 445 446  
 FT STRAND 448 448  
 FT TURN 455 456  
 FT TURN 463 464  
 FT TURN 466 469  
 FT HELIX 473 476  
 FT HELIX 477 490  
 FT STRAND 509 517  
 FT STRAND 522 531  
 FT TURN 535 536  
 FT STRAND 540 540  
 FT STRAND 543 550  
 FT TURN 553 554  
 FT HELIX 557 559  
 FT STRAND 561 563  
 FT STRAND 567 567  
 FT STRAND 576 579  
 FT TURN 580 581  
 FT STRAND 582 588  
 FT TURN 590 591  
 FT STRAND 594 594  
 FT TURN 599 602  
 FT STRAND 603 611  
 FT TURN 614 615  
 FT HELIX 618 620  
 FT TURN 622 624  
 FT HELIX 625 626  
 FT STRAND 632 633  
 FT TURN 635 636  
 FT STRAND 638 641  
 FT TURN 642 643  
 FT STRAND 644 647  
 SQ SEQUENCE 880 AA; 95202 MW; 5EA9A6ABF45A4D9A CRC64;

Query Match 65.5%; Score 38; DB 1; Length 880;  
 Best Local Similarity 83.3%; Pred. No. 98;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 2 VMGQYW 7  
 Db 263 VMGAYW 268

RESULT 19  
 YE68\_METJA STANDARD; PRT; 1009 AA.

AC Q58663; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein MJ1468.  
 GN MJ1468.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 CC NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=8688087;  
 RA Bult C.J., White O., Olsen G.J., Olsen G.J., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerecavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirnesh E.F., Weisslock K.G., Merrick J.M., Glodok A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,  
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Frazer C.M., Smith H.O., Woese C.R., Venter J.C.,  
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";  
 RT Science 273:1058-1073(1996).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- SIMILARITY: Contains 5 PKD domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U67588; AAB99478.1; -.  
 DR PIR; C64483; C64483.  
 DR TIGR; MJ1468; -.  
 DR InterPro: IPR000601; PKD\_domain.  
 DR Pfam; PF00801; PKD; 5.  
 DR SMART; SM00089; PKD; 7.  
 DR PROSITE; PS0093; PKD; 5.  
 KW Hypothetical protein; Transmembrane; Repeat; Complete proteome.  
 FT TRANSMEM 6 POTENTIAL.  
 FT TRANSMEM 985 1005  
 FT DOMAIN 213 247 PKD 1.  
 FT DOMAIN 436 503 PKD 2.  
 FT DOMAIN 724 806 PKD 3.  
 FT DOMAIN 822 886 PKD 4.  
 FT DOMAIN 925 962 PKD 5.  
 FT DOMAIN 293 298 POLY-ASN  
 SQ SEQUENCE 1009 AA; 15119 MW; 135954933EAB7972 CRC64;  
 Query Match 65.5%; Score 38; DB 1; Length 1009;  
 Best Local Similarity 66.7%; Pred. No. 1,1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OS Cellulomonas fimi.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Micrococcineae; Cellulomonadaceae; Cellulomonas.  
 CC NCBI\_TaxID=1708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=91100298; PubMed=1987122;  
 RX Meinke A., Braun C., Gilkes N.R., Kilburn D.G., Miller R.C. Jr.,  
 RA Warren R.A.J.;  
 RT "Unusual sequence organization in CenB, an inverting endoglucanase  
 from Cellulomonas fimi.";  
 RT J. Bacteriol. 173:308-314(1991).  
 RN [2]  
 RP DOMAINS.  
 RC MEDLINE=92041609; PubMed=1938913;  
 RX Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;  
 RT "Multiple domains in endoglucanase B (CenB) from Cellulomonas fimi:  
 RT functions and relatedness to domains in other polypeptides.";  
 RL J. Bacteriol. 173:7126-7135(1991).  
 CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE  
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:  
 CC (1) ENDOLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;  
 CC (2) EXOCELLULOBIOTRANSFERASES THAT CUT THE DISACCHARIDE CELLULOSE  
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;  
 CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYSE THE CELLULOSE AND OTHER  
 CC SHORT CELLULO-OLIGOSACCHARIDES TO GLUCOSE.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.  
 CC -1- MISCELLANEOUS: THE LINKER REGION (ALSO TERMED "HINGE") MAY BE A  
 CC POTENTIAL SITE FOR PROTEOLYSIS.  
 CC -1- SIMILARITY: MAY CONTAIN A SECOND CBD IN THE CATALYTIC DOMAIN.  
 CC -1- SIMILARITY: Contains 3 fibronectin type III domains.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY E (FAMILY 9 OF GLYCOSYL  
 CC HYDROLASES).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M64644; AAA23086.1; -.  
 DR PIR; A39199; A39199.  
 DR HSSP; P26221; ITR4.  
 DR InterPro: IPR001919; Bac\_cellose-bind.  
 DR InterPro: IPR001956; CBD\_3.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR001701; Glyco\_hydro\_9.  
 DR Pfam; PF00553; CBM\_2; 1.  
 DR Pfam; PF00942; CBM\_3; 1.  
 DR Pfam; PF00041; fn3; 3.  
 DR Pfam; PF00759; Glyco\_hydro\_9; 1.  
 DR SMART; SM00637; CBD\_II; 1.  
 DR SMART; SM00060; FN3; 3.  
 DR PROSITE; PS00561; CBD\_BACTERIAL; 1.  
 DR PROSITE; PS00592; GLYCOSYL\_HYDROL\_F9\_1; 1.  
 DR PROSITE; PS00698; GLYCOSYL\_HYDROL\_F9\_2; 1.  
 KW Cellulose degradation; Hydrolyase; Glycosidase; Repeat; Signal.  
 FT SIGNAL 1 33  
 FT CHAIN 34 1045  
 FT CATALYTIC 34 643  
 FT DOMAIN 644 650  
 FT DOMAIN 651 733  
 FT DOMAIN 734 748  
 FT DOMAIN 749 830  
 FT DOMAIN 831 846  
 FT DOMAIN 847 930  
 FT DOMAIN 931 944  
 FT DOMAIN 945 1045  
 FT ACT\_SITE 410 410  
 FT ACT\_SITE 449 449  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.

FT ACT\_SITE 458 458 BY SIMILARITY.  
FT DISULFID 946 1044 BY SIMILARITY.  
SQ SEQUENCE 1045 AA; 108990 MW; AC2F7B84E4E3C4F0 CRC64;  
Query Match 65.5%; Score 38; DB 1; Length 1045;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VMGOYV 7  
Db 251 VMGOYV 256

RESULT 21  
POL\_SIVAG STANDARD; PRT; 1046 AA.  
ID POL\_SIVAG  
AC P27580;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE POL polypeptide [Contains: Protease (Retropesin) (EC 3.4.23.-);  
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].  
GN POL.  
OS Simian immunodeficiency virus (AGM3 isolate) (SIV-AGM).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11730;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90232731; PubMed=2158689;  
RA Baler M., Garber C., Mueller C., Cichutek K., Kurth R.;  
RT "Complete nucleotide sequence of a simian immunodeficiency virus from  
African green monkeys: a novel type of intragroup divergence.";  
RL Virology 176:216-221(1990).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-  
phosphomonoester.  
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
+ {DNA} (N).  
CC -1- PM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE  
DETERMINED.  
CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.  
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO  
KNOWN AS THE RETROPEPSIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M30931; AAA91914.1; -.  
DR HSPSP; P03366; IHRH.  
DR MEROPS; A02.003; -.  
DR InterPro; IPR001995; Asparticase\_rtrv.  
DR InterPro; IPR001969; Asparticase\_site.  
DR InterPro; IPR001037; Integrase\_C.  
DR InterPro; IPR003308; Integrase\_Zn.  
DR InterPro; IPR002156; RNaseH.  
DR InterPro; IPR001584; Rve.  
DR InterPro; IPR000477; RVTse.  
DR Pfam; PF00552; Integrase\_1.  
DR Pfam; PF00075; RNaseH; 1.  
DR Pfam; PF00665; Irv; 1.  
DR Pfam; PF00077; Irv; 1.  
DR Pfam; PF00078; Irv; 1.  
DR PROSITE; PS00141; ASP\_PROTASE; 1.  
DR PROSITE; PS00175; ASP\_PROT\_RETROV; 1.  
KW AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;  
Nuclease; Transferase; RNA-directed DNA polymerase.  
FT CHAIN 1 195  
FT ACT\_SITE 118 118 BY SIMILARITY.

SQ SEQUENCE 1046 AA; 119328 MW; 9068415C43AD0A6B CRC64;  
Query Match 65.5%; Score 38; DB 1; Length 1046;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 WGOYV 9  
Db 597 WADYMOV 603

RESULT 22  
POL\_SIVAG STANDARD; PRT; 1047 AA.  
ID POL\_SIVAG  
AC P27573;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE POL polypeptide [Contains: Protease (Retropesin) (EC 3.4.23.-);  
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].  
GN POL.  
OS Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM).  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90156504; PubMed=2304139;  
RA Johnson P.R., Fomsgard A., Allan J., Gravel M., London W.T.,  
RA Olmstead R.A., Hirsch V.M.;  
RT "Simian immunodeficiency viruses from African green monkeys display  
unusual genetic diversity.";  
RL J. Virol. 64:1086-1092(1990).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-  
phosphomonoester.  
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
+ {DNA} (N).  
CC -1- PM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE  
DETERMINED.  
CC -1- MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM  
KENYA.  
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO  
KNOWN AS THE RETROPEPSIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M29975; AAA91906.1; -.  
DR HSPSP; P03366; IHRH.  
DR MEROPS; A02.003; -.  
DR InterPro; IPR001995; Asparticase\_rtrv.  
DR InterPro; IPR001969; Asparticase\_site.  
DR InterPro; IPR001037; Integrase\_C.  
DR InterPro; IPR003308; Integrase\_Zn.  
DR InterPro; IPR002156; RNaseH.  
DR InterPro; IPR001584; Rve.  
DR InterPro; IPR000477; RVTse.  
DR Pfam; PF00552; Integrase\_1.  
DR Pfam; PF00075; RNaseH; 1.  
DR Pfam; PF00077; Irv; 1.  
DR Pfam; PF00665; Irv; 1.  
DR Pfam; PF00078; Irv; 1.  
DR PROSITE; PS00141; ASP\_PROTASE; 1.  
DR PROSITE; PS00175; ASP\_PROT\_RETROV; 1.  
KW AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;  
Nuclease; Transferase; RNA-directed DNA polymerase.  
FT CHAIN 113 113  
FT ACT\_SITE 1047 AA; 118871 MW; A38DDDA39F268E5 CRC64;  
SQ SEQUENCE 1047 AA; 118871 MW; A38DDDA39F268E5 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 1047;  
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WGYWQV 9  
 |||||  
 Db 592 WADYWQV 598

RESULT 23  
 POL\_SIVAT STANDARD; PRT; 1061 AA.  
 AC P05895;  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE POL polyprotein (Contains: Protease (Retroviral) (EC 3.4.23.-);  
 DE Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)).  
 GN POL.  
 OS Simian immunodeficiency virus (Tyo-1 isolate) (SIV-AGM).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11731;  
 RN [1]  
 RP MEDLINE=88232906; PubMed=3374586;  
 RA Fukasawa M., Miura T., Hasegawa A., Morikawa S., Tsujimoto H.,  
 RA Miki K., Kitanura T., Hayami M.;  
 RT "Sequence of simian immunodeficiency virus from African green monkey,  
 RT Nature 333:457-461(1988)."  
 RL Nature 333:457-461(1988).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-  
 CC phosphomonoester.  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
 CC + {dNp} (N).  
 CC -1- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE  
 CC DETERMINED.  
 CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO  
 CC KNOWN AS THE RETROPEPSIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X07805; CA30658.1; ALT\_SEQ.  
 DR HSSP; P26315; 2WP.  
 DR HIV; X07805; POLSAGMTY.  
 DR MEROPS; A02.003; -;  
 DR InterPro; IPR001995; Asparticase, rtrv.  
 DR InterPro; IPR001969; Asparticase, site.  
 DR InterPro; IPR001037; Integrase\_C.  
 DR InterPro; IPR003308; Integrase\_Zn.  
 DR InterPro; IPR002156; RNaseH.  
 DR InterPro; IPR001584; Rve.  
 DR InterPro; IPR000477; RVTse.  
 DR Pfam; PF00552; Integrase; 1.  
 DR Pfam; PF02022; Integrase\_Zn; 1.  
 DR Pfam; PF00075; rnsesH; 1.  
 DR Pfam; PF00665; rve; 1.  
 DR Pfam; PF00077; rvc; 1.  
 DR Pfam; PF00078; rvd; 1.  
 DR PROSITE; PS00141; ASP\_PROTASE; 1.  
 DR PROSITE; PS00175; ASP\_PROT\_RETROV; 1.  
 KM AIBS; Polyprotein, Hydrolyase; Aspartyl protease; Endonuclease;  
 KM Nuclease; Transferase; RNA-directed DNA polymerase.  
 FT CHAIN 1 210  
 FT ACT SITE 134 134 BY SIMILARITY.  
 SO SEQUENCE 1061 AA; 120612 MW; 13DD4104CB432A4 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 1061;  
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WGYWQV 9  
 |||||  
 Db 613 WADYWQV 619

RESULT 24  
 RM09\_MOUSE STANDARD; PRT; 256 AA.  
 AC O99N94;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 60S ribosomal protein L9, mitochondrial precursor (19mt) (Fragment).  
 GN MRPL9.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP MEDLINE=21293042; PubMed=11279069;  
 RA Suzuki T., Terasaki M., Takemoto-Hori C., Hanada T., Ueda T., Wada A.,  
 RA Watanabe K.;  
 RT "Structural compensation for the deficit of rRNA with proteins in the  
 RT mammalian mitochondrial ribosome. Systematic analysis of protein  
 RT components of the large ribosomal subunit from mammalian  
 RT mitochondria.";  
 RL J. Biol. Chem. 276:21724-21736(2001).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE L9P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AB049637; BAB40842.1; -;  
 DR MGD; MGI:213721; Mrp19.  
 DR InterPro; IPR000244; Ribosomal\_L9.  
 DR Pfam; PF01281; Ribosomal\_L9\_N; 1.  
 KM Ribosomal protein; Mitochondrion; Transic peptide.  
 FT NON TER 1 1  
 FT TRANSIT 1 1  
 FT CHAIN 1 256  
 FT SEQUENCE 256 AA; 29460 MW; FECA2F8D1ACB46 CRC64;  
 SO SEQUENCE 256 AA; 29460 MW; FECA2F8D1ACB46 CRC64;  
 Query Match 63.8%; Score 37; DB 1; Length 256;  
 Best Local Similarity 80.0%; Pred. No. 42;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobium.  
 OX NCBI\_TaxID=375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=110R1P15; PubMed=1850420;  
 RX MEDLINE=91210304; PubMed=1850420;  
 RA Ramseder T.M., Winteler H.V., Hennecke H.;  
 RT "Discovery and sequence analysis of bacterial genes involved in the  
 RT biogenesis of c-type cytochromes";  
 RL J. Biol. Chem. 266:7793-7803(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USDA 110;  
 RX MEDLINE=22484998; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,  
 RA Sasamoto S., Watanabe A., Ideasa K., Iriyuchi M., Kawashima K.,  
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:189-197(2002).  
 CC -1- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE  
 CC BIOGENESIS OF C-TYPE CYTOCHROMES.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE CCMC/CYCZ/HELC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M60874; AAA26194.1; -.  
 DR EMBL; AP005936; BAC45734.1; -.  
 DR PIR; C39741; C39741.  
 DR InterPro; IPR002541; CYTC\_asm.  
 DR InterPro; IPR003557; CYTC\_Biog\_Ccmc.  
 DR Pfam; PF01578; CYTC\_asm\_1.  
 DR PRINTS; PRO1386; CCMCBIOGNIS.  
 DR TIGRFAMs; TIGR01191; ccmc\_1.  
 KW Cytochrome c-type biogenesis; Transport; Transmembrane;  
 KM Inner membrane; Complete proteome.  
 FT TRANSMEM 19 39 POTENTIAL.  
 FT TRANSMEM 61 81 POTENTIAL.  
 FT TRANSMEM 92 112 POTENTIAL.  
 FT TRANSMEM 126 146 POTENTIAL.  
 FT TRANSMEM 157 177 POTENTIAL.  
 FT TRANSMEM 198 218 POTENTIAL.  
 SQ SEQUENCE 263 AA; 28831 MW; A02EF75769F94EC0 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 263;  
 Best Local Similarity 57.1%; Pred. No. 43;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VWGQYQ 8  
 :|||:  
 :|||:  
 Db 115 MMGTWYB 121

Search completed: August 14, 2003, 09:06:18  
 Job time : 14.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 60 Seconds  
(without alignments)  
38.708 Million cell updates/sec

Title: US-09-214-836-2  
Perfect score: 58  
Sequence: 1 KWVGQYQV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mmc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_prodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	86.2	626	11	09CZB2 mus musculus
2	49	84.5	264	16	08XZ36 Oxe36 escherichia
3	49	84.5	549	16	08CVC9 O8CVC9 escherichia
4	43	74.1	305	2	045818 O45818 chlorella
5	42	72.4	98	16	08RD90 O8RD90 thermococcus
6	42	72.4	281	16	09KPY3 O9KPY3 vibrio chol
7	41	70.7	73	12	08OR33 O8OR33 human papill
8	41	70.7	73	12	09DWY8 O9DWY8 human papill
9	41	70.7	756	6	09SKV0 O9SKV0 bos taurus
10	40	69.0	73	12	09DWY4 O9DWY4 human papill
11	40	69.0	277	16	08XB56 O8XB56 escherichia
12	40	69.0	277	16	08ZCH5 O8ZCH5 escherichia
13	40	69.0	277	16	08FFB2 O8FFB2 escherichia
14	40	69.0	313	16	08ZJG2 O8ZJG2 yersinia pe
15	40	69.0	333	16	08DKT3 O8DKT3 synechococ
16	40	69.0	390	17	08PUV6 O8PUV6 methanosaar

17	40	69.0	400	16	P74474 P74474 synechocyst
18	40	69.0	458	5	O18533 O18533 schistosoma
19	40	69.0	489	10	O04483 O04483 arabidopsis
20	40	69.0	525	16	O8U7J6 O8U7J6 agrobacteri
21	40	69.0	537	10	O9SHY8 O9SHY8 arabidopsis
22	40	69.0	580	16	O8Y7Q0 O8Y7Q0 anabaena sp
23	40	69.0	1451	5	O01737 O01737 caenorhabdi
24	40	69.0	1884	4	O9ULD7 O9ULD7 homo sapien
25	40	69.0	1885	4	O81ZJ3 O81ZJ3 homo sapien
26	39	67.2	114	16	O9A81 O9A81 caulobacter
27	39	67.2	145	9	O34084 O34084 streptococ
28	39	67.2	145	9	O9MBX8 O9MBX8 streptococ
29	39	67.2	167	4	O9BRH6 O9BRH6 homo sapien
30	39	67.2	238	11	O8R5C1 O8R5C1 mus musculu
31	39	67.2	267	10	O9ZP33 O9ZP33 lycopersico
32	39	67.2	313	16	O8J324 O8J324 treponema p
33	39	67.2	416	16	O987L1 O987L1 rhizobium l
34	39	67.2	449	16	O8CK63 O8CK63 streptomyc
35	39	67.2	486	11	O91YV6 O91YV6 mus musculu
36	39	67.2	497	11	O8BXD5 O8BXD5 mus musculu
37	39	67.2	515	12	O8B5P8 O8B5P8 tobacco rin
38	39	67.2	515	12	O8B5P7 O8B5P7 tobacco rin
39	39	67.2	537	17	O9H81 O9H81 halobacteri
40	39	67.2	551	10	O8S5S5 O8S5S5 oryza sativ
41	39	67.2	585	11	O8BL59 O8BL59 mus musculu
42	39	67.2	585	11	O8BHJ9 O8BHJ9 mus musculu
43	39	67.2	586	4	O96FM9 O96FM9 homo sapien
44	39	67.2	586	4	O95J91 O95J91 homo sapien
45	39	67.2	742	5	O9W322 O9W322 dtrotophila

## ALIGNMENTS

RESULT 1

ID Q9CZB2 PREDIMINARY; PRT; 626 AA.

AC Q9CZB2;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

DE N/A.

GN SI OR SI.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

CK NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y., Arakawa T., Hara A., Fukunishi Y., Komio H., Adachi S., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada S., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schiraldi L.M., Staudli F., Suzuki R., Tomita M., Wagner U., Maehiro T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guernicchi S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombetris P., Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S., Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK012808; BAB28486.1; --

DR MGD; MGI:98301; Sl.

DR InterPro; IPR000601; PKD\_domain.  
 DR Pfam; PF00801; PKD; 1.  
 DR SMART; SM00089; PKD; 1.  
 DR PROSITE; PS00093; PKD; 1.  
 SQ SEQUENCE 626 AA; 66301 MW; 76C0A06C63212674 CRC64;

Query Match 86.2%; Score 50; DB 11; Length 626;  
 Best Local Similarity 77.8%; Pred. No. 7.4;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KVMGYWQV 9  
 |||||  
 Db 153 KVMGYWQV 161

## RESULT 2

OQ8X36 PRELIMINARY; PRT; 264 AA.  
 AC OQ8X36;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Hypothetical protein z3480.  
 GN Z3480 OR ECS3110.  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
 RL Nature 409:529-533(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,  
 RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,  
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22(2001).  
 DR EMBL; AE005454; AAG57356.1; -;  
 DR EMBL; AP002560; BAB3653.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 264 AA; 29288 MW; 257E81A5E46A9489 CRC64;

Query Match 84.5%; Score 49; DB 16; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VMGQYWQ 8  
 |||||  
 Db 124 VMGQYWQ 130

## RESULT 3

OQ8CV9 PRELIMINARY; PRT; 549 AA.  
 AC OQ8CV9;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein yfaQ precursor.

GN YFAQ OR C2769.  
 OS Escherichia coli O6.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=217992;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928;  
 RX MEDLINE=22388234; PubMed=12471157;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 RT of uropathogenic Escherichia coli.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:117020-117024(2002).  
 DR EMBL; AB016763; AA081223.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 549 AA; 61590 MW; PFEAB9B9CD22A8B6 CRC64;

Query Match 84.5%; Score 49; DB 16; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 9.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VMGQYWQ 8  
 |||||  
 Db 124 VMGQYWQ 130

## RESULT 4

OQ45818 PRELIMINARY; PRT; 305 AA.  
 AC OQ45818;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 33.7 kDa protein (Behc).  
 GN BHCG.  
 OS Chloroflexus aurantiacus.  
 OC Bacteria; Chloroflexi; Chloroflexales; Chloroflexaceae; Chloroflexus.  
 OX NCBI\_TaxID=1108;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J10-FL;  
 RX MEDLINE=94192803; PubMed=7511541;  
 RA Niedermeier G., Shiozawa J.A., Lotzspeich F., Feick R.G.;  
 RT "The primary structure of two chlorosome proteins from Chloroflexus  
 RT aurantiacus.";  
 RL FEBS Lett. 342:61-65(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20433268; PubMed=10976061;  
 RX Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;  
 RT "Molecular evidence for the early evolution of photosynthesis.";  
 RL Science 289:1724-1730(2000).  
 DR EMBL; Z34000; CA83969.1; -;  
 DR EMBL; AF288602; AAG15233.1; -;  
 DR InterPro; IPR006372; Chl\_synth.  
 DR InterPro; IPR005377; UblA.  
 DR Pfam; PF01040; UblA; 1.  
 DR TIGRFAMs; TIGR01476; chlor\_syn\_Bchg; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 305 AA; 33674 MW; P990F92F2D1C2B07 CRC64;

Query Match 74.1%; Score 43; DB 2; Length 305;  
 Best Local Similarity 83.3%; Pred. No. 43;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VMGQYW 7  
 |||||  
 Db 245 VMGQYW 250



RESULT 5  
Q8RD90 PRELIMINARY; PRT; 98 AA.  
AC Q8RD90:  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-OCT-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Hypothetical protein TEO156.  
GN TEO156.  
OS Thermobacterium tengcongensis.  
OC Bacteria; Firmicutes; Clostridia; Thermobacteriales;  
OC Thermobacteriaceae; Thermobacter.  
OX NCBI\_TaxID=119072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M84 / JCM 11007;  
RX MEDLINE=21992816; PubMed=11997336;  
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
Tan H., Chen R., Wang J., Yu J., Yang H.;  
RT "A complete sequence of T. tengcongensis genome.";  
RL Genome Res. 12:689-700(2002).  
DR EMBL, AF012988; AAM23457.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 98 AA; 11135 MW; 01317FPC55898A13 CRC64;

Query Match 72.4%; Score 42; DB 16; Length 98;  
Best Local Similarity 71.4%; Pred. No. 20;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KWGOYV 7  
Db 35 KWGOYV 41

RESULT 6  
Q9KPY3 PRELIMINARY; PRT; 281 AA.  
ID Q9KPY3  
AC Q9KPY3:  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein VC2229.  
GN VC2229.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=El Tor N16961 / Serotype O1;  
RX MEDLINE=20406833; PubMed=10953301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
Dodson R.J., Hatt D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
Ermlaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
McDonald L., Uitterlbeck T., Fleischmann R.D., Nieman W.C., White O.,  
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
cholerae.";  
RL Nature 406:477-483(2000).  
DR EMBL, AB004294; AAF95373.1;  
DR TIGR, VC2229;  
DR InterPro, IPR000583; GATase\_2.  
DR Pfam, PF00310; GATase\_2; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 281 AA; 31824 MW; 7CA75AD3494DFDD0 CRC64;

Query Match 72.4%; Score 42; DB 16; Length 281;  
Best Local Similarity 71.4%; Pred. No. 56;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWGOYV 7  
Db 97 ELWGOYV 103

RESULT 7  
Q8OR33 PRELIMINARY; PRT; 73 AA.  
ID Q8OR33  
AC Q8OR33:  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-OCT-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Major capsid protein (Fragment).  
GN L1.  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PA1MWS12;  
RA Forslund O., Ly H., Reid C., Higgins G.;  
RT "Human papillomavirus DNA in tumors, perilesional and buttock skin of  
immunocompetent and immunosuppressed patients.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AF489719; AAL88647.1;  
DR InterPro, IPR002210; PV\_capsid\_L1.  
DR Pfam, PF00500; late\_protein\_L1; 1.  
DR ProDom, PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 73 AA; 8493 MW; F1D1A87307D39765 CRC64;

Query Match 70.7%; Score 41; DB 12; Length 73;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 WGOYV 9  
Db 42 WGOYV 48

RESULT 8  
Q9DWT8 PRELIMINARY; PRT; 73 AA.  
ID Q9DWT8  
AC Q9DWT8:  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FA50;  
RA Antonsson A., Hossain S., Simon M., Hansson B.G.;  
RT "Skin HPV found on foreheads.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AY009882; AAG27044.1;  
DR InterPro, IPR002210; PV\_capsid\_L1.  
DR Pfam, PF00500; late\_protein\_L1; 1.  
DR ProDom, PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 73 AA; 8479 MW; F1D5B6C307D39062 CRC64;

Query Match 70.7%; Score 41; DB 12; Length 73;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 WGOYV 9

Db 42 WGEYWDV 48

## RESULT 9

ID Q95KV0 PRELIMINARY; PRT; 756 AA.  
AC Q95KV0;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE 1kB kinase-beta.  
GN BIKKETA.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OC NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rottenberg S., Dobbelaere D.A.B., Heussler V.T.;  
RT "Identification and characterisation of the bovine 1kB kinases (IKKs)  
alpha, beta and gamma."  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; AJ414556; CAC93687.1; -.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 756 AA; 86647 MW; A072D1561A1765 CRC64;

Query Match 70.7%; Score 41; DB 6; Length 756;  
Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KYMGQYW 7  
Db 428 KYMGQYW 434

## RESULT 10

ID Q9DWY4 PRELIMINARY; PRT; 73 AA.  
AC Q9DWY4;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Major capsid protein L1 (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OC NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Antonsen A., Hossain S., Simon M., Hanson B.G.;  
RT "Skin HPV found on foreheads."  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY009886; AAG27048.1; -.  
DR InterPro; IPR002210; PV\_capsid\_L1.  
DR Pfam; PF00500; late\_protein\_L1; 1.  
DR ProDom; PD000544; PV\_capsid\_L1; 1.  
FT NON\_TER 1 73  
SQ SEQUENCE 73 AA; 8323 MW; 8A994051AD736407 CRC64;  
Query Match 69.0%; Score 40; DB 12; Length 73;

Best Local Similarity 57.1%; Pred. No. 30;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGYWQV 9  
Db 42 WGEYWDI 48

## RESULT 11

ID Q8XB6 PRELIMINARY; PRT; 277 AA.  
AC Q8XB6;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Sulfate, thiosulfate transport system permease T protein.  
GN CYSU OR Z3689 OR ECG3295.  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OC NCBI\_TaxID=83334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE=2107935; PubMed=11206551;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamakis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."  
RL Nature 409:529-533 (2001).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / R1MD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,  
RA Kunata S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
O157:H7 and genomic comparison with a laboratory strain K-12."  
RL DNA Res. 8:11-22 (2001).  
DR EMBL; AB005472; AAG57542.1; -.  
DR EMBL; AP002561; BAB36718.1; -.  
DR InterPro; IPR000515; BPD\_transp.  
DR InterPro; IPR005667; Sulph\_transp2.  
DR Pfam; PF00528; BPD\_transp; 1.  
DR TIGRFAMs; TIGR00969; 3a0106s02; 1.  
DR PROSITE; PS00402; BPD\_TRANSP\_INN\_MEMBER; 1.  
KW Complete proteome.  
SQ SEQUENCE 277 AA; 30308 MW; 3EBBEFADD2CE5788 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 277;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGYWQV 9  
Db 44 WAQYWEV 50

## RESULT 12

ID Q8ZCH5 PRELIMINARY; PRT; 277 AA.  
AC Q8ZCH5;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Sulfate transport system permease protein CysT (inner membrane  
permease T of sulfate/thiosulfate ABC transporter).  
GN CYST OR YPO3014 OR CYSU OR Y1467.

```

OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
NX NCB1_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsis K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds S., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP EMBL; AJ414154; CAC82257.1; -
DR EMBL; AE013749; AAM85038.1; -
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp.1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; 1.
KW Complete proteome.
SQ SEQUENCE 277 AA; 30017 MW; 0BBB42B40B3C08A CRC64;

Query Match 69.0%; Score 40; DB 16; Length 277;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGQYQV 9
Db 44 WAQYWEV 50

RESULT 13
ID Q8FBF2 PRELIMINARY; PRT; 277 AA.
AC Q8FBF2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Sulfate transport system permease protein cyst.
GN CYSU OR C2958.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCB1_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raako D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016764; AAN81408.1; -
KW Complete proteome.
SQ SEQUENCE 277 AA; 30360 MW; B58FE3C6103F554D CRC64;

```

```

Query Match 69.0%; Score 40; DB 16; Length 277;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MGQYQV 9
Db 44 WAQYWEV 50

RESULT 14
ID Q8ZJG2 PRELIMINARY; PRT; 313 AA.
AC Q8ZJG2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein YPO0146.
GN YPO0146 OR Y3925.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
NX NCB1_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsis K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds S., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP EMBL; AJ414154; CAC89009.1; -
DR EMBL; AE013997; AAM87469.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 313 AA; 35133 MW; 69A851CC8B35E26F CRC64;

Query Match 69.0%; Score 40; DB 16; Length 313;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVMGQYQV 9
Db 15 KMYSQYQV 23

RESULT 15
ID Q8DKT3 PRELIMINARY; PRT; 333 AA.
AC Q8DKT3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE T110772 protein.
GN T110772
OS Synecchococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
OX NCB1_TaxID=32046;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriuguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohira C., Matsuno M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1."
RL DNA Res. 9:123-130(2002).
DR EMBL: AF005371; BAC08323.1; -.
KW Complete proteome.
SQ SEQUENCE 333 AA; 36246 MW; 39816B7DA1711E80 CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 16; Length 333;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYWG 8
DB 158 WGOYWG 163

RESULT 16
Q8PUV6 PRELIMINARY; PRT; 390 AA.
AC Q8PUV6;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Galactosyltransferase.
GN MM2222.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaeae; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=1125824;
RA Deppeineier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wietzer A., Baumeister S., Jacobi C.,
RA Brueggemann H., Hienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL: AE013463; AAM31918.1; -.
DR InterPro: IPR001296; Glyco. Trans. 1.
DR Pfam: PF00534; Glycos. transf. 1; I.
KW Transferase; Complete proteome.
SQ SEQUENCE 390 AA; 43768 MW; ED0DD163FBDADB4 CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 17; Length 390;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGOY 7
DB 126 KVMGOY 132

RESULT 17
P74474 PRELIMINARY; PRT; 400 AA.
AC P74474;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE D-alanyl-D-alanine carboxypeptidase.
GN SLR1924.
OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231.
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Hoshouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
DR EMBL: D90915; BAA18575.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR Pfam: PF00144; Beta-lactamase; 1.
KW Carboxypeptidase; Complete proteome.
SQ SEQUENCE 400 AA; 44316 MW; 75510481820E462F CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 16; Length 400;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOY 7
DB 335 WGOY 339

RESULT 18
O18533 PRELIMINARY; PRT; 458 AA.
AC O18533;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Preprocathepsin C precursor (EC 3.4.14.1).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Chinese;
RX MEDLINE=97442731; PubMed=9297696;
RA Brindley P.J., Kallina B.H., Dalton J.P., Day S.R., Wong J.Y.,
RA Smythe M.L., McManus D.P.;
RT "Proteolytic degradation of host hemoglobin by schistosomes."
RL Mol. Biochem. Parasitol. 89:1-9(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Chinese;
RX MEDLINE=98409270;
RA Hota-Jamriska L., Tort J.F., Dalton J.P., Day S.R., Fan J., Aaskov J.,
RA Brindley P.J.;
RT "Cathepsin C from Schistosoma japonicum: cDNA encoding the
RT preproenzyme and phylogenetic relationships."
RL Eur. J. Biochem. 255:527-534(1998).
DR EMBL: U77932; AAC32040.1; -.
DR HSSP: P00787; ITHE.
DR MEROPS: C01.070; -.
DR InterPro: IPR000668; Peptidase C1.
DR InterPro: IPR000169; SHprot. acsite.
DR Pfam: PF00112; Peptidase_C1; 1.
DR PRINTS: PR00705; PAPA1N.
DR ProDom: PD000156; Peptidase_C1; 1.
DR SMART: SMO0645; Pept. C1; 1.
DR PROSITE: PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE: PS00639; THIOI_PROTEASE_HIS; 1.
KW Hydrolyase; Protease; Signal; Thiol. protease.
FT SIGNAL 1 22
FT CHAIN 222 458
SQ SEQUENCE 458 AA; 52698 MW; ADA976566C4142C CRC64;

```

Query Match 69.0%; Score 40; DB 5; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WGOYW 7  
 Db 426 WGOYW 430

## RESULT 19

004483 PRELIMINARY; PRT; 489 AA.  
 AC 004483;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE F5114.19 protein.  
 GN Arabidopsis thaliana (Mouse-ear cress).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Vysotskaia V.S., Osborne B.I., Toriumi M., Yu G., Oji O., Shen Y.K.,  
 RA Buehler E., Conway A.B., Conway A.R., Dewar K., Feng J., Kim C.,  
 RA Kutz D., Li Y., Shinn P., Sun H., Davis R.W., Ecker J.R.,  
 RA Federpspiel N.A., Theologis A.;  
 RT "The sequence of BAC F5114 from Arabidopsis thaliana chromosome 1.";  
 RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Theologis A.;  
 RA Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.  
 RL EMBL; AC001229; AAB60915.1; -;  
 DR InterPro: IPR001878; Znf\_CCHC.  
 DR Pfam; PF00098; Zf-CCHC; 1.  
 DR SMART; SM00343; Znf\_C2HC; 1.  
 SQ SEQUENCE 489 AA; 56649 MW; E7482BF8637C0226 CRC64;

Query Match 69.0%; Score 40; DB 10; Length 489;  
 Best Local Similarity 71.4%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 WVGQYWQ 8  
 Db 357 WVGQYWQ 363

## RESULT 20

08U7J6 PRELIMINARY; PRT; 525 AA.  
 AC 08U7J6;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Ribitol kinase.  
 GN ATU4453 OR AGR L. 826.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 CC Rhizobiaceae; Rhizobium.  
 OC NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Serubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Boye D. Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Neeter E.M.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 C58.";  
 RL Science 294:2317-2323 (2001).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Ourollo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,  
 RA Houmlet K., Gordon J., Vaudin M., Iatchouk O., Bpp A., Liu F.,  
 RA Wollam C., Allinger M., Doughty D., Scott C., Iappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gureon J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328 (2001).  
 DR EMBL; AB009374; AAL45247.1; -;  
 DR EMBL; AB008240; AAK8987.1; -;  
 DR InterPro: IPR00577; FGXY\_kin.  
 DR InterPro: IPR006003; Pentulose\_kinase.  
 DR Pfam; PF00370; FGXY; 1.  
 DR Pfam; PF02782; FGXY\_C; 1.  
 DR TIGRPFams; TIGR01315; 5c\_CHO\_kinase; 1.  
 KW Kinase; Complete proteome.  
 SQ SEQUENCE 525 AA; 56072 MW; 0C96C97306BED7C0 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 525;  
 Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 WVGQYWQ 8  
 Db 298 WVGQYWQ 304

## RESULT 21

09SHY8 PRELIMINARY; PRT; 537 AA.  
 AC 09SHY8;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE F1E22.4.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chao O., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,  
 RA Williams S., Altrafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,  
 RA Hansen N.F., Huitzer L., Kremetskaia I., Lenz C., Li J., Liu S.,  
 RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,  
 RA Davis R.W., Federpspiel N.A., Theologis A., Ecker J.R.;  
 RT "Genomic sequence for Arabidopsis thaliana BAC F1E22.";  
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AC007234; AAF3844.1; -;  
 DR InterPro: IPR001878; Znf\_CCHC.  
 DR Pfam; PF00098; Zf-CCHC; 1.  
 DR SMART; SM00343; Znf\_C2HC; 1.  
 SQ SEQUENCE 537 AA; 62418 MW; A68275787B2FD5CE CRC64;

Query Match 69.0%; Score 40; DB 10; Length 537;  
 Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 WVGQYWQ 8

Db 404 VMGSYWK 410

## RESULT 22

Q8YT00 PRELIMINARY; PRT; 580 AA.  
AC Q8YT00;  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DE ABC transporter ATP-binding protein.  
GN A1R2663.  
OC Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
RT cyanobacterium Anabaena sp. strain PCC 7120.";  
RL DNA Res. 8:205-213(2001).  
DR EMBL, AP003590; BB74362.1; -.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR001140; ABC\_TM\_transp.  
DR InterPro; IPR003439; ABC\_transporter.  
DR InterPro; IPR002078; Sig54\_interact.  
DR Pfam; PF00664; ABC\_membrane; 1.  
DR Pfam; PF00005; ABC\_tran; 1.  
DR ProDom; PD000006; ABC\_transporter; 1.  
DR SMART; SM00382; AAA; 1.  
DR PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
DR PROSITE; PS00675; SIGMA54\_INTERACT\_1; 1.  
KM ATP-binding; Complete proteome.  
SQ SEQUENCE 580 AA; 66605 MW; AB278D7AEAF24C31 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 580;  
Best Local Similarity 44.4%; Pred. No. 2.3e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYWK 9  
Db 7 QIMQGFWD 15

## RESULT 23

CO1737 PRELIMINARY; PRT; 1451 AA.  
AC CO1737;  
DT 01-JUL-1997 (TRENBLrel. 04, Created)  
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE F20H11.2 protein.  
GN F20H11.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;  
RA Wilson R., Moesener J., Graves T.;  
RT "The sequence of C. elegans cosmid F20H11.";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AF002197; AAD34660.1; -.  
DR WormPep; F20H11.2; CE20701.  
DR InterPro; IPR001650; Helicase\_C.  
DR Pfam; PF00271; Helicase\_C; 1.  
KM ATP-binding; Helicase; Hydrolase.  
SQ SEQUENCE 1451 AA; 161681 MW; BCC357BDE6F8E01 CRC64;

Query Match 69.0%; Score 40; DB 5; Length 1451;  
Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMGQYWK 7  
Db 571 VMGQFW 576

## RESULT 24

CO12J3 PRELIMINARY; PRT; 1884 AA.  
AC CO12J3;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Hypothetical protein KIAA1283 (Fragment).  
GN KIAA1283.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20039619; PubMed=10574462;  
RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XV.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 6:337-345(1999).  
DR EMBL, AB03109; BAA6597.1; -.  
DR HSSP; P01024; 1C3D.  
DR InterPro; IPR002890; A2M\_N.  
DR InterPro; IPR002350; Kazal.  
DR InterPro; IPR001599; Macroglobulin2.  
DR Pfam; PF00207; A2M; 1.  
DR Pfam; PF01835; A2M\_N; 1.  
DR Pfam; PF00050; Kazal; 1.  
DR SMART; SM00280; KAZAL; 1.  
DR PROSITE; PS00477; ALPHA\_2\_MACROGLOBULIN; 1.  
KM Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 1884 AA; 206524 MW; D3C078F26B951D1A CRC64;

Query Match 69.0%; Score 40; DB 4; Length 1884;  
Best Local Similarity 75.0%; Pred. No. 7.5e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVMGQYWK 8  
Db 100 KVMGQW 107

## RESULT 25

CO12J3 PRELIMINARY; PRT; 1885 AA.

AC Q81ZJ3;  
DT 01-MAR-2003 (TIREMBLrel. 23, Created)  
DT 01-MAR-2003 (TIREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TIREMBLrel. 23, Last annotation update)  
DE Alpha-2 macroglobulin family protein VIP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li Z.; Wu X.; Engvall E.;  
RT "Cloning and expression of VIP, a novel alpha 2 macroglobulin family  
RT member.";  
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AY101765; AAM5084.1; -;  
SQ SEQUENCE 1885 AA; 20665 MW; 3FB4A8551FBF326D CRC64;  
Query Match 69.0%; Score 40; DB 4; Length 1885;  
Best Local Similarity 75.0%; Pred. No. 7.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KVMGQYWG 8  
Db 101 KVMGQYWG 108

Search completed: August 14, 2003, 09:10:13  
Job time : 62 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 23, 2003, 23:32:40 ; Search time 2188.5 Seconds

(without alignments)  
168.237 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGOYMAV 9

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 288871 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODL=frame+ p2n.model -DEV=xlh  
-O=/cgnr\_1/USPRO/spool/US09214836/runat\_14082003\_085039\_7593/app.query.fasta\_1.398  
-DB=GenBdl -QWMT=lastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09214836 @cgnr\_1.1.3608 @runat\_14082003\_085039\_7593 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUEY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenBdl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: gb\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pac:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_scs:\*  
28: em\_un:\*

29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	91.4	36	A46001	A46001 Sequence 9
2	53	91.4	1986	AR269285	AR269285 Sequence
3	53	91.4	1986	AX133406	AX133406 Sequence
4	53	91.4	1986	AX133655	AX133655 Sequence
5	53	91.4	1986	AX192347	AX192347 Sequence
6	53	91.4	1986	BT007202	BT007202 Homo sapi
7	53	91.4	1986	BT007991	BT007991 Synthetic
8	53	91.4	2026	HSU01874	U01874 Human me20m
9	53	91.4	2114	HUMGPMSS	M3295 Human 95 KD
10	53	91.4	2115	A45993	A45993 Sequence 1
11	53	91.4	2115	AR269281	AR269281 Sequence
12	53	91.4	2130	AR167365	AR167365 Sequence
13	53	91.4	2130	AX274950	AX274950 Sequence
14	53	91.4	2130	AX354933	AX354933 Sequence
15	53	91.4	2130	S73003	S73003 gp100-melan
16	53	91.4	2131	AX474662	AX474662 Sequence
17	53	91.4	2131	HUMPMEL	M7348 Human Pmel
18	53	91.4	2134	BC001414	BC001414 Homo sapi
19	53	91.4	2534	AX133528	AX133528 Sequence
20	53	91.4	2758	AK092881	AK092881 Homo sapi
21	50	86.2	2172	AR063067	AR063067 Sequence
22	50	86.2	2172	AR091800	AR091800 Sequence
23	50	86.2	2172	AR162997	AR162997 Sequence
24	50	86.2	2172	AR287974	AR287974 Sequence
25	49	84.5	1881	AX474660	AX474660 Sequence
26	49	84.5	1881	MMU14133	U14133 Mus musculu
27	49	84.5	64323	AL356976	AL356976 Human DNA
28	49	84.5	151951	AC084300	AC084300 Homo sapi
29	49	84.5	160456	AC110997	AC110997 Homo sapi
30	49	84.5	170470	AC022696	AC022696 Homo sapi
31	49	84.5	177565	AP002769	AP002769 Homo sapi
32	49	84.5	200688	AC073266	AC073266 Homo sapi
33	49	84.5	210317	AC105094	AC105094 Homo sapi
34	48	82.8	24	A45999	A45999 Sequence 7
35	48	82.8	24	AR269284	AR269284 Sequence
36	48	82.8	697	HSAS329943	AJ329943 Homo sapi
37	48	82.8	113687	AC069281	AC069281 Homo sapi
38	48	82.8	227968	AF053356	AF053356 Homo sapi
39	48	82.8	230218	AC094458	AC094458 Homo sapi
40	48	82.8	231982	AC130118	AC130118 Rattus no
41	48	82.8	237927	AC130252	AC130252 Rattus no
42	48	82.8	291147	AC094912	AC094912 Rattus no
43	47	81.0	33591	CEFI6D3	Z78062 Caenorhabdi
44	47	81.0	106465	HSJ765F13	AL109853 Human DNA
45	47	81.0	113286	AP005556	AP005556 Oryza sat

RESULT 1

## ALIGNMENTS

A46001  
LOCUS A46001 36 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 9 from Patent EP068350.  
ACCESSION A46001  
VERSION A46001.1 GI:2300273  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE  
AUTHORS 1 (bases 1 to 36)  
TITLE Adema, G.J. and Figdor, C.G.  
JOURNAL Melanoma associated antigenic polypeptide, epitopes thereof and  
vaccines against melanoma  
COMMENT Patent: EP 068350-A 9 23-AUG-1995;  
AKZO NOBEL NV (NL)  
Other publication ZA 9501239 951019  
Other publication JP 7278193 951024  
Other publication FI 950665 950817  
Other publication CA 2142575 950817  
Other publication AU 1227295 950824.  
Location/Qualifiers  
FEATURES  
source 1..36  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
/cell\_type="MELANOCYT"  
/tissue\_type="MELANOMA"  
CDS 1..36  
/note="unnamed protein product; Protein sequence is in  
conflict with the conceptual translation"  
BASE COUNT 9 a 8 c 11 g 8 t  
ORIGIN

Alignment Scores:  
Pred. No.: 0.752 Length: 36  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 6 Gaps: 0  
US-09-214-836-1 (1-9) x A46001 (1-36)

QY 1 LysHTTPGlyGlnTYTTPAlaVal 9  
Db 7 AAGACCTGGGCGCAATACTGCGCAAGTT 33

RESULT 2  
AR269285 AR269285 36 bp mRNA linear PAT 10-APR-2003  
LOCUS  
DEFINITION Sequence 9 from patent US 6500919.  
ACCESSION AR269285  
VERSION AR269285.1 GI:29700350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 36)  
TITLE Adema, G.J. and Figdor, C.G.  
JOURNAL Melanoma associated antigenic polypeptide, epitopes thereof and  
vaccines against melanoma  
COMMENT Patent: US 6500919-A 9 31-DEC-2002;  
Location/Qualifiers  
FEATURES  
source 1..36  
/organism="unknown"  
BASE COUNT 9 a 8 c 11 g 8 t  
ORIGIN

Alignment Scores:  
Pred. No.: 0.752 Length: 36  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 6 Gaps: 0  
US-09-214-836-1 (1-9) x A46001 (1-36)

Pred. No.: 0.752 Length: 36  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 6 Gaps: 0  
US-09-214-836-1 (1-9) x AR269285 (1-36)

QY 1 LysHTTPGlyGlnTYTTPAlaVal 9  
Db 7 AAGACCTGGGCGCAATACTGCGCAAGTT 33

RESULT 3  
AX133406 AX133406 1986 bp DNA linear PAT 15-MAY-2001  
LOCUS  
DEFINITION Sequence 1 from Patent WO0130847.  
ACCESSION AX133406  
VERSION AX133406.1 GI:14139665  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS 1  
TITLE Berinsteijn, N., Tartaglia, J., Moingeon, P., Barber, B. and Tine, J.A.  
JOURNAL Modified gp100 and uses thereof  
COMMENT Patent: WO 0130847-A 1 03-MAY-2001;  
Aventis Pasteur Limited (CA)  
Location/Qualifiers  
FEATURES  
source 1..1986  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="modified gp 100"

BASE COUNT 431 a 552 c 552 g 451 t  
ORIGIN

Alignment Scores:  
Pred. No.: 21.8 Length: 1986  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 6 Gaps: 0  
US-09-214-836-1 (1-9) x AX133406 (1-1986)

QY 1 LysHTTPGlyGlnTYTTPAlaVal 9  
Db 460 AAGACCTGGGCGCAATACTGCGCAAGTT 486

RESULT 4  
AX133655 AX133655 1986 bp DNA linear PAT 15-MAY-2001  
LOCUS  
DEFINITION Sequence 109 from Patent WO0130382.  
ACCESSION AX133655  
VERSION AX133655.1 GI:14139697  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS 1  
TITLE Berinsteijn, N., Tartaglia, J., Moingeon, P. and Barber, B.  
JOURNAL Method of inducing and/or enhancing an immune response to tumor  
antigens  
COMMENT Patent: WO 0130382-A 109 03-MAY-2001;  
Aventis Pasteur Limited (CA)  
Location/Qualifiers  
FEATURES  
source 1..1986  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="modified gp100"

CDS

1. 1986  
/note="unnamed protein product"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="CAC38954.1"  
/db\_xref="GI:14139698"  
/translation="MDLVLRCLHLAVIGALLAVGATKVRNODWLGVSRLRTKAV  
NROLYPEWTEAORLDCWKGQVSLKVNDSPTLLIGANASFSIALNFGSQVLPDGOV  
IWNNTTINSQVWGQGVPOETDDACIPDGGPCSGSWSOKRSFYVMKTKGOV  
OVIGPVSGLSIGTGKRAMLGTHMEVTVYHRRGSRVYPLAHSSAFTIDQVPSVS  
VSOIRALDGNKHFRLRNPFLPALDLHPSGTYLAELASTYWDPSGSGTILSALVY  
THYLEBGPVTAQVLOALPLTSCGSSPVGTTDGRPTAEAPNTTAAQVPTTEVAG  
TTTPOAPTAEPBSGTSVQVPTTEVISTAPVQMPAESTGMPEKVPVSEVNGTLLAE  
STPATGNTPAEVSIVLISGTTAAQVTTWEVETTARELPPEBGPASSIMSTESI  
TSGSLGPLDGTATRLVLRQVLDVLRVGSFSTVLDIVOGISAEILQAVPSGEED  
AFELTVSCOGGLPREACMEISSPCGPPARLCOVLPSPACQVLHQLIKGSGTVC  
LNVSLADTNSLAIVSTQILMGPQAGLQVPLVIGILLVMAVVLASLIYRRRLMKOD  
FSVQPLHSSSHMLRPRIFCSCTIGNSPLISQGV"

BASE COUNT 431 a 552 c 552 g 451 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 21.8 Length: 1986  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
Gaps: 0

US-09-214-836-1 (1-9) x AX133655 (1-1986)

Qy 1 LysThrTPGlyGlnTyrTrpAlaVal 9  
Db 460 AAGACCTGGGCGCAATACGTGCAAGTT 486

RESULT 5  
AX192347 1986 bp DNA linear PAT 15-AUG-2001  
LOCUS Sequence 1 from Patent WO0149317.  
DEFINITION AX192347  
ACCESSION AX192347  
VERSION AX192347.1 GI:15210325  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Embage, P., Barber, B.H., Sambhara, S. and Sia, C.D.  
TITLE Enhancing the immune response to an antigen by presensitizing with  
the antigen  
the antigen  
Patent: WO 0149317-A 1 12-JUL-2001;  
JOURNAL Aventis Pasteur Limited (CA)  
location/Qualifiers

FEATURES  
source  
1. 1986  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="modified gp 100"

BASE COUNT 431 a 552 c 552 g 451 t  
ORIGIN

Alignment Scores:  
Pred. No.: 21.8 Length: 1986  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
Gaps: 0

US-09-214-836-1 (1-9) x AX192347 (1-1986)

Qy 1 LysThrTPGlyGlnTyrTrpAlaVal 9  

Db 460 AAGACCTGGGCGCAATACGTGCAAGTT 486

RESULT 6  
LOCUS BT007202 1986 bp mRNA linear PRI 13-MAY-2003  
DEFINITION Homo sapiens silver homolog (mouse) mRNA, complete cds.  
ACCESSION BT007202  
VERSION BT007202.1 GI:30583242  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1986)  
AUTHORS Kainine, N., Chen, X., Rolfe, A., Halleck, A., Hines, L., Eisenstein, S.,  
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y.,  
Phelan, M. and Farmer, A.  
TITLE Cloning of human full-length CDSs in BD Creator (TM) System Donor  
vector  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1986)  
AUTHORS Kainine, N., Chen, X., Rolfe, A., Halleck, A., Hines, L., Eisenstein, S.,  
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y.,  
Phelan, M. and Farmer, A.  
TITLE Direct Submission  
JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow  
Circle, Palo Alto, CA 94303, USA

COMMENT This CDS clone is a part of a collection of human full length  
expression clones generated by BD Biosciences Clontech and the  
Harvard Institute of Proteomics. Each CDS has been cloned in two  
forms: with and without stop-codon (to allow fusion with C-terminal  
tag). The CDS has been directionally cloned using BD In-Fusion(TM)  
cloning system between the SalI and HindIII sites of the pDNR-DUAL  
vector. Additional sequences in the clone: 'ACC' after SalI site  
and before 'ATG' to provide Kozak consensus sequence; 'GG' after  
last codon and before HindIII site to maintain reading frame.  
Clone distribution: <http://bioinfo.clontech.com/orfclones>.

FEATURES

source  
1. 1986  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="GH00199X1.0"  
/clone\_lib="BD Creator (TM) CDS Library derived from MGC  
collection"  
/lab\_host="DH5alpha TI resistant"  
/note="Vector: pDNR-Dual"  
1. 1986  
/codon\_start=1  
/product="silver homolog (mouse)"  
/protein\_id="AAP35866.1"  
/db\_xref="GI:30583243"  
/translation="MDLVLRCLHLAVIGALLAVGATKVRNODWLGVSRLRTKAV  
NROLYPEWTEAORLDCWKGQVSLKVNDSPTLLIGANASFSIALNFGSQVLPDGOV  
IWNNTTINSQVWGQGVPOETDDACIPDGGPCSGSWSOKRSFYVMKTKGOV  
OVIGPVSGLSIGTGKRAMLGTHMEVTVYHRRGSRVYPLAHSSAFTIDQVPSVS  
VSOIRALDGNKHFRLRNPFLPALDLHPSGTYLAELASTYWDPSGSGTILSALVY  
THYLEBGPVTAQVLOALPLTSCGSSPVGTTDGRPTAEAPNTTAAQVPTTEVAG  
TTTPOAPTAEPBSGTSVQVPTTEVISTAPVQMPAESTGMPEKVPVSEVNGTLLAE  
STPATGNTPAEVSIVLISGTTAAQVTTWEVETTARELPPEBGPASSIMSTESI  
TSGSLGPLDGTATRLVLRQVLDVLRVGSFSTVLDIVOGISAEILQAVPSGEED  
AFELTVSCOGGLPREACMEISSPCGPPARLCOVLPSPACQVLHQLIKGSGTVC  
LNVSLADTNSLAIVSTQILMGPQAGLQVPLVIGILLVMAVVLASLIYRRRLMKOD  
FSVQPLHSSSHMLRPRIFCSCTIGNSPLISQGV"

CDS

BASE COUNT 431 a 554 c 550 g 451 t  
ORIGIN

Alignment Scores:  
Pred. No.: 21.8 Length: 1986  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0

DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x BT007202 (1-1986)

QY 1 LysThrTPGlyGlnTYrTPAlaVal 9  
 |||||  
 |||||

DB 460 AAGACCTGGGGCCAACTGCGCAAGTT 486

RESULT 7  
 BT007291

LOCUS 1986 bp mRNA linear SYN 13-MAY-2003

DEFINITION Synthetic construct Homo sapiens silver homolog (mouse) mRNA.

ACCESSION BT007291

VERSION BT007291.1 GI:30584820

KEYWORDS FLI CDNA.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 1986)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Pheilan,M., Raphael,J., Moreira,D., Kelley,T., Labaer,U., Lin,Y.,  
 Koundinya,M., and Farmer,A.

AUTHORS

TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor vector

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1986)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,U., Lin,Y.,  
 Pheilan,M., and Farmer,A.

AUTHORS

TITLE Direct Submission

COMMENT Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

FEATURES

source

1. 1986  
 /organism="synthetic construct"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:32630"  
 /clone="GH001991.0"  
 /clone\_1ib="BD Creator (TM) CDS Library derived from MGC collection"  
 /lab\_host="DH5alpha T1 resistant"  
 /note="vector: pDNR-Dual"  
 1. >1986  
 /note="Mutations: 1985:Stop->Leu"  
 /codon\_start=1  
 /transl\_table=11  
 /product="Homo sapiens silver homolog (mouse)"  
 /protein\_id="AAP36663.1"  
 /db\_xref="GI:30584821"  
 /translation="MDLVLRKCLHLAVIGALLAVGATKVPNNQDMLGVSRQLRTKAM  
 NQLYPTWTEAORLDICWGGVSLKVSNDGPTLIGANASFSIALNFGPSOKVLPDGOV  
 IWNNTITNSQWVGQGVPOETDADICFPDGGPCPGSGMSOKRSFYVWKMGQVY  
 QVLGGPVSGLSIGTRAMLGTHMEVYTHRRGSRSYVPLAHSSAFITTDQVPSVS  
 VSQLRALDGNKHFRLNQLPTFALQLDHPSGYLAEDISTYWDPDSSGTLISRLVV  
 THTYLERPVYAVVLAQAIPLTSCGSPVGTGDGRPTAEANTTAAGVPTTEVVG  
 TTPGQAPLAEPSGTSVQVPTTEVISTAPVQMPAEISGTMPKPEKVPVSWGTTLAEM  
 STPEAKMTPEAVSIVLSGTTAAOVTTTEMTARELPPEBGPASSIMTESI  
 TGSILPDLGTRATRLKRVQPLDCVLYRGSRSVTLIDYOGISASRTLOAPSGED  
 AFELTVSCQGLPKEACMEISPGCQPPAQRLCQVLPSPACQVLHQLKGGSTYC  
 LNVSLADNLSAVSTQLMPQDAGLGQVPLVIGLLVLAVALVSLIYRRRLMKOD  
 FSVPLPHSSSHMLRLPRIFCSCPIGENSPILSGOOV"

CDS

BASE COUNT 430 a 554 c 550 g 452 t

ORIGIN

Alignment Scores:

Pred. No.: 21.8 Length: 1986

Score: 53.00 Matches: 8

Percent Similarity: 88.89% Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 91.38% Indels: 0

DB: 12 Gaps: 0

US-09-214-836-1 (1-9) x BT007291 (1-1986)

QY 1 LysThrTPGlyGlnTYrTPAlaVal 9  
 |||||  
 |||||

DB 460 AAGACCTGGGGCCAACTGCGCAAGTT 486

RESULT 8  
 HSU01874

LOCUS 2026 bp mRNA linear PRI 26-MAY-1994

DEFINITION Human me20m mRNA, complete cds.

ACCESSION U01874

VERSION U01874.1 GI:494939

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 2026)  
 Marsh,G.A., Marken,J.S., Neubauer,M., Aruffo,A., Hellstrom,I.,  
 Hellstrom,K.E. and Marguardt,H.

AUTHORS

TITLE Cloning and expression of the gene for the melanoma-associated ME20 antigen

JOURNAL DNA Cell Biol. 13 (2), 87-95 (1994)

REFERENCE 2 (bases 1 to 2026)  
 Neubauer,M.G.

AUTHORS

TITLE Direct Submission

COMMENT Submitted (16-SEP-1993) Michael G. Neubauer, Bristol-Myers Squibb Pharmaceutical Research Institute, 3005 1st Ave, Seattle, WA 98121, USA

FEATURES

source

1. 2026  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="h12-2"  
 /cell\_line="melanoma H3606"  
 /clone\_1ib="cdm8"  
 7. 1995  
 /standard\_name="melanoma-associated ME20 antigen"  
 /codon\_start=1  
 /product="me20m"  
 /protein\_id="AA18479.1"  
 /db\_xref="GI:494940"  
 /translation="MDLVLRKCLHLAVIGALLAVGATKVPNNQDMLGVSRQLRTKAM  
 NQLYPTWTEAORLDICWGGVSLKVSNDGPTLIGANASFSIALNFGPSOKVLPDGOV  
 IWNNTITNSQWVGQGVPOETDADICFPDGGPCPGSGMSOKRSFYVWKMGQVY  
 QVLGGPVSGLSIGTRAMLGTHMEVYTHRRGSRSYVPLAHSSAFITTDQVPSVS  
 VSQLRALDGNKHFRLNQLPTFALQLDHPSGYLAEDISTYWDPDSSGTLISRLVV  
 THTYLERPVYAVVLAQAIPLTSCGSPVGTGDGRPTAEANTTAAGVPTTEVVG  
 TTPGQAPLAEPSGTSVQVPTTEVISTAPVQMPAEISGTMPKPEKVPVSWGTTLAEM  
 STPEAKMTPEAVSIVLSGTTAAOVTTTEMTARELPPEBGPASSIMTESI  
 TGSILPDLGTRATRLKRVQPLDCVLYRGSRSVTLIDYOGISASRTLOAPSGED  
 AFELTVSCQGLPKEACMEISPGCQPPAQRLCQVLPSPACQVLHQLKGGSTYC  
 LNVSLADNLSAVSTQLMPQDAGLGQVPLVIGLLVLAVALVSLIYRRRLMKOD  
 FSVPLPHSSSHMLRLPRIFCSCPIGENSPILSGOOV"

CDS

sig peptide  
 mat\_peptide

BASE COUNT 437 a 564 c 564 g 461 t

ORIGIN

Alignment Scores:  
Pred. No.: 22.1 Length: 2026  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x HSU01874 (1-2026)

QY 1 LysThrTPGlyGlnTyrTrpAlaVal 9  
Db 466 AAGACTGGGGCCAACTGGCAAGTT 492

RESULT 9  
HUMGPMS  
LOCUS Human 95 kd melanocyte-specific secreted glycoprotein mRNA, 3' end.  
DEFINITION M32295 GI:183559  
VERSION M32295.1  
KEYWORDS melanocyte-specific secreted glycoprotein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Vogel, A.  
TITLE Sequence of a melanocyte specific secreted glycoprotein  
JOURNAL Unpublished (1990)  
COMMENT Original source text: Human melanoma cell line, cDNA to mRNA, clone 8.

FEATURES  
source  
Location/Qualifiers  
1..2114  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/note="melanocyte-specific secreted glycoprotein"

## CDS

/codon\_start=1  
/protein\_id="AA03930.1"  
/translation="RGIRKMTMDLVLRKCLHLAVIGALLAVGATKVPBNDMLGVSR  
QLRTKAMRQLYPEWTEAQRDLDCWRGQVSLKXSNDEPTLIGANASRIALNPFSGSOK  
VLPGQVIVWNTTINSQWGGQPVYRQETDACPDPGCPGSGMSQRSPYTV  
KTWQYQVLDGVPVSGSLIGTRAKLGHTEVTVYHRGSRSVPLAHSSAFITD  
QVPSVSVSLRALDGNKHLRNQPLFALQHDPSGYLAADLSYWDGSSGTL  
ISRALVHTYLAERGPVTAQVLAALPLTSCGSPVGTGHRPTAEADNTTAAQV  
PTTEVAGTTPGQAPABSPGTSVQVPTTEVISTAPVQMPAESTGMPREKVPSEV  
GTTLAEMSTPEPATGMPPAEVSIVLSGTTAQTTEVETARELPPEEGPDAS  
IMSTESTIGSLGPIIDGTRATRLVKRQVPLDCVLRYSRFTVLDIVGITSALLOA  
VPSGEGDAFELTVSCQGLPKPKACMEISPGCQPAQRLCPVLPSPACQLVHLQILK  
GGSGTYCLNVLASLADNLSLAVSTOLIMGQAGAGQVPLVIGILVMAVVLASLIYR  
RLMKOPFSVQLPHSSSHMLRLPASSLVPLVLIAPSSVGSRSRYSHML"

BASE COUNT 469 a 586 c 575 g 484 t

ORIGIN

Alignment Scores:  
Pred. No.: 22.9 Length: 2114  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x HUMGPMS (1-2114)

QY 1 LysThrTPGlyGlnTyrTrpAlaVal 9  
Db 481 AAGACTGGGGCCAACTGGCAAGTT 507

RESULT 10

A45993  
LOCUS A45993 2115 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 1 from Patent EP0668350.  
ACCESSION A45993  
VERSION A45993.1 GI:2300268  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2115)  
AUTHORS Adams, G.J. and Figdor, C.G.  
TITLE Melanoma associated antigenic polypeptide, epitopes thereof and  
vaccines against melanoma  
JOURNAL Patent: EP 0668350-A 1 23-AUG-1995;  
AKZO NOBEL NV (NL)  
COMMENT Other publication ZA 950123 951019  
Other publication JP 7278193 951024  
Other publication FI 950665 950817  
Other publication CA 2142575 950817  
Other publication AU 1227295 950824.

## FEATURES

source  
1..2115  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
/cell\_type="MELANOCYTE"  
/feature\_type="MELANOMA"  
1..81  
22..2007  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CA02869.1"  
/db\_xref="GI:2300269"

/translation="MDLVLRKCLHLAVIGALLAVGATKVPBNDMLGVSRQLRTKAMRQLYPEWTEAQRDLDCWRGQVSLKXSNDEPTLIGANASRIALNPFSGSOK  
VLPGQVIVWNTTINSQWGGQPVYRQETDACPDPGCPGSGMSQRSPYTV  
KTWQYQVLDGVPVSGSLIGTRAKLGHTEVTVYHRGSRSVPLAHSSAFITD  
QVPSVSVSLRALDGNKHLRNQPLFALQHDPSGYLAADLSYWDGSSGTLISRALV  
HTYLAERGPVTAQVLAALPLTSCGSPVGTGHRPTAEADNTTAAQV  
PTTEVAGTTPGQAPABSPGTSVQVPTTEVISTAPVQMPAESTGMPREKVPSEV  
GTTLAEMSTPEPATGMPPAEVSIVLSGTTAQTTEVETARELPPEEGPDASIMSTESI  
TGSLGPIIDGTRATRLVKRQVPLDCVLRYSRFTVLDIVGITSALLOA  
VPSGEGDAFELTVSCQGLPKPKACMEISPGCQPAQRLCPVLPSPACQLVHLQILKGGSGTYC  
LNVLADTNLSLAVSTOLIMGQAGAGQVPLVIGILVMAVVLASLIYRRIMKOD  
FSVQQLPHSSSHMLRLPRICSCIGNSPILSGQV"

misc\_signal  
misc\_signal

BASE COUNT 469 a 587 c 575 g 484 t  
ORIGIN  
/function="TRANSMEMBRANE REGION"

Alignment Scores:  
Pred. No.: 23 Length: 2115  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 6 Gaps: 0

US-09-214-836-1 (1-9) x A45993 (1-2115)

QY 1 LysThrTPGlyGlnTyrTrpAlaVal 9  
Db 481 AAGACTGGGGCCAACTGGCAAGTT 507

RESULT 11  
LOCUS AR269281 2115 bp mRNA linear PAT 10-APR-2003  
DEFINITION Sequence 1 from patent US 6500919.  
ACCESSION AR269281  
VERSION AR269281.1 GI:29700346  
KEYWORDS  
SOURCE unknown.

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2115)
TITLE	Adema, G.J. and Figdor, C.G.
JOURNAL	Melanoma associated antigenic polypeptide, epitopes thereof and vaccines against melanoma
FEATURES	Patent: US 6500919-A 1 31-DEC-2002;
SOURCE	Location/Qualifiers
BASE COUNT	1..2115
ORIGIN	/organism="unknown"
BASE COUNT	469 a 587 c 575 g 484 t
Alignment Scores:	
Pred. No.:	23
Score:	53.00
Percent Similarity:	88.89%
Best Local Similarity:	88.89%
Query Match:	91.38%
DB:	6
US-09-214-836-1 (1-9) x AR269281 (1-2115)	
RESULT 12	
LOCUS	AR167365
DEFINITION	Sequence 1 from patent US 6287569.
ACCESSION	AR167365
VERSION	AR167365.1 GI:17903140
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2130)
TITLE	Kipps, T.J. and Wu, Y.
JOURNAL	Vaccines with enhanced intracellular processing
FEATURES	Patent: US 6287569-A 1 11-SEP-2001;
SOURCE	Location/Qualifiers
BASE COUNT	1..2130
ORIGIN	/organism="unknown"
BASE COUNT	484 a 587 c 575 g 484 t
Alignment Scores:	
Pred. No.:	23.1
Score:	53.00
Percent Similarity:	88.89%
Best Local Similarity:	88.89%
Query Match:	91.38%
DB:	6
US-09-214-836-1 (1-9) x AR167365 (1-2130)	
RESULT 13	
LOCUS	AX274950
DEFINITION	Sequence 1 from Patent WO0170767.
ACCESSION	AX274950
VERSION	AX274950.1 GI:16547582
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1

AUTHORS		Nicolette, C.A.	
TITLE		Therapeutic anti-melanoma compounds	
JOURNAL		Patent: WO 0170767-A 1 27-SEP-2001;	
FEATURES		GENZYME CORPORATION (US)	
source		Location/Qualifiers	
		1. 2130	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
CDS		22..2007	
		/note="unnamed protein product"	
		/codon_start=1	
		/protein_id="CAD10318.1"	
		/db_xref="GI:16547583"	
		/translation="MDLVKRCILHLAVIGALLAVGATKYVPRNDMLVGSORLRTKAM NRQILPEWTEAKRLDCWRGQVSLKNSDGPILTIGANASISALNPFSGSRLPDGYW IWNNTTINSQVWGQPVYPOETDDACIPDGGPCPSGSWSQKRSFVYWKTDGYW QVLGGPVSGLSIGTRGMLGTHTMELFVTVHRSRSVPLAHSSAPFTINDVPFVS VSOLRALDGNKHFRLNRPALQHLDPGSLAEADLYTMPFGDSGTLISRALVW THYLRGVPYAOVYLOAATPLTSCSSPVGPTTGDHRLPTAAENPTAGVGPTEVVG TTTQCAPTAPSPGTSQVPTTEVYSIAPLQMPFASBTGWTPEKVPYMGTTLAM STPATGMPAEVSTIVLSGTTAAQVTTTWEVTTAKELFPEPEGDASSINTESTI TGSIGPLLDGATLRLVWRQVPLDVCVLYRGSFSVTLDIVQGLSEAEILQAVSGED AFETLVSQCGGLPEALAEISSLSPCCPPAQLCPVLPSPACOLVHLQIKGSGTVC LNSVLADTSLAVSTFQILMPGQAGVGLVIGILLVMAVVLASLIYRRRLMKOD FSVDFPHSSSHWRLPRIFCSPGIGNSLLSGQQ"	
BASE COUNT		484 a 587 c 575 g 484 t	
ORIGIN			
Alignment Scores:			
Pred. No.:		23.1 Length: 2130	
Score:		53.00 Matches: 8	
Percent Similarity:		88.89% Conservative: 0	
Best Local Similarity:		88.89% Mismatches: 1	
Query Match:		91.38% Indels: 0	
DB:		6 Gaps: 0	
US-09-214-836-1 (1-9) x AX274950 (1-2130)			
OY		1 LysThrTrpGlyGlnTyrTrpAlaVal 9	
Db		481 AAGACCTGGGGCCCAATACTGGCAAGTT 507	
RESULT 14			
LOCUS		AX354933 2130 bp DNA linear PAT 06-FEB-2002	
AX354933			
DEFINITION		Sequence 1 from Patent WO0192294.	
ACCESSION		AX354933	
VERSION		AX354933.1 GI:18619617	
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE		1	
AUTHORS		Nicolette, C.A.	
TITLE		Therapeutic anti-melanoma compounds	
JOURNAL		Patent: WO 0192294-A 1 06-DEC-2001;	
FEATURES		GENZYME CORPORATION (US)	
source		Location/Qualifiers	
		1. 2130	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
BASE COUNT		484 a 587 c 575 g 484 t	
ORIGIN			
Alignment Scores:			
Pred. No.:		23.1 Length: 2130	
Score:		53.00 Matches: 8	
Percent Similarity:		88.89% Conservative: 0	
Best Local Similarity:		88.89% Mismatches: 1	
Query Match:		91.38% Indels: 0	

DB: 6 Gaps: 0

US-09-214-836-1 (1-9) x AX354933 (1-2130)

QY 1 LysThrTPGlyGlnTyrTTPAlaVal 9  
|||||  
481 AAGACCTGGGCGCAATCTGGCAAGTT 507

RESULT 15

LOCUS S73003 2130 bp mRNA linear PRI 26-JAN-1995

DEFINITION gp100-melanocyte lineage-specific antigen/Fmel17 homolog [human,  
mRNA, 2130 nt].

ACCESSION S73003

VERSION S73003.1

KEYWORDS GI:639589

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Adema, G.J., de Boer, A.J., Vogel, A.M., Loenen, W.A. and Figdor, C.G.  
1 (bases 1 to 2130)  
Molecular characterization of the melanocyte lineage-specific  
antigen gp100

JOURNAL J. Biol. Chem. 269 (31), 20126-20133 (1994)

MEDLINE 94327568

PUBMED 7519602

REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbon 154938] from the original journal article.  
This sequence comes from Fig. 6.

FEATURES

source

1. .2130  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/gene="gp100"  
22. .2007  
/gene="gp100"  
/note="melanocyte lineage-specific antigen/Fmel17 homolog;  
melanoma marker protein; this sequence comes from Fig. 6"  
/codon\_start=1  
/protein\_id="AAC60634.1"  
/db\_xref="GI:639590"  
/translation="MDLVLRKCLHLAVIGALLAVGATKVPKRNODMLGVSRLQRTKAM  
NRQLYPEWTEAQRDLDCWRGQVSLKVNNDGPTLLIGANASPSIALNFPQSOVLDPGOV  
IWNVNTIINSQVWGGQPVYPOETDADCIIPDGGPCPSGSSQKRSFYVWKVKGQV  
QVLCGPVSGLSIGTGRAMLGTHMEVTVYHGRGSRVYPLHSSSAFTITDOVPSVS  
VSOLRALDGGKHFRLNOLPLTALQHLDPGSLAEADLSYTWDPDSSGTLISRAVY  
THTYLRGPVTAQVVLQALPLTSCGSSPVGTTDGHRTAEAPNTTAAAGVPTTEVVG  
TTGQAPTAEPSTGTSVQVPTTEVISTAPVOMPTASTGTMTPEKVPVSEVGTLLAEK  
STPATGMPTEAEVSIIVLSGTTAAQVTTTEVETARLPIPEEGDPASSIMSTESI  
TGSIGPLDGTATLRLVKQVPLDCVLRYSFVTLDIYVGISSABTILQAVPSGEGD  
AFELTVSCOGGLPKKACMEIISPGCOPPAORLCPVLPSPACQVLAHLQILKSGGTYC  
LNVSLADTNSLAVVSTOLIMPGEGAGLGOVRLIYGLILVMAVLAVALIYRRLMKOD  
FSPVQLPHSSSHMLRLPRIFCSCPIGNSPLSSGQV"

BASE COUNT 484 a 587 c 575 g 484 t

ORIGIN

Alignment Scores:

Pred. No.:	23.1	Length:	2130
Score:	53.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	91.38%	Indels:	0
		Gaps:	0

US-09-214-836-1 (1-9) x S73003 (1-2130)

QY 1 LysThrTPGlyGlnTyrTTPAlaVal 9  
|||||  
481 AAGACCTGGGCGCAATCTGGCAAGTT 507

RESULT 16

LOCUS AX474662 2131 bp DNA linear PAT 12-AUG-2002

DEFINITION Sequence 3 from Patent EP1222928.

ACCESSION AX474662

VERSION AX474662.1

KEYWORDS GI:22214011

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Moelling, K., Nawrath, M. and Pavlovic, J.  
Pharmaceutical compositions for treating or preventing cancer,  
especially melanoma  
Patent: EP 1222928-A 3 17-JUL-2002;  
Universitaet Zuerich Institut fuer Medizinische Virologie (CH)

JOURNAL

FEATURES

source

1. .2131  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
12. .2018  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAD43667.1"  
/db\_xref="GI:22214012"  
/translation="MDLVLRKCLHLAVIGALLAVGATKVPKRNODMLGVSRLQRTKAM  
NRQLYPEWTEAQRDLDCWRGQVSLKVNNDGPTLLIGANASPSIALNFPQSOVLDPGOV  
IWNVNTIINSQVWGGQPVYPOETDADCIIPDGGPCPSGSSQKRSFYVWKVKGQV  
QVLCGPVSGLSIGTGRAMLGTHMEVTVYHGRGSRVYPLHSSSAFTITDOVPSVS  
VSOLRALDGGKHFRLNOLPLTALQHLDPGSLAEADLSYTWDPDSSGTLISRAVY  
THTYLRGPVTAQVVLQALPLTSCGSSPVGTTDGHRTAEAPNTTAAAGVPTTEVVG  
TTGQAPTAEPSTGTSVQVPTTEVISTAPVOMPTASTGTMTPEKVPVSEVGTLLAEK  
STPATGMPTEAEVSIIVLSGTTAAQVTTTEVETARLPIPEEGDPASSIMSTESI  
TGSIGPLDGTATLRLVKQVPLDCVLRYSFVTLDIYVGISSABTILQAVPSGEGD  
AFELTVSCOGGLPKKACMEIISPGCOPPAORLCPVLPSPACQVLAHLQILKSGGTYC  
LNVSLADTNSLAVVSTOLIMPGEGAGLGOVRLIYGLILVMAVLAVALIYRRLMKOD  
FSPVQLPHSSSHMLRLPRIFCSCPIGNSPLSSGQV"

BASE COUNT 475 a 588 c 578 g 490 t

ORIGIN

Alignment Scores:

Pred. No.:	23.1	Length:	2131
Score:	53.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	91.38%	Indels:	0
		Gaps:	0

US-09-214-836-1 (1-9) x AX474662 (1-2131)

QY 1 LysThrTPGlyGlnTyrTTPAlaVal 9  
|||||  
471 AAGACCTGGGCGCAATCTGGCAAGTT 497

RESULT 17

LOCUS HUMPMEL 2131 bp mRNA linear PRI 08-JAN-1995

DEFINITION Human Pmel 17 mRNA, complete cds.

ACCESSION M77348

VERSION M77348.1

KEYWORDS Pmel 17 protein; melanocyte.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Kwon, B.S., Chintamaneni, C., Kozak, C.A., Copeland, N.G.,  
Gilbert, D.J., Jenkins, N., Barton, D., Francke, U., Kobayashi, Y. and  
Kim, K.K.  
A melanocyte-specific gene, Pmel 17, maps near the silver coat

color locus on mouse chromosome 10 and is in a syntenic region on human chromosome 12  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (20), 9228-9232 (1991)  
 MEDLINE 92021023  
 PUBMED 1924386  
 COMMENT Original source text: Homo sapiens skin CDNA to mRNA.  
 FEATURES location/Qualifiers  
 source 1..2131  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="primary culture"  
 /cell\_type="melanocyte"  
 /tissue\_type="skin"  
 1..2131  
 /gene="Pmel 17"  
 1..2121  
 /gene="Pmel 17"  
 12..2018  
 /gene="Pmel 17"  
 /codon\_start=1  
 /product="Pmel 17 protein"  
 /protein\_id="AA60121.1"  
 /db\_xref="GI:190106"  
 /translation="MDLVKRCILHAVIGALLAVGATKVPKPNQDMLGVSRQLRTKAM  
 NROLYPEWTEAQRDLDCRGGQVSLKVNDSGPTLIGANASFSIALNPFQSGVLPDGOV  
 IWNNTTINSQVWGQVVPQETDCAICFPDGGPCSGSWSQKRSFYVWKTGQV  
 QVLGGPVGSLSTIGRAMLGHTMEVTVYHRGSRVPLAHSSAFTITTOVPSVS  
 VSQRLADGKNGHFLRNQPLFALQHPSPGSLAEADLSYTMDFGSSGTLISRLAV  
 THTYLPGPVTAQVLAQAIPLTSCSSPVGCTDGRPTAEAPNTAGOVPTTEVG  
 TTGQAPPAEBSGTSVQVPTTEVISTAPVOMPTAESGMPPEKVPVSEWGTIAEM  
 STEPATGTPAEBSIVVLSGTTAAQVTTETETARELPPEPEBGDASSIMSTESI  
 TGSIGPLDGTATLVRKQVPLDCLVLRGVSFVTLDIVOGIESAIIQVLPVSGEGD  
 AFELTVSCQGGLPKAEKMEISSPGCQPAQRLCPVLPSPACQVLVHLQILKSGSTYC  
 LNVSLADTNSLAVSTQILMPVPGILITGQEGLDQVRLVIGILVLAADVASTLYR  
 RRLMKQDSVPLPHSSSHWLRIPFCSCPIGNSPLISGQV"

BASE COUNT 475 a 588 c 578 g 490 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 23.1 Length: 2131  
 Score: 53.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 91.38% Indels: 0  
 DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x HUMPMEL (1-2131)

Qy 1 LysThrTPGlyGlnTyTTPAlaVal 9  
 DB 471 AAGACTGGGGCCCAATCTGCAAGTT 497

RESULT 18  
 BC001414 2134 bp mRNA linear PRI 12-JUL-2001  
 LOCUS Homo sapiens, silver (mouse homolog) like, clone MGC:2169  
 DEFINITION IMAGE:3139788, mRNA, complete cds.  
 ACCESSION BC001414  
 VERSION BC001414.1 GI:12655122  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-DEC-2000) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

## COMMENT

Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@hagri.nih.gov](mailto:nisc_mgc@hagri.nih.gov)  
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,  
 Benjamin, B., Blakesley, R.W., Boulard, G.G., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,  
 Lin, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Snyder, B., Stantirpop, S., Thomas, P.J.,  
 Tjongson, E.E., Touchman, J.W., Tsurgoun, C., Vogt, J.L., Walker, M.A.,  
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 4 Row: 1 Column: 8  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 639589.  
 Location/Qualifiers  
 1..2134

FEATURES  
 source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /db\_xref="taxon:9606"  
 /clone="MGC:2169 IMAGE:3139788"  
 /tissue\_type="Placenta, choriocarcinoma"  
 /clone\_id="NIH MGC 21"  
 /lab\_host="DH10B-R"  
 /note="vector: pOTB7"  
 20..2005  
 /codon\_start=1  
 /product="silver (mouse homolog) like"  
 /protein\_id="AAH01414.1"  
 /db\_xref="GI:12655123"  
 /translation="MDLVKRCILHAVIGALLAVGATKVPKPNQDMLGVSRQLRTKAM  
 NROLYPEWTEAQRDLDCRGGQVSLKVNDSGPTLIGANASFSIALNPFQSGVLPDGOV  
 IWNNTTINSQVWGQVVPQETDCAICFPDGGPCSGSWSQKRSFYVWKTGQV  
 QVLGGPVGSLSTIGRAMLGHTMEVTVYHRGSRVPLAHSSAFTITTOVPSVS  
 VSQRLADGKNGHFLRNQPLFALQHPSPGSLAEADLSYTMDFGSSGTLISRLAV  
 THTYLPGPVTAQVLAQAIPLTSCSSPVGCTDGRPTAEAPNTAGOVPTTEVG  
 TTGQAPPAEBSGTSVQVPTTEVISTAPVOMPTAESGMPPEKVPVSEWGTIAEM  
 STEPATGTPAEBSIVVLSGTTAAQVTTETETARELPPEPEBGDASSIMSTESI  
 TGSIGPLDGTATLVRKQVPLDCLVLRGVSFVTLDIVOGIESAIIQVLPVSGEGD  
 AFELTVSCQGGLPKAEKMEISSPGCQPAQRLCPVLPSPACQVLVHLQILKSGSTYC  
 LNVSLADTNSLAVSTQILMPVPGILITGQEGLDQVRLVIGILVLAADVASTLYR  
 RRLMKQDSVPLPHSSSHWLRIPFCSCPIGNSPLISGQV"

BASE COUNT 490 a 584 c 576 g 484 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 23.1 Length: 2134  
 Score: 53.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 91.38% Indels: 0  
 DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x BC001414 (1-2134)

Qy 1 LysThrTPGlyGlnTyTTPAlaVal 9  
 DB 479 AAGACTGGGGCCCAATCTGCAAGTT 505

RESULT 19  
 AX133528 2534 bp DNA linear PAT 15-MAY-2001  
 LOCUS Sequence 123 from Patent WO0130847.  
 DEFINITION  
 ACCESSION AX133528



```

VERSION      AX133528.1 GI:14139680
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS      Bernstetn,N., Tartaglia,J., Moingeon,P., Barber,B. and Time,J.A.
TITLE        Modified gp100 and uses thereof
JOURNAL      Patent: WO 0130847-A 123 03-MAY-2001;
              Aventis Pasteur Limited (CA)
FEATURES     Location/Qualifiers
              source
              1..2534
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
              /note="modified gp 100"
BASE COUNT   622 a 632 c 657 g 623 t
ORIGIN
Alignment Scores:
Pred. No.:      26.7      Length:      2534
Score:          53.00     Matches:      8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match:    91.38% Indels:      0
DB:             6 Gaps:      0
US-09-214-836-1 (1-9) x AX133528 (1-2534)
Qy            1 LysThrTrpGlyGlnTyrTrpAlaVal 9
Db            836 AAGACCTGGGCGCAATCTGCGCAAGTT 862
RESULT 20
LOCUS        AK092881 2758 bp mRNA linear PRI 15-JUL-2002
DEFINITION   Homo sapiens cDNA FLJ35562 f1s, clone SPLEN2005272, highly similar
              to MELANOCYTE PROTEIN PMEL 17 PRECURSOR.
ACCESSION    AK092881
KEYWORDS     oligo capping, f1s (full insert sequence).
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1
AUTHORS      Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
              Ono,Y., Hotuta,T., Hirooka,S., Murakawa,K., Takiguchi,S.,
              Kuranu,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
              Yasushita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
              Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Igono,Y.,
              Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K.,
              Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M.,
              Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
              Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
              NEDO human cDNA sequencing project
              Unpublished
              2 (bases 1 to 2758)
              Isogai,T. and Yamamoto,J.
              Direct Submission
              Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
              (E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
              Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
              (E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
              NEDO human cDNA sequencing project supported by Ministry of
              Economy, Trade and Industry of Japan; cDNA full insert sequencing:
              Research Association for Biotechnology (RAB); cDNA library
              construction: Helix Research Institute (HRI) (supported by Japan
              Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
              HRI, and Biotechnology Center, National Institute of Technology and
              Evaluation; clone selection for full insert sequencing: HRI and
              RAB; annotation: HRI and RAB.
              Location/Qualifiers
              1..2758
FEATURES     source

```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SPLEN2005272"
/tissue="spleen"
/clone_id="SPLEN2"
/note="Cloning vector: PMEL8SFL3"
BASE COUNT   600 a 747 c 733 g 678 t
ORIGIN
Alignment Scores:
Pred. No.:      28.7      Length:      2758
Score:          53.00     Matches:      8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match:    91.38% Indels:      0
DB:             9 Gaps:      0
US-09-214-836-1 (1-9) x AK092881 (1-2758)
Qy            1 LysThrTrpGlyGlnTyrTrpAlaVal 9
Db            1124 AAGACCTGGGCGCAATCTGCGCAAGTT 1150
RESULT 21
LOCUS        AR063067 2172 bp DNA linear PAT 29-SEP-1999
DEFINITION   Sequence 26 from patent US 5844075.
ACCESSION    AR063067
VERSION      AR063067.1 GI:5990758
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 2172)
AUTHORS      Kawakami,Y. and Rosenberg,S.A.
TITLE        Melanoma antigens and their use in diagnostic and therapeutic
              methods
JOURNAL      Patent: US 5844075-A 26 01-DEC-1998;
              Location/Qualifiers
              source
              1..2172
              /organism="unknown"
BASE COUNT   512 a 594 c 578 g 488 t
ORIGIN
Alignment Scores:
Pred. No.:      73.1      Length:      2172
Score:          50.00     Matches:      7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    86.21% Indels:      0
DB:             6 Gaps:      0
US-09-214-836-1 (1-9) x AR063067 (1-2172)
Qy            1 LysThrTrpGlyGlnTyrTrp 7
Db            498 AAGACCTGGGCGCAATCTGCG 518
RESULT 22
LOCUS        AR091800 2172 bp DNA linear PAT 07-SEP-2000
DEFINITION   Sequence 26 from patent US 5994523.
ACCESSION    AR091800
VERSION      AR091800.1 GI:10018554
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 2172)
AUTHORS      Kawakami,Y. and Rosenberg,S.A.
TITLE        Melanoma antigens and their use in diagnostic and therapeutic
              methods

```

JOURNAL Patent: US 5994523-A 26 30-NOV-1999;  
FEATURES Location/Qualifiers  
SOURCE 1..2172  
BASE COUNT 512 a 594 c 578 g 488 t  
ORIGIN

Alignment Scores:  
Pred. No.: 73.1 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0  
DB: 6 Gaps: 0

US-09-214-836-1 (1-9) x AR091800 (1-2172)

QY 1 LysThrTPGlyGlnTyrTTP 7  
|||||  
Db 498 AAGACCTGGGGCCAACTACTGG 518

RESULT 23  
AR162997  
LOCUS AR162997 2172 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 26 from patent US 6270778.  
ACCESSION AR162997  
VERSION AR162997.1 GI:16233468  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2172)  
AUTHORS Kawakami,Y. and Rosenberg,S.A.  
TITLE Melanoma antigens and their use in diagnostic and therapeutic methods  
JOURNAL Patent: US 6270778-A 26 07-AUG-2001;  
FEATURES Location/Qualifiers  
SOURCE 1..2172  
BASE COUNT 512 a 594 c 578 g 488 t  
ORIGIN

Alignment Scores:  
Pred. No.: 73.1 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0  
DB: 6 Gaps: 0

US-09-214-836-1 (1-9) x AR162997 (1-2172)

QY 1 LysThrTPGlyGlnTyrTTP 7  
|||||  
Db 498 AAGACCTGGGGCCAACTACTGG 518

RESULT 24  
AR287974  
LOCUS AR287974 2172 bp mRNA linear PAT 12-JUN-2003  
DEFINITION Sequence 26 from patent US 6537560.  
ACCESSION AR287974  
VERSION AR287974.1 GI:31675132  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2172)  
AUTHORS Kawakami,Y. and Rosenberg,S.A.  
TITLE Melanoma antigens and their use in diagnostic and therapeutic methods  
JOURNAL Patent: US 6537560-A 26 25-MAR-2003;  
FEATURES Location/Qualifiers  
SOURCE 1..2172

BASE COUNT 512 a 594 c 578 g 488 t  
ORIGIN

Alignment Scores:  
Pred. No.: 73.1 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0  
DB: 6 Gaps: 0

US-09-214-836-1 (1-9) x AR287974 (1-2172)

QY 1 LysThrTPGlyGlnTyrTTP 7  
|||||  
Db 498 AAGACCTGGGGCCAACTACTGG 518

RESULT 25  
AX474660  
LOCUS AX474660 1881 bp DNA linear PAT 12-AUG-2002  
DEFINITION Sequence 1 from Patent EP1222928.  
ACCESSION AX474660  
VERSION AX474660.1 GI:22214009  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Moelling,K., Nawrath,M. and Pavlovic,J.  
TITLE Pharmaceutical compositions for treating or preventing cancer, especially melanoma  
JOURNAL Patent: EP 1222928-A 1 17-JUL-2002;  
FEATURES Location/Qualifiers  
SOURCE 1..1881  
BASE COUNT 417 a 537 c 500 g 427 t  
ORIGIN

Alignment Scores:  
Pred. No.: 94.6 Length: 1881  
Score: 49.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 84.48% Indels: 0  
DB: 6 Gaps: 0

US-09-214-836-1 (1-9) x AX474660 (1-1881)

QY 1 LysThrTPGlyGlnTyrTTPAlaVal 9  
|||||  
Db 460 AAGACCTGGGGAAATACTGGCAAGTT 486

Mon Aug 25 09:47:39 2003

us-09-214-836-1.rge

Page 11

Search completed: August 24, 2003, 02:53:47  
Job time : 2201.5 secs

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 23, 2003, 23:25:17 ; Search time 196.5 Seconds  
(without alignments)  
123.638 Million cell updates/sec

Title: US-09-214-836-1  
Perfect score: 58  
Sequence: 1 KTWGQYMAV 9

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

```
MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2.1/USPTO/US09214836/runat.14082003.085039.7585/app.query.fasta_1.398
-DB=N.Geneseq.19Jun03 -QFMT=fasta -SUFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25
-MODE=LOCAL -OUTFMT=pcio -NORF=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09214836 @CGN 1.1.401 @runat.14082003.085039.7585 -NCPU=6 -ICPU=3
-NO_MMAR -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

## Database :

```
N.Geneseq.19Jun03:*
1: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSt/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	53	91.4	36	16	AAT05466	Sequence encoding
2	53	91.4	51	22	AAL26956	Human SNP oligonuc
3	53	91.4	90	24	ABK6650	Human DNA encoding
4	53	91.4	90	24	ABK6651	Human DNA encoding
5	53	91.4	1986	22	AAD07346	Modified tumour-as
6	53	91.4	1986	22	AAH22098	Human gp100W nucle
7	53	91.4	1986	22	AAH20120	Modified gp100W en
8	53	91.4	2115	16	AAO96055	Sequence encoding
9	53	91.4	2130	19	ABO76195	Human tumour anti
10	53	91.4	2130	22	AAH43500	Human melanoma ant
11	53	91.4	2130	24	AAH43596	CDNA encoding huma
12	53	91.4	2131	16	AAT03760	Melanoma-specific
13	53	91.4	2131	18	AAT96726	PMEL17 CDNA. Homo
14	53	91.4	2131	24	AAL49164	Human gp100 coding
15	53	91.4	2534	22	AAH22099	Plasmid C5H6gp100M
16	53	91.4	1638	24	ABK6828	Human DNA for mela
17	50	86.2	2172	16	AAT02716	MART-1 melanoma an
18	50	86.2	2172	22	AAH45525	DNA encoding Melan
19	49	84.5	1881	24	AAL49163	Murine gp100 codin
20	48	82.8	24	16	AAT05465	Sequence encoding
21	48	82.8	227968	24	ABK83497	Human cDNA differe
22	47	81.0	215	25	ABK45137	Bovine EST associa
23	45	77.6	493	22	AAH5451	Human polynucleoti
24	45	77.6	771	22	AAL20608	Human breast cance
25	45	77.6	31051	22	AAK73223	Human immune/haema
26	44	75.9	453	24	ABN64229	Human cancer relat
27	44	75.9	1030	22	AAH61041	Human polynucleoti
28	44	75.9	1085	22	AAH59255	Human polynucleoti
29	44	75.9	1589	24	ABH78737	DNA encoding human
30	44	75.9	1663	24	ABH78736	DNA encoding human
31	44	75.9	2110	25	AAH47654	Human PHD1 CDNA.
32	44	75.9	3913	25	ABH7742	Aspergillus fumiga
33	44	75.9	4608	25	ABH79566	Aspergillus fumiga
34	44	75.9	8159	22	AAH19600	Human expressed po
35	44	75.9	8159	22	ABA06824	Human genomic DNA
36	44	75.9	8159	22	AAH29006	Genomic sequence #
37	44	75.9	8159	22	AAH29758	Human endocrine po
38	44	75.9	8159	22	AAL02776	Human reproductive
39	44	75.9	8159	22	AAH02943	Human reproductive
40	44	75.9	8159	22	AAH35096	DNA #46 encoding h
41	44	75.9	8159	24	ABH4841	Human polynucleoti
42	44	75.9	8159	24	ABH07841	Novel human nuclei
43	44	75.9	8159	25	ABH74525	Secreted protein g
44	44	75.9	8159	25	ABH26059	Human secreted pro
45	44	75.9	8165	22	AAH95599	Human expressed po

## ALIGNMENTS

RESULT 1  
AAT05466  
AAT05466 standard; CDNA to mRNA; 36 BP.

AC AAT05466;  
25-JAN-1996 (first entry)

DB Sequence encoding immunogenic peptide of melanoma antigen gp100.

KW Melanoma; antigen; vaccine; immunogen; primer; probe; detection;

IX Identification; tumour; gp100; ss.

OS Homo sapiens.

XX Key  
FH Location/Qualifiers  
CDS 1..36

```
FT      /+tag= a
FT      /product= Immunogenic peptide.
FT      protein_bind 1.33
FT      /+tag= b
FT      protein_bind 7.36
FT      /+tag= c
FT      protein_bind 7.33
FT      /+tag= d
FT      protein_bind 10.36
FT      /+tag= e
XX
XX      EP668350-A1.
XX      PD
XX      23-AUG-1995.
XX
XX      14-FEB-1995; 95EP-0200348.
XX
XX      21-DEC-1994; 94EP-0203709.
XX      PR
XX      16-FEB-1994; 94EP-0200337.
XX
XX      (ALKU ) AKZO NOBEL NV.
XX      PA
XX      Adema GJ, Figgdor CG;
XX      PI
XX      WPI; 1995-284790/38.
XX      DR
XX      P-PSDB; AAR78642.
XX
XX      Melanoma associated antigen gp100 - used in vaccines and for the
XX      PT detection of tumours
XX
XX      Claim 7; Page 27; 40pp; English.
XX
XX      Immunogenic peptides derived from the melanoma associated antigen
XX      CC (See AAR78635-45) may be used in the production of vaccines.
XX      CC Nucleotide sequences encoding the immunogenic peptides may be used
XX      CC as primers and probes in the detection of melanoma cells. Tumour
XX      CC infiltrating lymphocytes capable of binding to the melanoma
XX      CC associated antigen can be cultured ex vivo and returned to melanoma
XX      CC particles, and when radiolabelled, they may be used to identify
XX      CC tumour deposits.
XX
XX      Sequence 36 BP; 9 A; 8 C; 11 G; 8 T; 0 other;
XX      SQ
XX
XX      Alignment Scores:
XX      Pred. No.: 0.315 Length: 36
XX      Score: 53.00 Matches: 8
XX      Percent Similarity: 88.89% Conservative: 0
XX      Best Local Similarity: 88.89% Mismatches: 1
XX      Query Match: 91.38% Indels: 0
XX      DB: 16 Gaps: 0
XX
XX      US-09-214-836-1 (1-9) x AAT05466 (1-36)
XX
XX      QY 1 LysThrTPGlyGlnTyrTrpAlaVal 9
XX      DB 7 AAGACCTGGGGCCCACTACTGCAAGTT 33
XX
XX      RESULT 2
XX      AAL26956/c
XX      ID AAL26956 standard; DNA; 51 BP.
XX
XX      AAL26956;
XX      AC
XX      24-JAN-2002 (first entry)
XX      DE
XX      Human SNP oligonucleotide #164.
XX
XX      Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX      KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX      KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX      KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX      KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX      KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
```

```
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX      Homo sapiens.
XX      OS
XX      WO200147944-A2.
XX      PN
XX      05-JUL-2001.
XX      PD
XX      28-DEC-2000; 2000WO-US35498.
XX      PF
XX      28-DEC-1999; 99US-0173419.
XX      PR
XX      27-DEC-2000; 2000US-0173419.
XX      XX
XX      (CURA-) CURAGEN CORP.
XX      PA
XX      Shinkets RA, Leach M;
XX      PI
XX      WPI; 2001-465210/50.
XX      DR
XX
XX      Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX      PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX      PT cancer, autoimmune diseases and infections -
XX      PS
XX      Claim 1; Page 1443; 4143pp; English.
XX
XX      The present invention relates to oligonucleotides encoding polymorphic
XX      CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX      CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX      CC histones, kinases, colony stimulating factors, complement related
XX      CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX      CC G-protein coupled receptors and thioesterases. The present sequence is
XX      CC one such oligonucleotide. The oligonucleotides and the peptides encoded
XX      CC by them may be used in the prevention, diagnosis and treatment of
XX      CC diseases associated with inappropriate expression of the proteins listed
XX      CC above. Disorders that may be prevented, diagnosed and/or treated include
XX      CC multifactorial diseases with a genetic component, such as autoimmune
XX      CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX      CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX      CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX      CC leukaemia), diseases of the nervous system and an infection of pathogenic
XX      CC organisms.
XX      CC
XX      Sequence 51 BP; 15 A; 17 C; 9 G; 10 T; 0 other;
XX      SQ
XX
XX      Alignment Scores:
XX      Pred. No.: 0.464 Length: 51
XX      Score: 53.00 Matches: 8
XX      Percent Similarity: 88.89% Conservative: 0
XX      Best Local Similarity: 88.89% Mismatches: 1
XX      Query Match: 91.38% Indels: 0
XX      DB: 22 Gaps: 0
XX
XX      US-09-214-836-1 (1-9) x AAL26956 (1-51)
XX
XX      QY 1 LysThrTPGlyGlnTyrTrpAlaVal 9
XX      DB 37 AAGACCTGGGGTCACTACTGCAAGTT 11
XX
XX      RESULT 3
XX      ABK36650
XX      ID ABK36650 standard; DNA; 90 BP.
XX      AC
XX      ABK36650;
XX      AC
XX      08-MAY-2002 (first entry)
XX      DE
XX      Human DNA encoding gp100 segment 10.
XX
XX      Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX      KW viral infection; human immunodeficiency virus; melanoma;
XX      KW bacterial infection; Salmonella; Legionella; parasitic infection;
XX      KW Trypanosoma; Toxoplasma; Giardia; ds.
```

```

XX OS Homo sapiens.
XX PN WO200190197-A1.
XX PD 29-NOV-2001.
XX PF 25-MAY-2001; 2001WO-AU00622.
XX PR 26-MAY-2000; 2000AU-0007761.
XX PA (AUSU ) UNIV AUSTRALIAN NAT.
XX P1 Thomson SA, Ramshaw IA;
XX P2 WPI; 2002-147575/19.
XX P3 P-PSDB; AAU84830.
XX PT New synthetic polypeptides having several different segments of at
XX PT least one parent polypeptide linked together differently compared to
XX PT the linkage in the parent polypeptide, for inducing immune response
XX PT against a pathogen or cancer
XX PS Example 3; Fig 27; 364pp; English.
XX CC The invention relates to a new synthetic polypeptide (I) comprising
XX CC several different segments of at least one parent polypeptide linked
XX CC together in a different relationship relative to their linkage in the
XX CC parent polypeptide to impede, abrogate or otherwise alter at least one
XX CC function associated with the parent polypeptide and for inducing an
XX CC immune response against a pathogen or cancer. Also included are a
XX CC synthetic polynucleotide encoding and a computer system for
XX CC designing the synthetic polypeptides. The synthetic polypeptides and
XX CC polynucleotides are referred to as a Savine. The synthetic polypeptide is
XX CC useful for modulating immune responses preferably directed against a
XX CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,
XX CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone
XX CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.
XX CC Compositions comprising the polypeptide may be used in the treatment or
XX CC prophylaxis against viral (such as infections caused by HIV (human
XX CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX CC Trypanosoma, Toxoplasma and Giardia) infections. The present
XX CC sequence encodes a peptide derived from a parent protein used to
XX CC construct a savine of the invention.
XX SQ Sequence 90 BP; 23 A; 17 C; 32 G; 18 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0.872 Length: 90
XX Score: 53.00 Matches: 8
XX Percent Similarity: 88.89% Conservative: 0
XX Best Local Similarity: 88.89% Mismatches: 1
XX Query Match: 91.38% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-214-836-1 (1-9) x ABK36650 (1-90)
XX
XX Oy 1 LysThrTrpGlyGlnTyrTrpAlaVal 9
XX Db 61 AAGACATGGGAGCATATTGGCAAGTG 87
XX
XX RESULT 4
XX ABK36651
XX ID ABK36651 standard; DNA; 90 BP.
XX AC ABK36651;
XX XX 08-MAY-2002 (first entry)
XX

```

```

DE DE Human DNA encoding gp100 segment 11.
XX XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX XX viral infection; human immunodeficiency virus; melanoma;
XX XX bacterial infection; Salmonella; Legionella; parasitic infection;
XX XX Trypanosoma; Toxoplasma; Giardia; de.
XX OS Homo sapiens.
XX PN WO200190197-A1.
XX PD 29-NOV-2001.
XX PF 25-MAY-2001; 2001WO-AU00622.
XX PR 26-MAY-2000; 2000AU-0007761.
XX PA (AUSU ) UNIV AUSTRALIAN NAT.
XX P1 Thomson SA, Ramshaw IA;
XX P2 WPI; 2002-147575/19.
XX P3 P-PSDB; AAU84831.
XX PT New synthetic polypeptides having several different segments of at
XX PT least one parent polypeptide linked together differently compared to
XX PT the linkage in the parent polypeptide, for inducing immune response
XX PT against a pathogen or cancer
XX PS Example 3; Fig 27; 364pp; English.
XX CC The invention relates to a new synthetic polypeptide (I) comprising
XX CC several different segments of at least one parent polypeptide linked
XX CC together in a different relationship relative to their linkage in the
XX CC parent polypeptide to impede, abrogate or otherwise alter at least one
XX CC function associated with the parent polypeptide and for inducing an
XX CC immune response against a pathogen or cancer. Also included are a
XX CC synthetic polynucleotide encoding and a computer system for
XX CC designing the synthetic polypeptides. The synthetic polypeptides and
XX CC polynucleotides are referred to as a Savine. The synthetic polypeptide is
XX CC useful for modulating immune responses preferably directed against a
XX CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,
XX CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone
XX CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.
XX CC Compositions comprising the polypeptide may be used in the treatment or
XX CC prophylaxis against viral (such as infections caused by HIV (human
XX CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX CC Trypanosoma, Toxoplasma and Giardia) infections. The present
XX CC sequence encodes a peptide derived from a parent protein used to
XX CC construct a savine of the invention.
XX SQ Sequence 90 BP; 17 A; 26 C; 29 G; 18 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 0.872 Length: 90
XX Score: 53.00 Matches: 8
XX Percent Similarity: 88.89% Conservative: 0
XX Best Local Similarity: 88.89% Mismatches: 1
XX Query Match: 91.38% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-214-836-1 (1-9) x ABK36651 (1-90)
XX
XX Oy 1 LysThrTrpGlyGlnTyrTrpAlaVal 9
XX Db 16 AAAACCTGGGCGCAATCTGCGAGTTC 42
XX
XX RESULT 5
XX AAD07346

```

```

ID AAD07346 standard; DNA; 1986 BP.
XX
XX AAD07346;
AC
XX 18-SEP-2001 (first entry)
XX
XX Modified tumour-associated antigen, GP100 DNA.
DE
XX
XX Tumour-associated antigen; TAA; GP100 antigen; cytostatic; gene therapy;
KM immune response; tetanus toxoid; TT; diptheria toxoid; DT; prophylactic;
KM vaccine; cancer; therapeutic; ds.
XX
XX Synthetic.
OS
XX
XX Key location/Qualifiers
FH 1.1986
FT CDS /*tag= a
FT /product= "Modified tumour-associated antigen, GP100"
XX
XX WO200149317-A2.
XX
XX 12-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-CA00005.
XX
XX 05-JAN-2000; 2000US-0174587.
XX
XX (AVET ) AVENTIS PASTEUR LTD.
XX
XX Emtege P, Barber BH, Samhara S, Sia CDY;
XX
XX WPI: 2001-441790/47.
XX
XX P-PSDB; AAB05116.
XX
XX Enhancing immune response to antigen such as tumor antigen for treating
PT cancer in an animal involves administering an inducing agent to the
PT animal followed by administering inducing agent-antigen mixture -
XX
XX Example 1; Fig 1; 62pp; English.
XX
XX The invention relates to a method of enhancing an immune response against
CC tumour-associated antigens (TAAs), such as GP100 and carcinoembryonic
CC antigen (CEA) in an animal. The method involves priming of the animal
CC with an inducing agent such as tetanus toxoid (TT) or diptheria toxoid
CC (DT), subsequently followed by administration of an inducing agent-
CC antigen mixture. The method provides the enhancement or augmentation of
CC the immune response to the antigen and/or improves a vaccination protocol
CC by allowing use of less antigen. The immunisation of the animal with
CC tumour-associated antigen is useful for the prophylactic or therapeutic
CC treatment of cancer. The present DNA sequence encodes modified tumour-
CC associated antigen, GP100 related to the invention.
XX
XX Sequence 1986 BP; 431 A; 552 C; 552 G; 451 T; 0 other;
SQ

```

Alignment Scores:

Pred. No.:	27	Length:	1986
Score:	53.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	91.38%	Indels:	0
DB:	22	Gaps:	0

US-09-214-836-1 (1-9) x AAD07346 (1-1986)

```

QY 1 LysThrTPGlyGlnTyrTrpAlaVal 9
AC |||||
XX |||||
DB 460 AAGACCTGGGCGCAATCTGGCAAGTT 486

```

RESULT 6

AAH22098 standard; cDNA; 1986 BP.

AAH22098;

```

XX
XX 17-AUG-2001 (first entry)
DT
XX
XX Human gp100M nucleotide sequence.
DE
XX
XX Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
KM modified gp100; vaccine; gene therapy; cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200130847-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-CA01254.
XX
XX 22-OCT-1999; 99US-0160879.
PR 07-AUG-2000; 2000US-0223325.
XX
XX (AVET ) AVENTIS PASTEUR LTD.
XX
XX PA
XX
XX PI Berinstein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
XX
XX WPI: 2001-316326/33.
XX
XX P-PSDB; AAB98206.
XX
XX New isolated and purified gp100 useful for the prophylactic treatment
PT of cancer -
XX
XX Claim 2; Fig 1; 89pp; English.
XX
XX The present invention describes an isolated and purified modified gp100
CC molecule (gp100M) capable of modulating an immune response in an animal.
CC gp100M has cytostatic activity and can be used in vaccine production and
CC gene therapy. Nucleic acids and proteins of the invention are useful as
CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
CC AAB98098 to AAB98206 represent sequence used in the exemplification of
CC the present invention. More specifically AAB98098 to AAB98205 represent
CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
CC AAH22106 represent primers used in the present invention; AAH22099
CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
CC gp100M protein given in AAB22106.
XX
XX Sequence 1986 BP; 431 A; 552 C; 552 G; 451 T; 0 other;
SQ

```

Alignment Scores:

Pred. No.:	27	Length:	1986
Score:	53.00	Matches:	8
Percent Similarity:	88.89%	Conservative:	0
Best Local Similarity:	88.89%	Mismatches:	1
Query Match:	91.38%	Indels:	0
DB:	22	Gaps:	0

US-09-214-836-1 (1-9) x AAH22098 (1-1986)

```

QY 1 LysThrTPGlyGlnTyrTrpAlaVal 9
AC |||||
XX |||||
DB 460 AAGACCTGGGCGCAATCTGGCAAGTT 486

```

RESULT 7

AAH20120 standard; cDNA; 1986 BP.

AAH20120;

08-AUG-2001 (first entry)

Modified gp100M encoding cDNA sequence SEQ ID NO:109.

Virus; adenovirus; poxvirus; alphavirus; immune response; gp100; tumour antigen; CEA; carcinoembryonic antigen; immunostimulant; cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer; ss.



```

XX OS Virus.
XX OS Synthetic.
XX PN WO200130382-A1.
XX XX 03-MAY-2001.
XX XX 20-OCT-2000; 2000WO-CA01253.
XX PF 22-OCT-1999; 99US-0160879.
XX PR 07-AUG-2000; 2000US-0223325.
XX XX (AVET ) AVENTIS PASTEUR LTD.
XX PA Berinstein N, Tartaglia J, Moingeon P, Barber B;
XX PI WPI; 2001-308587/32.
XX DR P-PSDB; AAB97816.
XX XX
XX PT Inducing immune response to tumor antigen, useful in immunotherapy of
XX PT cancer, by administering the antigen to a lymphatic site
XX PS Disclosure; Fig 6; 60pp; English.
XX XX
XX CC The present invention describes a method for inducing an immune response,
XX CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or
XX CC nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys
XX CC (Macaca fascicularis) were injected with a modified form of gp100 antigen
XX CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals
XX CC of (a) developed a cell-mediated response (indicated by production of
XX CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but
XX CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far
XX CC greater antibody response to gp100. The method is used in immunotherapy
XX CC of a wide range of cancers through induction of a specific immune
XX CC response (humoral and cellular) against the tumour antigens. When
XX CC administered to a lymphatic site, Ag (or (I)) induces a stronger immune
XX CC response than administration by other routes and may also break tolerance
XX CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to
XX CC AAB97815 represent peptides derived from gp100 which stimulate interferon
XX CC (IFN)-gamma production; AAB20120 encodes the modified gp100 protein given
XX CC in AAB97816; AAB20121 encodes the modified carcinoembryonic antigen (CEA)
XX CC protein given in AAB97817; and AAB97818 represents a CEA modified antigen
XX CC peptide, all of which are used in the exemplification of the present
XX CC invention.
XX SQ Sequence 1986 BP; 431 A; 552 C; 552 G; 451 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 27 Length: 1986
XX Score: 53.00 Matches: 8
XX Percent Similarity: 88.89% Conservative: 0
XX Best Local Similarity: 88.89% Mismatches: 1
XX Query Match: 91.38% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-214-836-1 (1-9) x AAB20120 (1-1986)
XX QY 1 LysThrTrpGlyGlnTyrTTPAlaVal 9
XX DB 460 AAGACTGGGGCCCAATCTGCAAGTT 486
XX
XX RESULT 8
XX AAQ96055
XX ID AAQ96055 standard; CDNA to mRNA; 2115 BP.
XX AC AAQ96055;
XX XX 22-JAN-1996 (first entry)
XX DT
XX DE Sequence encoding melanoma associated antigen gp100.
XX XX Melanoma; antigen; vaccine; immunogen; primer; probe; detection;
XX KW

```

```

KW identification; tumour; gp100; ds.
XX OS Homo sapiens.
XX XX Location/Qualifiers
XX FH Key 22..2007
XX FT CDS
XX FT
XX FT
XX FT misc_signal
XX FT /tag= a
XX FT /product= Melanoma associated antigen gp100.
XX FT 1..81
XX FT /tag= b
XX FT 1792..1870
XX FT /tag= c
XX FT /label= Transmembrane domain.
XX FT 262..264
XX FT /tag= d
XX FT /bound moeity= Carbohydrate.
XX FT 337..359
XX FT /tag= e
XX FT 352..354
XX FT /tag= f
XX FT misc_binding
XX FT 982..984
XX FT /tag= g
XX FT 1723..1725
XX FT /tag= h
XX XX
XX XX EP668350-A1.
XX XX 23-AUG-1995.
XX XX
XX XX 14-FEB-1995; 95EP-0200348.
XX PF
XX PR 21-DEC-1994; 94EP-0203709.
XX PR 16-FEB-1994; 94EP-0200337.
XX XX
XX PA (ALKU ) AKZO NOBEL NV.
XX XX
XX PI Adema GJ, Figdor CG;
XX XX WPI; 1995-284790/38.
XX DR P-PSDB; AAB78646.
XX XX
XX PT Melanoma associated antigen gp100 - used in vaccines and for the
XX PT detection of tumours
XX XX
XX PS Claim 2; Page 19-22; 40pp; English.
XX XX
XX CC Immunogenic peptides derived from the melanoma associated antigen
XX CC may be used in the production of vaccines. Nucleotide sequences
XX CC encoding the immunogenic peptides may be used as primers and probes
XX CC in the detection of melanoma cells. Tumour infiltrating lymphocytes
XX CC capable of binding to the melanoma associated antigen can be
XX CC cultured ex vivo and returned to melanoma particles, and when
XX CC radioabelled, they may be used to identify tumour deposits.
XX XX
XX SQ Sequence 2115 BP; 469 A; 587 C; 575 G; 484 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 29 Length: 2115
XX Score: 53.00 Matches: 8
XX Percent Similarity: 88.89% Conservative: 0
XX Best Local Similarity: 88.89% Mismatches: 1
XX Query Match: 91.38% Indels: 0
XX DB: 16 Gaps: 0
XX
XX US-09-214-836-1 (1-9) x AAQ96055 (1-2115)
XX QY 1 LysThrTrpGlyGlnTyrTTPAlaVal 9
XX DB 481 AAGACTGGGGCCCAATCTGCAAGTT 507
XX
XX RESULT 9
XX ABQ76195
XX ID ABQ76195 standard; DNA; 2130 BP.

```

XX AC ABQ76195;  
XX XX 21-OCT-2002 (first entry)  
XX DE Human tumour antigen gp100 DNA.  
XX KW Tumour antigen; human; vaccine; cellular immune response; immunogen;  
XX KW cancer; tumour; gp100; ds.  
XX OS Homo sapiens.  
XX EN US6287569-B1.  
XX PD 11-SEP-2001.  
XX PF 06-APR-1998; 98US-0056105.  
XX PR 10-APR-1997; 97US-043467P.  
XX XX (REGC ) UNIV CALIFORNIA.  
XX PI Kipsps TJ, Wu Y;  
XX DR WPI; 1998-583198/49.  
XX PT Generating cellular immune response in patient to target protein -  
XX PT comprises introducing vector with nucleotide sequence encoding  
XX PT immunogen comprising protein processing signal into cell of patient  
XX PS Disclosure; Column 17-18; 61pp; English.  
XX XX  
XX CC This invention describes a novel method for generating a cellular immune  
XX CC response in a patient to a target protein or its fragment. The method  
XX CC involves introducing a vector containing a nucleotide sequence encoding  
XX CC a chimeric immunogen comprising a protein processing signal and the  
XX CC target protein or its fragment. The immunogen is produced by the cells  
XX CC and processed so that the target protein or its fragment is presented to  
XX CC the patient's immune system and a cellular immune response is initiated.  
XX CC The method and vectors can be used as a form of vaccination and could be  
XX CC used to generate a cellular immune response in patients to, e.g.,  
XX CC cancerous tumors. The cellular immune response is the predominant immune  
XX CC response in the patient. This sequence represents a DNA fragment which  
XX CC encodes the human tumour antigen gp100 described in the method of the  
XX CC invention.  
XX CC Note: The information in this spec has been previously disclosed in  
XX CC WO199845444 however this spec contained no sequence information.  
XX CC  
XX SQ Sequence 2130 BP; 484 A; 587 C; 575 G; 484 T; 0 other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 29.2 Length: 2130  
XX Score: 53.00 Matches: 8  
XX Percent Similarity: 88.89% Conservative: 0  
XX Best Local Similarity: 88.89% Mismatches: 1  
XX Query Match: 91.38% Indels: 0  
XX DB: 19 Gaps: 0  
XX  
XX US-09-214-836-1 (1-9) x ABQ76195 (1-2130)  
XX QY 1 LysTnTrpGlyGlnTyrTrpAlaVal 9  
XX DB 481 AAGACCTGGGGCCCAATCTGCGCAAGTT 507  
XX  
XX RESULT 10  
XX ID AAH43500 standard; cDNA; 2130 BP.  
XX AC AAH43500;  
XX XX  
XX DT 13-DEC-2001 (first entry)  
XX XX  
XX DE Human melanoma antigen gp100 coding sequence.

XX XX Major histocompatibility complex; MHC; human; melanoma antigen; gp100;  
XX KW HLA-A2 binding domain; mutation; antigen presenting cell; vaccine;  
XX KW immune effector cell; cancer; antibody; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 22..2007  
XX FT /\*tag= a  
XX FT /product= "gp100"  
XX FT  
XX WO200170767-A2.  
XX EN  
XX PD 27-SEP-2001.  
XX PF 19-MAR-2001; 2001WO-US08919.  
XX PR 20-MAR-2000; 2000US-190750P.  
XX PR 12-DEC-2000; 2000US-255019P.  
XX XX (GENZ ) GENZYME CORP.  
XX PA  
XX PI Nicolette CA;  
XX DR WPI; 2001-611469/70.  
XX DR P-PSDB; AAB47500.  
XX PT Novel synthetic compounds useful for stimulating an immune response in  
XX PT a subject and as components of anti-cancer vaccines, are designed to  
XX PT enhance binding to major histocompatibility complex molecules -  
XX PS Disclosure; Page 60-63; 67pp; English.  
XX XX  
XX CC This sequence encodes human melanoma antigen gp100. Peptides of the  
XX CC invention based on the sequence of residues 209-217 of human melanoma  
XX CC antigen gp100, which represents the putative HLA-A2 binding domain,  
XX CC are designed to enhance binding to major histocompatibility complex  
XX CC (MHC) molecules and to enhance immunoregulatory properties relative to  
XX CC their natural counterparts. The mutations in the claimed peptides  
XX CC confer tighter binding to the MHC. These peptides are useful for  
XX CC inducing an immune response in a subject, where they are delivered in  
XX CC the context of an MHC molecule which presents the compound on the  
XX CC surface of an antigen presenting cell. The peptide sequences are useful  
XX CC as components of anti-cancer vaccines and to expand immune effector cells  
XX CC that are specific for cancers characterized by expression of the  
XX CC melanoma antigen gp100. They are useful for diagnosis and treatment of  
XX CC diseases such as cancer, in particular against human melanoma and for  
XX CC generating antibodies that specifically recognize and bind the compounds.  
XX CC  
XX SQ Sequence 2130 BP; 484 A; 587 C; 575 G; 484 T; 0 other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 29.2 Length: 2130  
XX Score: 53.00 Matches: 8  
XX Percent Similarity: 88.89% Conservative: 0  
XX Best Local Similarity: 88.89% Mismatches: 1  
XX Query Match: 91.38% Indels: 0  
XX DB: 22 Gaps: 0  
XX  
XX US-09-214-836-1 (1-9) x AAH43500 (1-2130)  
XX QY 1 LysTnTrpGlyGlnTyrTrpAlaVal 9  
XX DB 481 AAGACCTGGGGCCCAATCTGCGCAAGTT 507  
XX  
XX RESULT 11  
XX ID AAS14396 standard; cDNA; 2130 BP.  
XX AC AAS14396;  
XX XX  
XX DT 26-MAR-2002 (first entry)  
XX XX

ID	AA03760	standard; DNA; 2131 BP.
XX		
AC	AA03760;	
XX		
DT	25-MAR-1996	(first entry)
XX		
DE	Melanoma-specific immunogen, pMEL17.	
XX		
KW	Melanoma; immunogen; epitope; homologue; vaccine; immunotherapy;	
RW	cytotoxic T cell; lymphocyte; HLA-A2; ss.	
XX		
OS	Homo sapiens.	
XX		
FN	W09522561-A2.	
PD	24-AUG-1995.	
XX		
PF	16-FEB-1995; 95WO-US01991.	
XX		
PR	29-APR-1994; 94US-0234784.	
PR	16-FEB-1994; 94US-0197399.	
XX		
PA	(UYVI-) UNIV VIRGINIA PATENT FOUND.	
XX		
PI	Cox AL, Engelhard VH, Hunt DF, Shabanowitz J, Slingluff CL;	
XX		
DR	WPI; 1995-302688/39.	
XX		
PT	Melanoma-specific immunogen comprises epitope(s) homologous with	
PT	pMEL-17 - are highly potent stimulators of HLA-A2+CTL's useful in	
PT	adoptive immuno-therapy	
XX		
PS	Disclosure; Page 19-20; 148pp; English.	
XX		
CC	A melanoma-specific immunogen homologous with pMEL-17 (AA03760)	
CC	comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the	
CC	group AA882098-R82194 capable of eliciting a CTL response. The epitopes	
CC	AA882098- AA882108 are of particular interest. The immunogen can be used	
CC	for partial protection in mammals against melanoma peptides which are	
CC	homologous with pMEL-17 are highly potent stimulators of HLA-A2+	
CC	CTLs in several cell lines and can be used in immunotherapy or	
CC	incorporated into immunogenic conjugates as vaccines.	
XX		
SQ	Sequence 2131 BP; 474 A; 589 C; 577 G; 491 T; 0 other;	
XX		
Alignment Scores:		
Pred. No.:	29.2	Length: 2131
Score:	53.00	Matches: 8
Percent Similarity:	88.89%	Conservative: 0
Best Local Similarity:	88.89%	Mismatches: 1
Query Match:	91.38%	Indels: 0
DB:	16	Gaps: 0
XX		
US-09-214-836-1 (1-9) x AA03760 (1-2131)		
Oy	1	lyeThrTrpGIyGlnTrpTrpAlaVal 9
Db	471	AAAGACCTGGGGCCAAATACCTGGCAAGTT 497
XX		
RESULT 13		
ID	AA096726	standard; cDNA; 2131 BP.
XX		
AC	AA096726;	
XX		
DT	08-APR-1998	(first entry)
XX		
DE	pMEL17 cDNA.	
XX		
KW	Melanoma; immunogen; cytotoxic T lymphocyte; CTL;	
RW	human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3;	
XX	HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection; ss.	
XX		

```

OS Homo sapiens.
XX
XX WO9734613-A1.
XX
XX 25-SEP-1997.
XX
XX PF 17-MAR-1997; 97WO-US04958.
XX
XX PR 04-OCT-1996; 96US-0027627.
XX
XX PR 19-MAR-1996; 96US-0013972.
XX
XX (UUVI-) UNIV VIRGINIA PATENT FOUND.
XX
XX PA Cox AL, Engelhard VH, Hendrikson RC, Hunt DF, Kittlesen D;
XX PI Shabanowitz J, Skipper J, Slingluff CL;
XX DR WPI, 1997-479982/44.
XX
XX PT Melanoma-specific immunogens of pMel-17 and tyrosinase - useful in
XX vaccination for producing melanoma-specific cytotoxic T lymphocytes
XX
XX PS Disclosure; Pages 30-31; 106pp; English.
XX
XX CC A novel melanoma specific immunogen comprises at least 1 melanoma
XX specific cytotoxic T lymphocyte (CTL) epitope, where at least
XX 1 of the epitopes is substantially homologous to a human leukocyte
XX antigen-A1 (HLA-A1) and HLA-A3 restricted epitope of a melanoma
XX antigen, either pMel-17, i.e. the protein encoded by present
XX sequence, or tyrosinase. The immunogen can be used in vaccines for
XX protection against melanoma in mammals.
XX
XX SQ Sequence 2131 BP; 475 A; 588 C; 578 G; 490 T; 0 other;

Alignment Scores:
Pred. No.: 29.2 Length: 2131
Score: 53.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 91.38% Indels: 0
DB: 18 Gaps: 0

US-09-214-836-1 (1-9) x AAT96726 (1-2131)
OY 1 LysThrTPGlyGlnTyrTrpAlaVal 9
DB 471 AAGACTGGGGCCCACTACTGCGCAAGT 497

RESULT 14
AAL49164
ID AAL49164 standard; cDNA; 2131 BP.
XX
XX AC AAL49164;
XX
XX DT 29-OCT-2002 (first entry)
XX
XX DE Human gp100 coding sequence.
XX
XX KM Human; gp100; cancer; vaccine; melanoma; tumour-associated antigen;
XX cytosolic; gene; ss.
XX
XX OS Homo sapiens.
XX
XX FT Key location/Qualifiers
XX CDS 12..2018
XX FT /*tag= a
XX FT /product= "gp100"
XX
XX PN EP1222928-A2.
XX
XX PD 17-JUL-2002.
XX
XX PF 09-JAN-2002; 2002EP-0000185.
XX
XX

```

```

PR 16-JAN-2001; 2001EP-0100914.
XX
XX (UWZU-) UNIV ZUERICH INST MEDIZINISCHE VIROLOGIE.
XX
XX XX Moelling K, Nawrath M, Pavlovic J;
XX
XX DR WPI, 2002-610269/66.
XX
XX DR P-Psdb; AAO18863.
XX
XX PT Pharmaceutical composition useful for treating cancer, comprises
XX nucleic acid molecule encoding tumor associated antigen and peptide
XX PT comprising a region corresponding to epitope of tumor associated
XX antigen
XX
XX PS Disclosure; Page 21-24; 34pp; English.
XX
XX CC The present invention relates to a pharmaceutical composition which
XX comprises a nucleic acid molecule encoding a tumour-associated antigen
XX and at least one peptide comprising a region corresponding to a putative
XX cytotoxic T cell, helper T cell or B cell epitope of a tumour-associated
XX antigen and/or cells pulsed with such peptide(s) in particular, the
XX CC tumour-associated antigen may be gp100. The composition is useful for the
XX CC treatment of cancer, especially melanoma. The present sequence is the
XX CC human gp100 coding sequence.
XX
XX SQ Sequence 2131 BP; 475 A; 588 C; 578 G; 490 T; 0 other;

Alignment Scores:
Pred. No.: 29.2 Length: 2131
Score: 53.00 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 1
Query Match: 91.38% Indels: 0
DB: 24 Gaps: 0

US-09-214-836-1 (1-9) x AAL49164 (1-2131)
OY 1 LysThrTPGlyGlnTyrTrpAlaVal 9
DB 471 AAGACTGGGGCCCACTACTGCGCAAGT 497

RESULT 15
AAH22099
ID AAH22099 standard; DNA; 2534 BP.
XX
XX AC AAH22099;
XX
XX DT 17-AUG-2001 (first entry)
XX
XX DE Plasmid CSH6gp100M H6 promoted human gp100M nucleotide sequence.
XX
XX KM Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
XX modified gp100; vaccine; gene therapy; cancer; circular; cyclic; ds.
XX
XX OS Homo sapiens.
XX
XX OS Vaccinia virus.
XX
XX PN WO200130847-A1.
XX
XX PD 03-MAY-2001.
XX
XX PF 20-OCT-2000; 2000WO-CA01254.
XX
XX PR 22-OCT-1999; 99US-0160879.
XX
XX PR 07-AUG-2000; 2000US-0223325.
XX
XX PA (AVET ) AVENTIS PASTEUR LTD.
XX
XX PI Berinstein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
XX
XX DR WPI, 2001-316326/33.
XX
XX PT New isolated and purified gp100 useful for the prophylactic treatment

```

PT of cancer -  
XX  
XX Example 2; Fig 3; 89pp; English.  
XX  
XX The present invention describes an isolated and purified modified gp100  
XX molecule (gp100M) capable of modulating an immune response in an animal.  
XX gp100M has cytoskeletal activity and can be used in vaccine production and  
XX gene therapy. Nucleic acids and proteins of the invention are useful as  
XX vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and  
XX AAH8098 to AAH98206 represent sequence used in the exemplification of  
XX the present invention. More specifically AAH98098 to AAH98205 represent  
XX peptides derived from gp100, AAH22084 to AAH22097 and AAH22100 to  
XX AAH22106 represent primers used in the present invention; AAH22099  
XX represents the plasmid nucleotide sequence comprising the Vaccinia virus  
XX H6 promoter and the human gp100 gene; and AAH22098 encodes the human  
XX gp100M protein given in AAH22106.  
SQ Sequence 2534 BP; 622 A; 632 C; 657 G; 623 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 35.4 Length: 2534  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 22 Gaps: 0  
  
US-09-214-836-1 (1-9) x AAH22099 (1-2534)  
QY 1 LysThrTPGlyGlnTYTTPAlaVal 9  
Db 836 AAGACCTGGGGCCAACTACTGCGCAGTT 862  
  
RESULT 16  
ABK36828  
ID ABK36828 standard; DNA; 16638 BP.  
AC ABK36828;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Human DNA for melanocyte differentiation antigens savine.  
XX  
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
XX viral infection; human immunodeficiency virus; melanoma;  
XX bacterial infection; Salmonella; Legionella; parasitic infection;  
XX Trypanosoma; Toxoplasma; Giardia; ds.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200190197-A1.  
XX  
XX 29-NOV-2001.  
XX  
XX 25-MAY-2001; 2001WO-AU00622.  
XX  
XX 26-MAY-2000; 2000AU-0007761.  
XX  
XX (AUSU ) UNIV AUSTRALIAN NAT.  
XX  
XX Thomson SA, Ramshaw IA;  
XX  
XX MPI; 2002-147575/19.  
XX  
XX P-PSDB; AAU85008.  
XX  
XX  
XX New synthetic polypeptides having several different segments of at  
XX least one parent polypeptide linked together differently compared to  
XX the linkage in the parent polypeptide, for inducing immune response  
XX against a pathogen or cancer -  
XX  
XX Example 3; Fig 27; 364pp; English.  
XX

CC The invention relates to a new synthetic polypeptide (I) comprising  
CC several different segments of at least one parent polypeptide linked  
CC together in a different relationship relative to their linkage in the  
CC parent polypeptide to impede, abrogate or otherwise alter at least one  
CC function associated with the parent polypeptide and for inducing an  
CC immune response against a pathogen or cancer. Also included are a  
CC synthetic polynucleotide encoding and a computer system for  
CC designing the synthetic polypeptides. The synthetic polypeptides and  
CC polynucleotides are referred to as a Savine. The synthetic polypeptide is  
CC useful for modulating immune responses preferably directed against a  
CC pathogen or a cancer. (e.g., cancers of the lung, breast, ovary, cervix,  
CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone  
CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.  
CC Compositions comprising the polypeptide may be used in the treatment or  
CC prophylaxis against viral (such as infections caused by HIV (human  
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic  
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
CC Trypanosoma, Toxoplasma and Giardia) infections. The present  
CC sequence encodes a savine protein of the invention.  
SQ Sequence 16638 BP; 3840 A; 5297 C; 3944 G; 3557 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 286 Length: 16638  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 24 Gaps: 0  
  
US-09-214-836-1 (1-9) x ABK36828 (1-16638)  
QY 1 LysThrTPGlyGlnTYTTPAlaVal 9  
Db 7252 AAAACCTGGGGCCAACTACTGCGCAGTCTC 7278  
  
RESULT 17  
AAT02716  
ID AAT02716 standard; cDNA; 2172 BP.  
AC AAT02716;  
XX  
XX 20-APR-1996 (first entry)  
XX  
XX MART-1 melanoma antigen cDNA25.  
XX  
XX cDNA25; MART-1; melanoma antigen recognised by T-cells;  
XX gp100 antigen derivative; melanoma; metastatic melanoma;  
XX tumour-associated antigen; immunogen; diagnosis; prognosis;  
XX prophylaxis; therapy; vaccine; ds.  
XX  
XX Mammalian.  
OS  
XX  
XX Key Location/Qualifiers  
FH 38..2038  
FT /\*tag= a  
FT /note= "cDNA25 melanoma antigen"  
XX  
XX WO9529193-A2.  
XX  
XX 02-NOV-1995.  
XX  
XX 21-APR-1995; 95WO-US05063.  
XX  
XX 05-APR-1995; 95US-0417174.  
XX  
XX 22-APR-1994; 94US-0231565.  
XX  
XX (USSH ) US SEC DEPT HEALTH.  
XX  
XX Kawakami Y, Rosenberg SA;  
XX

XX WPI; 1995-382963/49.  
 DR P-PSDB; AAR84854.  
 XX  
 PT DNA encoding melanoma antigens recognised by T-lymphocytes - also  
 PT vectors, host cells and antibodies, used to detect, treat and  
 PT immunise animal against melanoma.  
 XX  
 PS Disclosure; Fig 4A-4B; 184pp; English.  
 XX  
 CC The nucleic acid encodes cDNA25, a melanoma antigen (MART-1)  
 CC which is recognized by T-lymphocytes. cDNA25 is a derivative of  
 CC the melanocyte-melanoma-specific antigen gp100 (see AAR84855).  
 CC Antigen cDNA25 is a source of immunogenic peptides (see AAR84199)  
 CC which are optionally modified (see AAR84200-R84211) and used in  
 CC medicaments, especially vaccines, for the treatment or prevention  
 CC (by immunisation) of melanoma. Antibodies against cDNA25 and its  
 CC immunogenic peptides may be used in the detection and isolation  
 CC of the antigen from a sample, the detection of which is indicative  
 CC of a disease state (melanoma or metastatic melanoma).  
 XX  
 SQ Sequence 2172 BP; 512 A; 594 C; 578 G; 488 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 92.4 Length: 2172  
 Score: 50.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 86.21% Indels: 0  
 DB: 16 Gaps: 0  
 US-09-214-836-1 (1-9) x AAT02716 (1-2172)  
 QY 1 LysThrTpglYglnTYTtp 7  
 DB 498 AAGACCTGGGGCCAACTACTGG 518  
 RESULT 18  
 AAS45525  
 ID AAS45525 strand; cDNA; 2172 BP.  
 AC AAS45525;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE DNA encoding Melanoma antigen cDNA25.  
 XX  
 KW Human; MART-1; immunogenic; melanoma antigen recognised by T lymphocyte;  
 KW diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition;  
 KW in vivo tumour rejection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6270778-B1.  
 PD 07-AUG-2001.  
 XX  
 PF 12-MAR-1999; 99US-0267439.  
 XX  
 PR 05-MAY-1998; 98US-0073138.  
 PR 22-APR-1994; 94US-0231565.  
 PR 05-APR-1995; 95US-0417174.  
 XX  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Kawakami Y, Rosenberg SA;  
 DR WPI; 2001-595403/67.  
 DR P-PSDB; AAU28912.  
 XX  
 PT Immunogenic peptide useful in vaccines comprises specific amino acids  
 PT of new melanoma antigen recognised by T lymphocytes  
 XX

PS Example 3; Figure 4; 73pp; English.  
 XX  
 CC The invention relates to a novel immunogenic peptide comprising 5-20  
 CC contiguous amino acids of new melanoma antigen recognised by T  
 CC lymphocytes (MART-1). The peptide sequence contains at least one amino  
 CC acid modification of MART-1. The peptide is used in diagnostic and  
 CC therapeutic methods as an immunogen or vaccine to prevent or treat  
 CC melanoma, and for in vivo tumour recognition and rejection. AAS45524-  
 CC AAS45528 represent MART-1 coding sequences, PCR primers, and related  
 CC sequences of the invention.  
 XX  
 SQ Sequence 2172 BP; 512 A; 594 C; 578 G; 488 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 92.4 Length: 2172  
 Score: 50.00 Matches: 7  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 86.21% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-214-836-1 (1-9) x AAS45525 (1-2172)  
 QY 1 LysThrTpglYglnTYTtp 7  
 DB 498 AAGACCTGGGGCCAACTACTGG 518  
 RESULT 19  
 AAL49163  
 ID AAL49163 standard; cDNA; 1881 BP.  
 AC AAL49163;  
 XX  
 DT 29-OCT-2002 (first entry)  
 XX  
 DE Murine gp100 coding sequence.  
 XX  
 KW Mouse; gp100; cancer; vaccine; melanoma; tumour-associated antigen;  
 KW cytosolic; gene; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1881  
 FT /\*tag= a  
 FT /product= "gp100"  
 XX  
 PN EP122928-A2.  
 XX  
 PD 17-JUL-2002.  
 XX  
 PF 09-JAN-2002; 2002EP-0000185.  
 XX  
 PR 16-JAN-2001; 2001EP-0100914.  
 XX  
 PA (UZYU-) UNIV ZUERICH INST MEDIZINISCHE VIROLOGIE.  
 XX  
 PI Moelling K, Nawrath M, Pavlovic J;  
 DR WPI; 2002-610269/66.  
 DR P-PSDB; AAO18862.  
 XX  
 PT Pharmaceutical composition useful for treating cancer, comprises  
 PT nucleic acid molecule encoding tumor associated antigen and peptide  
 PT comprising a region corresponding to epitope of tumor associated  
 PT antigen  
 XX  
 PS Disclosure; Page 16-19; 34pp; English.  
 XX  
 CC The present invention relates to a pharmaceutical composition which  
 CC comprises a nucleic acid molecule encoding a tumour-associated antigen  
 CC and at least one peptide comprising a region corresponding to a putative  
 CC cytotoxic T cell, helper T cell or B cell epitope of a tumour-associated



or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](ftp:wipo.int/pub/published_pct_sequences).

Sequence 227968 BP; 53185 A; 60440 C; 61985 G; 52358 T; 0 other;

Alignment Scores:  
Pred. No.: 3,43e+04 Length: 227968  
Score: 48.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 82.76% Indels: 0  
DB: 24 Gaps: 0

US-09-214-836-1 (1-9) x ABX83497 (1-227968)

OY 3 TTPGlyGIntYrPALaVal 9  
|||  
Db 221007 TGGGGCAGATTTGGCAGTA 220987

RESULT 22  
ABX45137  
ID ABX45137 standard; cDNA; 215 BP.

AC ABX45137;

DT 21-FEB-2003 (first entry)

DE Bovine EST associated with lactation/muscle/fat deposition #10302.

KM Bovine; ss; EST; expressed sequence tag; lactation; LMPD;

KW muscle deposition; fat deposition; genome mapping; gene identification;

KW gene analysis; cattle breeding.

OS Bos Taurus.

XX US2002137139-A1.

PD 26-SEP-2002.

PF 24-SEP-2001; 2001US-0960352.

PR 12-JAN-1999; 99US-115707P.

PA 11-JAN-2000; 2000US-0480902.

PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

PI Byatt JC, Mathialagan N, Tao N, Warren WC;

DR WPI; 2003-110599/10.

XX New nucleic acid associated with lactation, and muscle and fat

PT deposition, useful for genome mapping; gene identification and

PT analysis, cattle breeding, or for genetically improving cattle

XX Claim 2; SEQ ID No 10302; 245pp; English.

PS The invention relates to a purified nucleic acid molecule associated with  
XX lactation or muscle and fat deposition (designated LMPD), derived  
CC from cattle, and the LMPD nucleic acid can specifically hybridise to a  
CC second nucleic acid molecule comprising any of 15112 nucleotide  
CC sequences, appearing as ABX34836-ABX49947, or complements of them.  
CC Also included are: (1) a transformed cell having a nucleic acid  
CC comprising an LMPD nucleic acid linked to a promoter and a 3' non-  
CC translated sequence that functions in the cell to cause termination of  
CC transcription and addition of polyadenylated ribonucleotides to a 3' end  
CC of the mRNA molecule; and (2) determining a level or pattern of a  
CC molecule in a bovine cell or tissue comprising: (a) incubating a marker  
CC nucleic acid (comprising any of the 15112 nucleic acid sequences or its  
CC complement or fragment) with a complementary nucleic acid molecule  
CC obtained from the bovine cell or tissue, where hybridisation between the  
CC marker nucleic acid and the complementary nucleic acid permits the  
CC detection of the molecule; and (b) detecting the level or pattern of the  
CC complementary nucleic acid, where the detection of the complementary  
CC nucleic acid is predictive of the level or pattern of the molecule.  
CC The LMPD nucleic acid is used for determining a level or pattern  
CC of a molecule in a bovine cell or tissue. It is useful for genome  
CC mapping, gene identification and analysis, cattle breeding, preparation  
CC of constructs for use in cattle gene expression, or for genetically  
CC improving cattle. The present sequence is one of the 15112 bovine  
CC LMPD EST (expressed sequence tag) nucleic acids.  
CC Note: The present sequence was not shown in the specification but  
CC was obtained in electronic format from the USPTO web site:  
CC [seqdata.uspto.gov/sequence.html?docid=20020137139](http://seqdata.uspto.gov/sequence.html?docid=20020137139).

XX SQ Sequence 215 BP; 79 A; 37 C; 34 G; 65 T; 0 other;

Alignment Scores:  
Pred. No.: 21.9 Length: 215  
Score: 47.00 Matches: 7  
Percent Similarity: 77.78% Conservative: 0  
Best Local Similarity: 77.78% Mismatches: 2  
Query Match: 81.03% Indels: 0  
DB: 25 Gaps: 0

US-09-214-836-1 (1-9) x ABX45137 (1-215)

OY 1 LysThrTPGlyGIntYrPALaVal 9  
|||  
Db 166 AAGCATGGGACAAATCTGCTGTC 192

RESULT 23

AA185451  
ID AA185451 standard; cDNA; 493 BP.

AC AA185451;

DT 06-NOV-2001 (first entry)

DE Human polynucleotide SEQ ID NO 5511.

KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukemia;

KW nervous system disorders; arthritis; inflammation; ss.

OS Homo sapiens.

XX WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US04927.

PR 28-FEB-2000; 2000US-0515126.

PA 18-MAY-2000; 2000US-0577409.



PA (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Drmanac RT;  
 XX WPI: 2001-514838/56.  
 DR P-PSDB: AAO05520.  
 XX Isolated nucleic acids and polypeptides, useful for preventing  
 PT diagnosing and treating e.g. leukaemia, inflammation and immune  
 PT disorders -  
 XX Claim 1; SEQ ID NO 511; 1399pp + Sequence Listing; English.  
 XX The invention relates to human polynucleotides (AA179941-AA193841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 493 BP; 120 A; 99 C; 118 G; 147 T; 9 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 117 Length: 493  
 Score: 45.00 Matches: 5  
 Percent Similarity: 88.69% Conservative: 3  
 Best Local Similarity: 55.56% Mismatches: 1  
 Query Match: 77.59% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-214-836-1 (1-9) x AA185451 (1-493)  
 Qy 1 LysThrTrpGlyGlnTyrTrpAlaVal 9  
 Db 408 AGGCGATGGGCGCAATTGCGCCATT 434  
 RESULT 24  
 AAL20608  
 ID AAL20608 standard; CDNA, 771 BP.  
 XX AAL20608;  
 AC  
 XX 07-DEC-2001 (first entry)  
 DT  
 XX Human breast cancer expressed polynucleotide 13065.  
 DB  
 XX Human, breast cancer; cell marker; cytostatic; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200151628-A2.  
 PN  
 XX 19-JUL-2001.  
 PD  
 XX 10-JAN-2001; 2001WO-US00798.  
 PF  
 XX 14-JAN-2000; 2000US-0176077.  
 PR 14-MAR-2000; 2000US-0189167.  
 PR 24-MAR-2000; 2000US-0192099.  
 PR 29-MAR-2000; 2000US-0193480.  
 PR 15-MAY-2000; 2000US-0205230.  
 PR 09-JUN-2000; 2000US-0211315.  
 PR 25-JUL-2000; 2000US-0220534.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lillie J, Xu Y, Wang Y, Steinmann K;  
 PI WPI: 2001-451856/48.  
 DR  
 XX New peptide useful as a marker for the diagnosis of breast cancer -  
 PT  
 XX Claim 1; Page 2317-2318; 3695pp; English.  
 XX The invention relates to human breast cancer expressed polynucleotides  
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is  
 CC afflicted with breast cancer by examining the correlation between the  
 CC expression of certain markers and the cancerous state of breast cells.  
 CC The polynucleotides and encoded polypeptides are potential markers for  
 CC detecting, diagnosing, monitoring, characterizing treating and  
 CC potentially preventing breast cancer. The polynucleotides and encoded  
 CC polypeptides are also useful for isolating compounds with cytostatic  
 CC activity.  
 XX Sequence 771 BP; 195 A; 205 C; 203 G; 168 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 192 Length: 771  
 Score: 45.00 Matches: 6  
 Percent Similarity: 87.50% Conservative: 1  
 Best Local Similarity: 75.00% Mismatches: 1  
 Query Match: 77.59% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-214-836-1 (1-9) x AAL20608 (1-771)  
 Qy 1 LysThrTrpGlyGlnTyrTrpAla 8  
 Db 701 AAAACTGGGGCGCATCTGCTGC 724  
 RESULT 25  
 AAK73223/C  
 ID AAK73223 standard; DNA; 31051 BP.  
 XX AAK73223;  
 AC  
 XX 06-NOV-2001 (first entry)  
 DT  
 XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28035.  
 DB  
 XX Human, immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW  
 XX Human; immune; gene therapy; vaccine; metastasis; ds.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200157182-A2.  
 PN  
 XX 09-AUG-2001.  
 PD  
 XX 17-JAN-2001; 2001WO-US01354.  
 PF  
 XX 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
 PR 18-APR-2000; 2000US-0198123.  
 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
 PR 28-JUN-2000; 2000US-0214886.  
 PR 30-JUN-2000; 2000US-0215135.  
 PR 07-JUL-2000; 2000US-0216647.  
 PR 07-JUL-2000; 2000US-0216880.  
 PR 11-JUL-2000; 2000US-0217487.  
 PR 11-JUL-2000; 2000US-0217496.  
 PR 14-JUL-2000; 2000US-0218290.  
 PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518-  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279-  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226686.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228287-  
PR 01-SEP-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 06-SEP-2000; 2000US-0230437-  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037-  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239335.  
PR 13-OCT-2000; 2000US-0239337.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246539.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251858.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI, 2001-483426/52.  
  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and  
PT metastasis -  
XX  
PS Disclosure: SEQ ID NO 28035; 3071bp + Sequence Listing; English.  
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patients own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703

CC to AAK87694 represent human immune/haematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
 CC represent sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 31051 BP; 6999 A; 8773 C; 8261 G; 7018 T; 0 other;

Alignment Scores:  
 Pred. No.: 1.16e+04 Length: 31051  
 Score: 45.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 85.71% Mismatches: 0  
 Query Match: 77.59% Indels: 0  
 DB: 22 Gaps: 0

US-09-214-836-1 (1-9) x AAK73223 (1-31051)

QY 3 TrpGlyGlnTyrTrpAlaVal 9  
 DB 20037 TGGGGCGAGTAATTGGGCAGTA 20017

Search completed: August 24, 2003, 01:40:45  
 Job time : 227.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - nucleic search, using frame\_plus\_p2n model

Run on: August 24, 2003, 01:25:55 ; Search time 47 Seconds  
(without alignments)  
84.520 Million cell updates/sec

Title: US-09-214-836-1  
Perfect score: 58  
Sequence: 1 KTWGQYMAV 9

Scoring table: BIOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues  
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-Q=/cgm2\_1/USFPO/seqpool/US09214836/runat\_14082003\_085041\_7665/app\_query.fasta\_1.398  
-DB=issued\_patents\_NA -QFMT=fastap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25  
-MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09214836 @CGN 1.1.76 @runat\_14082003\_085041\_7665 -NCP=6 -ICPU=3  
-NO\_MMAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgm2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgm2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgm2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgm2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgm2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgm2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	91.4	36	4	US-08-388-852B-9
2	53	91.4	2130	3	US-08-388-852B-1
3	53	91.4	2130	3	US-09-056-105-1
4	50	86.2	2172	2	US-08-417-174-26
5	50	86.2	2172	2	US-08-231-565A-26
6	50	86.2	2172	2	US-09-007-961-26
7	50	86.2	2172	2	US-09-267-439-26
8	50	86.2	2172	2	US-09-073-118-26
9	48	82.8	224	4	US-08-388-852B-7
10	47	81.0	951	4	US-09-252-991A-4794
11	44	75.9	65042	4	US-09-784-316-3
12	43	74.1	1847	4	US-08-858-207A-64

C 13	43	74.1	11887	4	US-08-961-527-146	Sequence 146, App
C 14	42	72.4	4088	2	US-08-317-310A-1	Sequence 1, Appli
C 15	42	72.4	4088	5	PCT-US95-13041-1	Sequence 1, Appli
C 16	41	70.7	629	1	US-08-592-135-135	Sequence 135, App
C 17	41	70.7	629	4	US-09-168-595-135	Sequence 135, App
C 18	41	70.7	1898	1	US-07-814-964-8	Sequence 8, Appli
C 19	41	70.7	1898	1	US-08-258-442-8	Sequence 8, Appli
C 20	41	70.7	1898	1	US-08-328-809-3	Sequence 3, Appli
C 21	41	70.7	1898	4	US-08-866-840-3	Sequence 3, Appli
C 22	41	70.7	1898	5	PCT-US92-11107-8	Sequence 8, Appli
C 23	41	70.7	2839	1	US-07-814-964-6	Sequence 6, Appli
C 24	41	70.7	2839	1	US-08-258-442-6	Sequence 6, Appli
C 25	41	70.7	2839	1	US-08-328-809-1	Sequence 1, Appli
C 26	41	70.7	2839	3	US-09-015-003-1	Sequence 1, Appli
C 27	41	70.7	2839	4	US-08-866-840-1	Sequence 1, Appli
C 28	41	70.7	2839	5	PCT-US92-11107-6	Sequence 6, Appli
C 29	41	70.7	3090	5	PCT-US93-06251-7	Sequence 7, Appli
C 30	41	70.7	152331	3	US-09-128-155-16	Sequence 16, Appli
C 31	41	70.7	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 32	40	69.0	216	1	US-08-482-282B-7	Sequence 7, Appli
C 33	40	69.0	216	1	US-08-486-036A-7	Sequence 7, Appli
C 34	40	69.0	216	4	US-09-005-298-7	Sequence 7, Appli
C 35	40	69.0	216	4	US-09-005-298-29	Sequence 29, Appli
C 36	40	69.0	216	4	US-08-768-619-7	Sequence 7, Appli
C 37	40	69.0	216	4	US-08-768-619-29	Sequence 29, Appli
C 38	40	69.0	216	5	PCT-US96-09848-7	Sequence 7, Appli
C 39	40	69.0	216	5	PCT-US96-09848-28	Sequence 28, Appli
C 40	40	69.0	291	1	US-08-482-282B-5	Sequence 5, Appli
C 41	40	69.0	291	4	US-08-486-036A-5	Sequence 5, Appli
C 42	40	69.0	291	4	US-09-005-298-5	Sequence 5, Appli
C 43	40	69.0	291	4	US-09-005-298-28	Sequence 28, Appli
C 44	40	69.0	291	4	US-08-768-619-5	Sequence 5, Appli
C 45	40	69.0	291	4	US-08-768-619-28	Sequence 28, Appli

## ALIGNMENTS

RESULT 1  
US-08-388-852B-9  
Sequence 9, Application US/08388852B  
Patent No. 650919  
GENERAL INFORMATION:  
APPLICANT: Adema, Gosee Jan, Figdor, Carl Gustav.  
TITLE OF INVENTION: Melanoma associated antigenic polypeptide.  
TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESS: Adema, Gosee Jan, Figdor, Carl Gustav  
STREET: Philips van Leydenlaan 25  
CITY: Nijmegen  
STATE: Brabant  
COUNTRY: the Netherlands  
ZIP: 6525 EX  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (ERO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,852B  
FILING DATE: February 15, 1995  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE: Melanoma  
TISSUE TYPE: Melanocyte  
CELL TYPE: Melanocyte

```

FEATURE:
NAME/KEY: CDS
LOCATION: 1...36
FEATURE:
NAME/KEY: protein bind
LOCATION: 1...33
FEATURE:
NAME/KEY: protein bind
LOCATION: 1...36
FEATURE:
NAME/KEY: protein bind
LOCATION: 7...33
FEATURE:
NAME/KEY: protein bind
LOCATION: 10...36
US-08-388-852B-9

Alignment Scores:
Pred. No.: 0.0928
Score: 53.00
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 91.38%
DB: 4
Gaps: 0

US-09-214-836-1 (1-9) x US-08-388-852B-9 (1-36)

QY 1 LysThrTrpGlyGlnTyrTrpAlaVal 9
Db 7 AAGACCTGGGGCCCAATCTGCGCAAGTT 33

RESULT 2
US-08-388-852B-1
; Sequence 1, Application US/08388852B
; Patent No. 6500919
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan, Figdor, Carl Gustav.
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide,
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide,
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Adema, Gosse Jan, Figdor, Carl Gustav
; STREET: Philips van Leydenlaan 25
; CITY: Nijmegen
; STATE: Brabant
; COUNTRY: the Netherlands
; ZIP: 6525 EX
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,852B
; FILING DATE: February 15, 1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2115 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Melanoma
; CELL TYPE: Melanocyte
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22...2005
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 1...81

```

```

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1792...1870
OTHER INFORMATION: //function = "transmembrane region"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 262...264
OTHER INFORMATION: //bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 337...339
OTHER INFORMATION: //bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 352...354
OTHER INFORMATION: //bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 982...984
OTHER INFORMATION: //bound moiety = "carbohydrate"
FEATURE:
NAME/KEY: misc_binding
LOCATION: 1723...1725
OTHER INFORMATION: //bound moiety = "carbohydrate"
US-08-388-852B-1

Alignment Scores:
Pred. No.: 7.66
Score: 53.00
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 91.38%
DB: 4
Gaps: 0

US-09-214-836-1 (1-9) x US-08-388-852B-1 (1-2115)

QY 1 LysThrTrpGlyGlnTyrTrpAlaVal 9
Db 481 AAGACCTGGGGCCCAATCTGCGCAAGTT 507

RESULT 3
US-09-056-105-1
; Sequence 1, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-1

Alignment Scores:
Pred. No.: 7.72
Score: 53.00
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 91.38%
DB: 3
Gaps: 0

US-09-214-836-1 (1-9) x US-09-056-105-1 (1-2130)

QY 1 LysThrTrpGlyGlnTyrTrpAlaVal 9

```

Db 481 AAGACCTGGGCGCAATCTGCAAGTT 507  
RESULT 4  
US-08-417-174-26  
Sequence 26, Application US/08417174  
Patent No. 5844075  
GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-08-417-174-26  
Alignment Scores:  
Pred. No.: 24 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x US-08-417-174-26 (1-2172)  
QY 1 LysThrTTPGlyGlnTyrTTP 7  
Db 498 AAGACCTGGGCGCAATCTGCG 518  
RESULT 5  
US-08-231-565A-26  
Sequence 26, Application US/08231565A  
Patent No. 5874560  
GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:

TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,565A  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-08-231-565A-26  
Alignment Scores:  
Pred. No.: 24 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x US-08-231-565A-26 (1-2172)  
QY 1 LysThrTTPGlyGlnTyrTTP 7  
Db 498 AAGACCTGGGCGCAATCTGCG 518  
RESULT 6  
US-09-007-961-26  
Sequence 26, Application US/09007961  
Patent No. 5994523  
GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/007,961  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-09-007-961-26

Alignment Scores:  
Pred. No.: 24 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0  
DB: 2 Gaps: 0

US-09-214-836-1 (1-9) x US-09-007-961-26 (1-2172)

QY 1 LysThrTpGlyGlnTyTTP 7  
Db 498 AAGACCTGGGGCCCAATACTGG 518

RESULT 7  
US-09-267-439-26  
Sequence 26, Application US/09267439  
Patent No. 6270778  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-09-267-439-26

Alignment Scores:  
Pred. No.: 24 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0  
DB: 3 Gaps: 0

US-09-214-836-1 (1-9) x US-09-267-439-26 (1-2172)

QY 1 LysThrTpGlyGlnTyTTP 7  
Db 498 AAGACCTGGGGCCCAATACTGG 518

RESULT 8  
US-09-073-138-26  
Sequence 26, Application US/09073138  
Patent No. 6537560  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,138  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2172  
TYPE: nucleotide  
STRANDEDNESS: Double  
TOPOLOGY: Unknown  
MOLECULE TYPE: CDNA  
US-09-073-138-26



```
Alignment Scores:
Pred. No.: 24
Score: 50.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 86.21%
DB: 4
Gaps: 0

US-09-214-836-1 (1-9) x US-09-073-138-26 (1-2172)

Cy 1 LysThrTPGlyGlnTYTTP 7
Db 498 AAGACTGGGCGCACTACTGG 518

RESULT 9
US-08-388-852B-7
; Sequence 7, Application US/0838852B
; Patent No. 6500919
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide,
; TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Adema, Gosse Jan; Figdor, Carl Gustav
; STREET: Philips van Leydenlaan 25
; CITY: Nijmegen
; STATE: Brabant
; COUNTRY: the Netherlands
; ZIP: 6525 EX
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,852B
; FILING DATE: February 15, 1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Melanoma
; CELL TYPE: Melanocyte
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1...24
; US-08-388-852B-7

Alignment Scores:
Pred. No.: 0.383
Score: 48.00
Percent Similarity: 87.50%
Best Local Similarity: 87.50%
Query Match: 82.76%
DB: 4
Gaps: 0

US-09-214-836-1 (1-9) x US-08-388-852B-7 (1-24)

Cy 2 ThrTPGlyGlnTYTTPAlaVal 9
Db 1 ACCTGGGCGCACTACTGGCAAGTT 24

RESULT 10
US-09-252-991A-4794
; Sequence 4794, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4794
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4794

Alignment Scores:
Pred. No.: 29.9
Score: 47.00
Percent Similarity: 100.00%
Best Local Similarity: 75.00%
Query Match: 81.03%
DB: 4
Gaps: 0

US-09-214-836-1 (1-9) x US-09-252-991A-4794 (1-951)

Cy 1 LysThrTPGlyGlnTYTTPAla 8
Db 62 AGGAGTTGGGCGCAGTACTGGGCA 85

RESULT 11
US-09-784-316-3
; Sequence 3, Application US/09784316
; Patent No. 6461843
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: CL001139
; CURRENT APPLICATION NUMBER: US/09/784,316
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 65042
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(65042)
; OTHER INFORMATION: n = A,T,C or G
; US-09-784-316-3

Alignment Scores:
Pred. No.: 8.87e+03
Score: 44.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 75.86%
DB: 4
Gaps: 0

US-09-214-836-1 (1-9) x US-09-784-316-3 (1-65042)

Cy 3 TrpGlyGlnTYTTPAla 8
Db 60796 TGGGGCAATATTGGCT 60813

RESULT 12
US-08-858-207A-64
; Sequence 64, Application US/08858207A
```

Patent No. 6348328  
GENERAL INFORMATION:  
APPLICANT: Black, Michael  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Nicholas, Richard  
APPLICANT: Stodola, Robert  
TITLE OF INVENTION: No. 6348328e1 Compounds  
NUMBER OF SEQUENCES: 552  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,207A  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimm, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1847 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-858-207A-64  
Alignment Scores:  
Pred. No.: 271 Length: 1847  
Score: 43.00 Matches: 6  
Percent Similarity: 88.89% Conservative: 2  
Best Local Similarity: 66.67% Mismatches: 1  
Query Match: 74.14% Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x US-08-858-207A-64 (1-1847)  
Qy 1 LysThrTrpGlyGlnTyrTrpAlaVal 9  
Db 1411 AAACTGGCGACAGTTCTGAGCGGTG 1437  
RESULT 13  
US-08-961-527-146/c  
Sequence 146, Application US/08961527  
Patent No. 6420135  
GENERAL INFORMATION:  
APPLICANT: Charles Kunesh  
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 391  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,527  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8512  
TELEFAX: (301) 309-8504  
INFORMATION FOR SEQ ID NO: 146:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1187 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-961-527-146  
Alignment Scores:  
Pred. No.: 2.04e+03 Length: 1187  
Score: 43.00 Matches: 6  
Percent Similarity: 88.89% Conservative: 2  
Best Local Similarity: 66.67% Mismatches: 1  
Query Match: 74.14% Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x US-08-961-527-146 (1-1187)  
Qy 1 LysThrTrpGlyGlnTyrTrpAlaVal 9  
Db 5132 AAACTGGCGACAGTTCTGAGCGGTG 5106  
RESULT 14  
US-08-317-310A-1/c  
Sequence 1, Application US/08317310A  
Patent No. 5858701  
GENERAL INFORMATION:  
APPLICANT: WHITE, Morris F.  
APPLICANT: SUN, Xiao Jian  
APPLICANT: PIERCE, Jacalyn H.  
TITLE OF INVENTION: THE IRS FAMILY OF GENES  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHYE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,310A  
FILING DATE: 03-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Louis Myers  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: JDP-022  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400

```
TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4088 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 60..4022
US-08-317-310A-1

Alignment Scores:
Pred. No.: 929          Length: 4088
Score: 42.00           Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 72.41%     Indels: 0
                        Gaps: 0
DB: 2

US-09-214-836-1 (1-9) x US-08-317-310A-1 (1-4088)

Qy 1 LysThrTTPGlyGlnTYTTP 7
Db 3098 AGGACGTGGGGCGAGTGTGG 3078

RESULT 15
PCT-US95-13041-1/c
; Sequence 1, Application PC/TUS9513041
; GENERAL INFORMATION:
;   APPLICANT: WHITE, Morris F.
;   APPLICANT: SUN, Xiao Jian
;   APPLICANT: PIERCE, Jacalyn H.
;   TITLE OF INVENTION: THE IRS FAMILY OF GENES
;   NUMBER OF SEQUENCES: 63
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: LAHIVE & COCKFIELD
;     STREET: 60 State Street, Suite 510
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: ASCII text
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US95/13041
;     FILING DATE: Herewith
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/317,310
;       FILING DATE: 03-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;         NAME: Louis Myers
;         REGISTRATION NUMBER: 35,965
;         REFERENCE/DOCKET NUMBER: JDP-022PC
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (617)227-7400
;         TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 4088 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 60..4022
PCT-US95-13041-1

Alignment Scores:
Pred. No.: 929          Length: 4088
Score: 42.00           Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 72.41%     Indels: 0
                        Gaps: 0
DB: 2

US-09-214-836-1 (1-9) x PCT-US95-13041-1 (1-4088)

Qy 1 LysThrTTPGlyGlnTYTTP 7
Db 3098 AGGACGTGGGGCGAGTGTGG 3078

RESULT 16
US-08-592-126-135
; Sequence 135, Application US/08592126
; Patent No. 5821091
; GENERAL INFORMATION:
;   APPLICANT: Gregory Dolganov
;   TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
;   NUMBER OF SEQUENCES: 151
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: Dehlinger & Associates
;     STREET: 350 Cambridge Avenue, Suite 250
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;   ZIP: 94306
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/592,126
;     FILING DATE:
;     CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Sholtz, Charles K.
;       REGISTRATION NUMBER: 38,615
;       REFERENCE/DOCKET NUMBER: 4600-0111
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (415) 324-0880
;         TELEFAX: (415) 324-0960
;   INFORMATION FOR SEQ ID NO: 135:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 629 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA to mRNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE: G115a.seq
US-08-592-126-135

Alignment Scores:
Pred. No.: 177          Length: 629
Score: 41.00           Matches: 5
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 71.43% Mismatches: 1
Query Match: 70.69%     Indels: 0
                        Gaps: 0
DB: 1

US-09-214-836-1 (1-9) x US-08-592-126-135 (1-629)

Qy 1 LysThrTTPGlyGlnTYTTP 7
Db 79 AAACATGGGGAGACTTCTGG 99
```

RESULT 17  
US-09-168-595-135  
Sequence 135, Application US/09168595  
Patent No. 6555666  
GENERAL INFORMATION:  
APPLICANT: Gregory Dolganov  
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/168,595  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,126  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholez, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 4600-0111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 629 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: G115a.seq  
US-09-168-595-135  
Alignment Scores:  
Pred. No.: 177  
Score: 41.00  
Percent Similarity: 85.71%  
Best Local Similarity: 71.43%  
Query Match: 70.69%  
DB: 4  
Length: 629  
Matches: 5  
Conservative: 1  
Mismatch: 1  
Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x US-09-168-595-135 (1-629)  
QY 1 LysTHTTTPGLYGLNYYTTP 7  
DB 79 AAAACATGGGAGAGTTCG 99  
RESULT 18  
US-07-814-964-8/c  
Sequence 8, Application US/07814964  
Patent No. 5359047  
GENERAL INFORMATION:  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pil, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellett, Patti

APPLICANT: Essigmann, John M.  
APPLICANT: Lippard, Stephen J.  
TITLE OF INVENTION: DNA Structure Specific Recognition  
TITLE OF INVENTION: Protein and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: 2 Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/814,964  
FILING DATE: 19911226  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/539,906  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-4787AA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1898 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: Human B cell  
CLONE: lambda-Pcl1  
US-07-814-964-8  
Alignment Scores:  
Pred. No.: 587  
Score: 41.00  
Percent Similarity: 87.50%  
Best Local Similarity: 62.50%  
Query Match: 70.69%  
DB: 1  
Length: 1898  
Matches: 5  
Conservative: 2  
Mismatch: 1  
Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x US-07-814-964-8 (1-1898)  
QY 2 ThTTPGLYGLNYYTTPAlaVal 9  
DB 1654 AGCTGGGGGAGAGTCTGCTAGTT 1631  
RESULT 19  
US-08-258-442-8/c  
Sequence 8, Application US/08258442  
Patent No. 5670621  
GENERAL INFORMATION:  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pil, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellett, Patti  
APPLICANT: Essigmann, John M.  
APPLICANT: Lippard, Stephen J.  
TITLE OF INVENTION: DNA Structure Specific Recognition

TITLE OF INVENTION: Protein and Uses Therefor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: 2 Millitia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/258,442  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/539,906  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-4787AAA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1898 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: Human B cell  
CLONE: lambda-Ptl  
US-08-258-442-8

Alignment Scores:  
Pred. No.: 587 Length: 1898  
Score: 41.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 1 Gaps: 0

US-09-214-836-1 (1-9) x US-08-258-442-8 (1-1898)

QY 2 ThrtTpglyglnTyTTPAlaVal 9  
DB 1654 AGCTGGGGGAGTACTGCTAGTT 1631

RESULT 20  
US-08-328-809-3/C  
Sequence 3, Application US/08328809  
GENERAL INFORMATION:  
APPLICANT: Lippard, Stephen J.  
APPLICANT: Essigmann, John M.  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pili, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellelt, Patti  
TITLE OF INVENTION: Uses For DNA Structure-Specific  
RECOGNITION PROTEINS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault  
STREET: 53 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/328,809  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fenton, Gillian M.  
REGISTRATION NUMBER: 36,508  
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7100  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1898 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: Human B cell  
CLONE: lambda-Ptl  
US-08-328-809-3

Alignment Scores:  
Pred. No.: 587 Length: 1898  
Score: 41.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 1 Gaps: 0

US-09-214-836-1 (1-9) x US-08-328-809-3 (1-1898)

QY 2 ThrtTpglyglnTyTTPAlaVal 9  
DB 1654 AGCTGGGGGAGTACTGCTAGTT 1631

RESULT 21  
US-08-866-840-3/C  
Sequence 3, Application US/08866840  
GENERAL INFORMATION:  
APPLICANT: Lippard, Stephen J.  
APPLICANT: Essigmann, John M.  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pili, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellelt, Patti  
TITLE OF INVENTION: Uses For DNA Structure-Specific  
RECOGNITION PROTEINS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault  
STREET: 53 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/866,840  
FILING DATE: 02-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fenton, Gillian M.  
REGISTRATION NUMBER: 36,508  
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1898 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: Human B cell  
CLONE: lambda-Pt1  
US-08-866-840-3

Alignment Scores:  
Pred. No.: 587 Length: 1898  
Score: 41.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 4 Gaps: 0

US-09-214-836-1 (1-9) x US-08-866-840-3 (1-1898)

Qy 2 ThrtTpglyglnTyTTPalaVal 9  
DB 1654 AGCTGGGGGAGTACTGGCTAGTT 1631

RESULT 22  
PCT-US92-11107-8/c  
Sequence 8, Application PC/TUS9211107  
GENERAL INFORMATION:  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pil, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellelt, Patti  
APPLICANT: Essigmann, John M.  
APPLICANT: Lippard, Stephen J.  
TITLE OF INVENTION: DNA Structure Specific Recognition  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: 2 Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/11107

FILING DATE: 19921218  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/539,906  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-4787AAA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1898 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: Human B cell  
CLONE: lambda-Pt1  
PCT-US92-11107-8

Alignment Scores:  
Pred. No.: 587 Length: 1898  
Score: 41.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 5 Gaps: 0

US-09-214-836-1 (1-9) x PCT-US92-11107-8 (1-1898)

Qy 2 ThrtTpglyglnTyTTPalaVal 9  
DB 1654 AGCTGGGGGAGTACTGGCTAGTT 1631

RESULT 23  
US-07-814-964-6/c  
Sequence 6, Application US/07814964  
Patent No. 5359047  
GENERAL INFORMATION:  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pil, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellelt, Patti  
APPLICANT: Essigmann, John M.  
APPLICANT: Lippard, Stephen J.  
TITLE OF INVENTION: DNA Structure Specific Recognition  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: 2 Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/814,964  
FILING DATE: 19911226  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/539,906  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-4787AAA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2839 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: human SSRP - composite of six overlapping  
CLONE: CDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 11q12  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 275..2404  
US-07-814-964-6

Alignment Scores:  
Pred. No.: 908 Length: 2839  
Score: 41.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 1 Gaps: 0

US-09-214-836-1 (1-9) x US-07-814-964-6 (1-2839)

OY 2 ThrtPglYgInTYTTPAlaVal 9  
Db 2372 AGCTGGGGGAGTACTGCTAGTT 2349

RESULT 24  
US-08-258-442-6/C  
Sequence 6, Application US/08258442  
Patent No. 5670621  
GENERAL INFORMATION:  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pil, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellelt, Patti  
APPLICANT: Essigmann, John M.  
APPLICANT: Lippard, Stephen J.  
TITLE OF INVENTION: DNA Structure Specific Recognition  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: 2 Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/258,442  
FILING DATE:

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/539,906  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-4787AAA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2839 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: human SSRP - composite of six overlapping  
CLONE: CDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 11q12  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 275..2404  
US-08-258-442-6

Alignment Scores:  
Pred. No.: 908 Length: 2839  
Score: 41.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 1 Gaps: 0

US-09-214-836-1 (1-9) x US-08-258-442-6 (1-2839)

OY 2 ThrtPglYgInTYTTPAlaVal 9  
Db 2372 AGCTGGGGGAGTACTGCTAGTT 2349

RESULT 25  
US-08-328-809-1/C  
Sequence 1, Application US/08328809  
Patent No. 5705334  
GENERAL INFORMATION:  
APPLICANT: Lippard, Stephen J.  
APPLICANT: Essigmann, John M.  
APPLICANT: Donahue, Brian A.  
APPLICANT: Toney, Jeffrey H.  
APPLICANT: Bruhn, Suzanne L.  
APPLICANT: Pil, Pieter M.  
APPLICANT: Brown, Steven  
APPLICANT: Kellelt, Patti  
TITLE OF INVENTION: Uses For DNA Structure-Specific  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault  
STREET: 53 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,809  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fenton, Gillian M.  
REGISTRATION NUMBER: 36,508  
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
FAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2839 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
ORGANISM: Homo sapiens  
CLONE: human SSRP - composite of six overlapping  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 11q12  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 275..2404  
US-08-328-809-1

Alignment Scores:  
Pred. No.: 908 Length: 2839  
Score: 41.00 Matches: 5  
Percent Similarity: 87.50% Conservative: 2  
Best Local Similarity: 62.50% Mismatches: 1  
Query Match: 70.69% Indels: 0  
DB: 1 Gaps: 0

US-09-214-836-1 (1-9) x US-08-328-809-1 (1-2839)

QY 2 ThTTpGlyGIntYrTpaAlaVal 9  
Db 2372 AGCTGGGGAGTACTGCTAGTT 2349

Search completed: August 24, 2003, 03:59:06  
Job time : 62 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 24, 2003, 02:54:20 ; Search time 150.5 Seconds  
(without alignments)  
134.442 Million cell updates/sec

Title: US-09-214-836-1  
Perfect score: 58  
Sequence: 1 KTMGQYAV 9

Scoring table:  
BLOSUM62 Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1517243 seqs, 1124081882 residues  
Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO.spool/US09214836/runat\_14082003\_085045\_7758/app\_query.fasta\_1.398  
-DB=Published.Applications.NA -OPMT=fastcap -SUFFIX=tmdb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blomsum62  
-TRANS=numan40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=25 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09214836@cgn2\_1.1.290@runat\_14082003\_085045\_7758  
-NCPU=6 -ICPU=3 -NO MAP -LARGESUBSTR -NEG\_SCORES=0 -WAIT -DSELOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	53	91.4	2130	9	US-09-862-260A-1 Sequence 1, Appl1

2	53	91.4	2130	10	US-09-812-238B-1	Sequence 1, Appl1
3	53	91.4	2130	14	US-10-207-655-76	Sequence 76, Appl1
4	53	91.4	2131	13	US-10-047-539-3	Sequence 3, Appl1
5	53	91.4	23770	14	US-10-035-637-8	Sequence 8, Appl1
6	50	86.2	2172	12	US-09-898-860-26	Sequence 26, Appl1
7	49	84.5	1881	13	US-10-047-539-1	Sequence 1, Appl1
8	47	81.0	215	10	US-09-960-352-10302	Sequence 10302, A
9	46	79.3	517	13	US-10-027-632-37178	Sequence 37178, A
10	46	79.3	517	13	US-10-027-632-75092	Sequence 75092, A
11	46	79.3	517	13	US-10-027-632-75093	Sequence 75093, A
12	45	77.6	1803	14	US-09-783-590-1345	Sequence 1345, Ap
13	45	77.6	1807	10	US-10-198-846-13052	Sequence 13052, A
14	44	75.9	458	11	US-09-918-995-565	Sequence 565, App
15	44	75.9	1839	13	US-10-027-632-97711	Sequence 97711, A
16	44	75.9	3913	14	US-10-128-714-100	Sequence 100, App
17	44	75.9	4608	14	US-10-128-714-5100	Sequence 5100, Ap
18	44	75.9	8159	9	US-09-764-891-5464	Sequence 910, App
19	44	75.9	8159	11	US-09-764-891-5464	Sequence 5464, Ap
20	44	75.9	8159	11	US-09-764-891-5631	Sequence 5631, Ap
21	44	75.9	8159	14	US-10-073-865-140	Sequence 140, App
22	44	75.9	8159	14	US-10-103-313-624	Sequence 624, App
23	44	75.9	8159	14	US-10-073-885-112	Sequence 112, App
24	44	75.9	8165	9	US-09-764-893-809	Sequence 909, App
25	44	75.9	8165	11	US-09-764-891-5463	Sequence 5463, Ap
26	44	75.9	8165	11	US-09-764-891-5630	Sequence 5630, Ap
27	44	75.9	8165	14	US-10-073-865-139	Sequence 139, App
28	44	75.9	8165	14	US-10-103-313-623	Sequence 623, App
29	44	75.9	8165	14	US-10-073-885-111	Sequence 111, App
30	44	75.9	13327	11	US-09-764-891-5627	Sequence 5627, App
31	44	75.9	65042	14	US-10-229-124-3	Sequence 3, Appl1
32	43	74.1	310	10	US-09-867-701-3370	Sequence 3370, Ap
33	43	74.1	346	14	US-09-796-692-2927	Sequence 2927, Ap
34	43	74.1	346	14	US-10-040-862-2927	Sequence 2927, Ap
35	43	74.1	467	11	US-09-918-995-23223	Sequence 23223, A
36	43	74.1	527	13	US-10-027-632-60202	Sequence 60202, A
37	43	74.1	1008	9	US-09-815-242-9572	Sequence 9572, Ap
38	43	74.1	6219	10	US-09-880-107-1761	Sequence 1761, Ap
39	40	72.4	303	10	US-09-974-300-6148	Sequence 6145, Ap
40	42	72.4	430	10	US-09-960-352-10480	Sequence 10480, A
41	42	72.4	442	13	US-10-027-632-43332	Sequence 43332, A
42	42	72.4	443	13	US-10-027-632-83331	Sequence 83331, A
43	42	72.4	443	13	US-10-027-632-30253	Sequence 30253, A
44	42	72.4	668	13	US-10-027-632-99172	Sequence 99172, A
45	42	72.4	922	10	US-09-764-868-335	Sequence 335, App

ALIGNMENTS

RESULT 1  
US-09-862-260A-1  
Sequence 1, Application US/09862260A  
Patent No. US20020082217A1  
GENERAL INFORMATION:  
APPLICANT: Nicolette, Charles A.  
TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
FILE REFERENCE: 126881210200  
CURRENT APPLICATION NUMBER: US/09/862,260A  
CURRENT FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/208,955  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/267,877  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2130  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-862-260A-1  
Alignment Scores: 13.5 Length: 2130  
Pred. No.: 53.00 Matches: 8  
Score:

Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 1  
DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x US-09-862-260A-1 (1-2130)

Qy 1 LysThrTPGlglnTyrTrpAlaVal 9  
DB 481 AAGACCTGGGGCCAACTACTGGCAAGTT 507

RESULT 2  
US-09-812-238B-1  
; Sequence 1, Application US/09812238B  
; Patent No. US20020169132A1  
; GENERAL INFORMATION:

APPLICANT: Nicolette, Charles  
TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
FILE REFERENCE: GZ 2094.00  
CURRENT APPLICATION NUMBER: US/09/812,238B  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 2130  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (22) .. (2004)  
US-09-812-238B-1

## Alignment Scores:

Pred. No.: 13.5 Length: 2130  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 10 Gaps: 0

US-09-214-836-1 (1-9) x US-09-812-238B-1 (1-2130)

Qy 1 LysThrTPGlglnTyrTrpAlaVal 9  
DB 481 AAGACCTGGGGCCAACTACTGGCAAGTT 507

RESULT 3  
US-10-207-655-76  
; Sequence 76, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390069.401C1  
CURRENT APPLICATION NUMBER: US/10/207,655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 76  
LENGTH: 2130  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-207-655-76

## Alignment Scores:

Pred. No.: 13.5 Length: 2130  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-207-655-76 (1-2130)

Qy 1 LysThrTPGlglnTyrTrpAlaVal 9  
DB 481 AAGACCTGGGGCCAACTACTGGCAAGTT 507

RESULT 4  
US-10-047-539-3  
; Sequence 3, Application US/10047539  
; Publication No. US20020177547A1  
; GENERAL INFORMATION:

APPLICANT: MOLLING, KARIN  
APPLICANT: PAVLOVIC, JOVAN  
APPLICANT: NAMRATH, MICHAEL  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING  
FILE REFERENCE: VOS-27  
CURRENT APPLICATION NUMBER: US/10/047,539  
CURRENT FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
PRIOR FILING DATE: 2001-01-16  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2131  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (12) .. (2018)  
US-10-047-539-3

## Alignment Scores:

Pred. No.: 13.5 Length: 2131  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 13 Gaps: 0

US-09-214-836-1 (1-9) x US-10-047-539-3 (1-2131)

Qy 1 LysThrTPGlglnTyrTrpAlaVal 9  
DB 471 AAGACCTGGGGCCAACTACTGGCAAGTT 497

RESULT 5  
US-10-035-637-8/C  
; Sequence 8, Application US/10035637  
; Publication No. US2003003167A1  
; GENERAL INFORMATION:

APPLICANT: Keiler, Tibor  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC  
FILE REFERENCE: MXI-166CP  
CURRENT APPLICATION NUMBER: US/10/035,637  
CURRENT FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 09/851,614  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USSN 60/203,126  
PRIOR FILING DATE: 2000-05-08  
PRIOR APPLICATION NUMBER: USSN 60/230,739  
PRIOR FILING DATE: 2000-09-07  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 23770  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (16489) ... (17094)

US-10-035-637-8

Alignment Scores:

Pred. No.: 149 Length: 23770  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-035-637-8 (1-23770)

Oy 1 LysThrTPGlyGlnTyrTrpAlaVal 9

Db 10671 AAGACCTGGGGCAATACGCAAGTT 10645

RESULT 6

US-09-898-860-26  
Sequence 26, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & PINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 2172

TYPE: nucleotide

STRANDEDNESS: Double

TOPOLOGY: Unknown

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Alignment Scores:

Pred. No.: 41.9 Length: 2172  
Score: 50.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.21% Indels: 0

DB: 12 Gaps: 0

US-09-214-836-1 (1-9) x US-09-898-860-26 (1-2172)

Oy 1 LysThrTPGlyGlnTyrTrp 7

Db 498 AAGACCTGGGGCAATACGCAAGTT 518

RESULT 7

US-10-047-539-1  
Sequence 1, Application US/10047539  
Publication No. US20020177547A1  
GENERAL INFORMATION:

APPLICANT: MOLLING, KARIN

APPLICANT: PAVLOVIC, JOVAN

APPLICANT: NAMRATH, MICHAEL

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING

FILE REFERENCE: VOS-27

CURRENT APPLICATION NUMBER: US/10/047,539

CURRENT FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: EP 01 10 0914.9

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 1

LENGTH: 1881

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1881)

US-10-047-539-1

Alignment Scores:

Pred. No.: 52.7 Length: 1881  
Score: 49.00 Matches: 7  
Percent Similarity: 88.89% Conservative: 1  
Best Local Similarity: 77.78% Mismatches: 1  
Query Match: 84.48% Indels: 0  
DB: 13 Gaps: 0

US-09-214-836-1 (1-9) x US-10-047-539-1 (1-1881)

Oy 1 LysThrTPGlyGlnTyrTrpAlaVal 9

Db 460 AAGACCTGGGGCAATACGCAAGTT 486

RESULT 8

US-09-960-352-10302  
Sequence 10302, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengping

APPLICANT: Byatt, John C.

APPLICANT: Machialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 10302

LENGTH: 215

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 44-LIB34-021-Q1-B1-C8

US-09-960-352-10302

Alignment Scores:  
Pred. No.: 12.8 Length: 215  
Score: 47.00 Matches: 7

```
Percent Similarity: 77.78% Conservative: 0
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 81.03% Indels: 0
DB: 10 Gaps: 0

US-09-214-836-1 (1-9) x US-09-960-352-10302 (1-215)

Qy 1 LysThrTpglyGlnTyTrpAlaVal 9
Db 166 AAGCAATGGGACATACCTGGCTGGTGC 192

RESULT 9
US-10-027-632-37178/c
; Sequence 37178, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37178
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-37178

Alignment Scores:
Pred. No.: 44.4 Length: 517
Score: 46.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 79.31% Indels: 0
DB: 13 Gaps: 0

US-09-214-836-1 (1-9) x US-10-027-632-37178 (1-517)

Qy 1 LysThrTpglyGlnTyTrp 7
Db 418 AAGACCTGGGGTAGACTACTGG 398

RESULT 10
US-10-027-632-75092
; Sequence 75092, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75092
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75092

Alignment Scores:
Pred. No.: 44.4 Length: 517
Score: 46.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 79.31% Indels: 0
DB: 13 Gaps: 0

US-09-214-836-1 (1-9) x US-10-027-632-75092 (1-517)

Qy 1 LysThrTpglyGlnTyTrp 7
Db 100 AAGACCTGGGGTAGACTACTGG 120

RESULT 11
US-10-027-632-75093
; Sequence 75093, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75093
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75093

Alignment Scores:
Pred. No.: 44.4 Length: 517
Score: 46.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 79.31% Indels: 0
DB: 13 Gaps: 0

US-09-214-836-1 (1-9) x US-10-027-632-75093 (1-517)

Qy 1 LysThrTpglyGlnTyTrp 7
```

|||||  
Db 100 AAGACTGGGCTAGTACTGG 120  
RESULT 12  
US-09-783-590-1345/C  
; Sequence 1345, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16, 2C1  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: US/09/783,590  
; PRIOR FILING DATE: 1995-04-12  
; PRIOR APPLICATION NUMBER: 08/346,731  
; PRIOR FILING DATE: 1994-11-21  
; NUMBER OF SEQ ID NOS: 12485  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1345  
; LENGTH: 297  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (239)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (274)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (275)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (276)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (289)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (292)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (295)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-1345  
Alignment Scores:  
Pred. No.: 37 Length: 297  
Score: 45.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 85.71% Mismatches: 0  
Query Match: 77.59% Indels: 0  
DB: 10 Gaps: 0  
US-09-214-836-1 (1-9) x US-09-783-590-1345 (1-297)  
QY 2 ThTTPGLyGIntYrTTPdAla 8  
Db 31 ACTGGGGGCAATCTGGGCT 11  
RESULT 13  
US-10-198-846-13052  
; Sequence 13052, Application US/10198846  
; Publication No. US2003009974A1  
; GENERAL INFORMATION:

APPLICANT: Lillie, James  
APPLICANT: Xu, Yongyao  
APPLICANT: Wang, Youzhen  
APPLICANT: Steinmann, Kathleen  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF BREAST CANCER  
FILE REFERENCE: MRI-049  
CURRENT APPLICATION NUMBER: US/10/198,846  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/306,220  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 14084  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13052  
LENGTH: 1803  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1, 20, 21, 1802, 1803  
OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-13052

Alignment Scores:  
Pred. No.: 223 Length: 1803  
Score: 45.00 Matches: 7  
Percent Similarity: 87.50% Conservative: 0  
Best Local Similarity: 87.50% Mismatches: 1  
Query Match: 77.59% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-198-846-13052 (1-1803)

QY 2 ThTTPGLyGIntYrTTPdAlaVal 9  
Db 95 ACTGGGGGCCAGTGTGGCAGTG 118

RESULT 14  
US-09-918-995-565  
; Sequence 565, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 565  
; LENGTH: 458  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(458)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-565

Alignment Scores:  
Pred. No.: 82.7 Length: 458  
Score: 44.00 Matches: 6  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 75.00% Mismatches: 0  
Query Match: 75.86% Indels: 0  
DB: 11 Gaps: 0

US-09-214-836-1 (1-9) x US-09-918-995-565 (1-458)

```

Oy      2  ThrttprgiyGintYrTTPALaVal 9
      :::|||||:::|||||
Db      237  TCTGTGGGGGACACTGGCGGCTC 260

RESULT 15
US-10-027-632-97711
: Sequence 97711, Application US/10027632
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: FILE REFERENCE: 108827,129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 97711
: LENGTH: 1839
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-97711

Alignment Scores:
Pred. No.:      331      Length:      1839
Score:          44.00    Matches:      6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match:     75.86% Indels:      0
DB:              13      Gaps:       0

US-09-214-836-1 (1-9) x US-10-027-632-97711 (1-1839)

Oy      2  ThrttprgiyGintYrTTPALaVal 9
      |||||:::|||||
Db      1239  ACTTGGGACACATGCTGCTGCTG 1262

RESULT 16
US-10-128-714-100
: Sequence 100, Application US/10128714
: Publication No. US20030119013A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Bo
: APPLICANT: Hu, Wengqi
: APPLICANT: Tishkoff, Daniel
: APPLICANT: Zamudio, Carlos
: APPLICANT: Eroskin, Alexey M
: APPLICANT: Lemieux, Sebastien M
: TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
: FILE REFERENCE: 10182-018-999
: CURRENT APPLICATION NUMBER: US/10/128,714
: CURRENT FILING DATE: 2002-04-23
: PRIOR APPLICATION NUMBER: US 60/285,697
: PRIOR FILING DATE: 2001-04-23
: PRIOR APPLICATION NUMBER: US 60/287,066
: PRIOR FILING DATE: 2001-04-27
: PRIOR APPLICATION NUMBER: US 60/295,890
: PRIOR FILING DATE: 2001-06-05
: PRIOR APPLICATION NUMBER: US 60/303,899

```

```

      ; PRIOR FILING DATE: 2001-07-09
      ; PRIOR APPLICATION NUMBER: US 60/316,362
      ; PRIOR FILING DATE: 2001-08-31
      ; NUMBER OF SEQ ID NOS: 8603
      ; SOFTWARE: PatentIn version 3.1
      ; SEQ ID NO 100
      ; LENGTH: 3913
      ; TYPE: DNA
      ; ORGANISM: Aspergillus fumigatus
      ; US-10-128-714-100

Alignment Scores:
Pred. No.: 701 Length: 3913
Score: 44.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 75.86% Indels: 0
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-128-714-100 (1-3913)

CY 1 LysThrTrpGlyGlnTyrTrp 7
   ::|||:|||::|||
Db 3745 CGCACTTGGGGGGAATCTGG 3765

RESULT 17
US-10-128-714-5100
; Sequence 5100, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Mengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-9999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5100
; LENGTH: 4608
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-5100

Alignment Scores:
Pred. No.: 826 Length: 4608
Score: 44.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 75.86% Indels: 0
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-128-714-5100 (1-4608)

CY 1 LysThrTrpGlyGlnTyrTrp 7
   ::|||:|||:|||::|||
Db 4326 CGCACTTGGGGGGAATCTGG 4346

```

```
RESULT 18
US-09-764-853-910/c
; Sequence 910, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 910
; LENGTH: 8159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (835)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-853-910

Alignment Scores:
Pred. No.: 1.46e+03 Length: 8159
Score: 44.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 75.86% Indels: 0
DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x US-09-764-853-910 (1-8159)

OY 2 ThrtTpglygIntYrTTPAlaVal 9
Db 7275 TCCTGGGGGCGAGCACTGGCGGCTC 7252

RESULT 19
US-09-764-891-5464/c
; Sequence 5464, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5464
; LENGTH: 8159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (835)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-5464

Alignment Scores:
Pred. No.: 1.46e+03 Length: 8159
Score: 44.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 75.86% Indels: 0
DB: 11 Gaps: 0

US-09-214-836-1 (1-9) x US-09-764-891-5464 (1-8159)

OY 2 ThrtTpglygIntYrTTPAlaVal 9
Db 7275 TCCTGGGGGCGAGCACTGGCGGCTC 7252
```

```
RESULT 20
US-09-764-891-5631/c
; Sequence 5631, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5631
; LENGTH: 8159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (835)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-5631

Alignment Scores:
Pred. No.: 1.46e+03 Length: 8159
Score: 44.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 75.86% Indels: 0
DB: 11 Gaps: 0

US-09-214-836-1 (1-9) x US-09-764-891-5631 (1-8159)

OY 2 ThrtTpglygIntYrTTPAlaVal 9
Db 7275 TCCTGGGGGCGAGCACTGGCGGCTC 7252

RESULT 21
US-10-073-865-140/c
; Sequence 140, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1209C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; CURRENT FILING DATE: 2002-02-14
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 140
; LENGTH: 8159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (835)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-073-865-140

Alignment Scores:
Pred. No.: 1.46e+03 Length: 8159
Score: 44.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 75.86% Indels: 0
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-073-865-140 (1-8159)

OY 2 ThrtTpglygIntYrTTPAlaVal 9
Db 7275 TCCTGGGGGCGAGCACTGGCGGCTC 7252
```

DB 7275 TCCTGGGGGAGCACTGGCGGCTC 7252

RESULT 22

US-10-103-313-624/c

Sequence 624, Application US/10103313

Publication No. US20030082758A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PJ207C1

CURRENT APPLICATION NUMBER: US/10/103,313

CURRENT FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 653

Prior Application removed - See file Wrapper or Palm

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 624

LENGTH: 8159

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (835)

OTHER INFORMATION: n equals a,t,g, or c

US-10-103-313-624

Alignment Scores:

Pred. No.: 1.46e+03 Length: 8159

Score: 44.00 Matches: 6

Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 75.00% Mismatches: 0

Query Match: 75.86% Indels: 0

DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-103-313-624 (1-8159)

OY 2 ThrtPgiyGIntYrTtpAlaVal 9

DB 7275 TCCTGGGGGAGCACTGGCGGCTC 7252

RESULT 23

US-10-073-885-112/c

Sequence 112, Application US/10073885

Publication No. US20030096346A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PJ203C1

CURRENT APPLICATION NUMBER: US/10/073,885

CURRENT FILING DATE: 2002-02-14

Prior Application removed - See file Wrapper or Palm

NUMBER OF SEQ ID NOS: 116

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 112

LENGTH: 8159

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (835)

OTHER INFORMATION: n equals a,t,g, or c

US-10-073-885-112

Alignment Scores:

Pred. No.: 1.46e+03 Length: 8159

Score: 44.00 Matches: 6

Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 75.00% Mismatches: 0

Query Match: 75.86% Indels: 0

DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x US-10-073-885-112 (1-8159)

OY 2 ThrtPgiyGIntYrTtpAlaVal 9

DB 7275 TCCTGGGGGAGCACTGGCGGCTC 7252

RESULT 24

US-09-764-853-909/c

Sequence 909, Application US/09764853

Patent No. US20020090672A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PJ206

CURRENT APPLICATION NUMBER: US/09/764,853

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 939

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 909

LENGTH: 8165

TYPE: DNA

ORGANISM: Homo sapiens

US-09-764-853-909

Alignment Scores:

Pred. No.: 1.46e+03 Length: 8165

Score: 44.00 Matches: 6

Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 75.00% Mismatches: 0

Query Match: 75.86% Indels: 0

DB: 9 Gaps: 0

US-09-214-836-1 (1-9) x US-09-764-853-909 (1-8165)

OY 2 ThrtPgiyGIntYrTtpAlaVal 9

DB 7279 TCCTGGGGGAGCACTGGCGGCTC 7256

RESULT 25

US-09-764-891-5463/c

Sequence 5463, Application US/09764891

Publication No. US20030077808A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC006

CURRENT APPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5463

LENGTH: 8165

TYPE: DNA

ORGANISM: Homo sapiens

US-09-764-891-5463

Alignment Scores:

Pred. No.: 1.46e+03 Length: 8165

Score: 44.00 Matches: 6

Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 75.00% Mismatches: 0

Query Match: 75.86% Indels: 0

DB: 11 Gaps: 0

US-09-214-836-1 (1-9) x US-09-764-891-5463 (1-8165)

OY 2 ThrtPgiyGIntYrTtpAlaVal 9

DB 7279 TCCTGGGGGAGCACTGGCGGCTC 7256

Search completed: August 24, 2003, 05:36:23

Job time : 163.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 24, 2003, 01:08:28 ; Search time 1896.5 Seconds  
(without alignments)  
115.339 Million cell updates/sec

Title: US-09-214-836-1  
Sequence: 1 KTWGQYWAY 9

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 22781392 segs, 1215238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgm2\_1/USPRO\_spool/US09214836/runat\_14082003\_085040\_7605/app\_query.fasta\_1.398  
-DB=EST -QFMT=fastap -SUFFIX=ref -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=25 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USPR=US09214836 @CGN 1.1 3596 @runat\_14082003\_085040\_7605 -NCPU=6 -ICPU=3  
-NO MAP -LARGQOUTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	91.4	304	13	BQ678421
2	53	91.4	384	13	BQ678421
3	53	91.4	436	14	CB792319
4	53	91.4	503	10	BE387921
5	53	91.4	506	10	BE389161
6	53	91.4	506	12	BM707920
7	53	91.4	515	10	BE407844
8	53	91.4	523	10	BE276871
9	53	91.4	531	10	BE280517
10	53	91.4	546	10	BE408811
11	53	91.4	577	14	CA397722
12	53	91.4	585	10	BE281030
13	53	91.4	587	14	CA392552
14	53	91.4	587	14	CA396509
15	53	91.4	594	12	BE743315
16	53	91.4	595	10	BE743315
17	53	91.4	603	12	BE743315
18	53	91.4	604	10	BE384038
19	53	91.4	605	12	BE761374
20	53	91.4	605	14	CA397065
21	53	91.4	606	12	BM722309
22	53	91.4	611	14	CA397499
23	53	91.4	616	10	BE389689
24	53	91.4	619	14	CA396195
25	53	91.4	622	10	BE384085
26	53	91.4	623	10	BE895835
27	53	91.4	628	10	BE276204
28	53	91.4	630	12	BE769568
29	53	91.4	640	12	BE766391
30	53	91.4	640	14	CA379865
31	53	91.4	649	10	BG477442
32	53	91.4	650	9	AL134961
33	53	91.4	655	10	BE388095
34	53	91.4	657	12	BE768036
35	53	91.4	660	10	BF978563
36	53	91.4	666	12	BE760391
37	53	91.4	667	12	BG764284
38	53	91.4	671	14	CA389877
39	53	91.4	673	12	BG766458
40	53	91.4	678	12	BG761457
41	53	91.4	680	10	BE277419
42	53	91.4	684	10	BF689653
43	53	91.4	684	12	BG770571
44	53	91.4	690	10	BE408713
45	53	91.4	698	12	BG766715

# ALIGNMENTS

RESULT 1  
LOCUS BQ678421  
DEFINITION AGENCOURT\_8281395 NIH\_MGC\_112 Homo sapiens cDNA IMAGE:6258718  
ACCESSION BQ678421  
VERSION BQ678421  
KEYWORDS BQ678421.1 GI:21791100  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 304)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.llnl.gov>  
 Plate: LHC2415 row: a column: 23  
 High quality sequence stop: 303.  
 Location/Qualifiers

## FEATURES

source

```

1..304
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6258718"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7, Site 1: XhoI, Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT      59 a      89 c      86 g      70 t
ORIGIN

```

## Alignment Scores:

```

Pred. No.:      37.2      Length:      304
Score:          53.00      Matches:      8
Percent Similarity: 88.89%      Conservative: 0
Best Local Similarity: 88.89%      Mismatches: 1
Query Match:    91.38%      Indels:      0
DB:             13      Gaps:      0

```

US-09-214-836-1 (1-9) x BQ678421 (1-304)

OY 1 LysThrTPGLyGlnTYTTPAlaVal 9  
 |||||  
 DB 13 AAGACTGGGGCCCAATCTGCAAGTT 39

## RESULT 2

BM708487

LOCUS

384 bp mRNA linear EST 28-FEB-2002  
 UI-E-C11-afu-b-14-0-UI\_r1 UI-E-C11 Homo sapiens cDNA clone

DEFINITION UI-E-C11-afu-b-14-0-UI 5', mRNA sequence.

ACCESSION

BM708487

VERSION

BM708487.1 GI:19021745

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 384)

AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

97044477

PUBMED

8889548

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MERRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

## FEATURES

source

Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics ([www.resgen.com](http://www.resgen.com)).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

```

1..384
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-C11-afu-b-14-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-C11"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-C11 is a normalized cDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA,
Genome Research, 6:791-806, 1996. First strand cDNA,
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is ACCGA.
This library was created for the program, Gene Discovery
in the Visual System, supported by National Eye Institute
(NEI)."
BASE COUNT      89 a      91 c      113 g      91 t
ORIGIN

```

## Alignment Scores:

```

Pred. No.:      51.8      Length:      384
Score:          53.00      Matches:      8
Percent Similarity: 88.89%      Conservative: 0
Best Local Similarity: 88.89%      Mismatches: 1
Query Match:    91.38%      Indels:      0
DB:             12      Gaps:      0

```

US-09-214-836-1 (1-9) x BM708487 (1-384)

OY 1 LysThrTPGLyGlnTYTTPAlaVal 9  
 |||||  
 DB 277 AAGACTGGGGCCCAATCTGCAAGTT 303

## RESULT 3

CB792319

LOCUS

436 bp mRNA linear EST 16-MAY-2003  
 AMGNNUC:NRHY4-00003-D6-A w Rat hypothalamus (10464) Rattus

DEFINITION AMGNNUC:NRHY4-00003-D6-A w Rat hypothalamus (10464) Rattus

ACCESSION

CB792319

VERSION

CB792319.1 GI:29880712

KEYWORDS

EST.

SOURCE

Rattus norvegicus

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1 (bases 1 to 436)

AUTHORS

Amgen EST Program.

TITLE

Amgen Rat EST Program

JOURNAL

Unpublished

COMMENT

Contact: Dan Fitzpatrick

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00003 row: d column: 6.

FEATURES  
Source Location/Qualifiers  
1. .436  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="nrhy4-00003-d6"  
/clone\_lib="W Rat hypothalamus (10464)"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat hypothalamus adult female Wistar rat avg. insert size 2.3 kb fraction 6 and 7"  
BASE COUNT 89 a 113 c 112 g 83 t 39 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 62 Length: 436  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 14 Gaps: 0  
US-09-214-836-1 (1-9) x CB792319 (1-436)  
Qy 1 Ly5ThrTTPGlyGlnTYTTPAlaVal 9  
Db 216 AAGACCTGGGCGCAATCTGGCAAGTT 242  
RESULT 4  
LOCUS BE387921 503 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601282169F1 NIH\_MGC\_44 Homo sapiens CDNA clone IMAGE:3603952 5',  
mRNA sequence.  
ACCESSION BE387921  
VERSION BE387921.1 GI:9333286  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
1 (bases 1 to 503)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCM249 row: j column: 17  
High quality sequence start: 25  
High quality sequence stop: 503.  
Location/Qualifiers  
1. .503  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3603952"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 119 a 115 c 147 g 122 t  
ORIGIN

Alignment Scores:  
Pred. No.: 76 Length: 503  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 10 Gaps: 0  
US-09-214-836-1 (1-9) x BE387921 (1-503)  
Qy 1 Ly5ThrTTPGlyGlnTYTTPAlaVal 9  
Db 449 AAGACCTGGGCGCAATCTGGCAAGTT 475  
RESULT 5  
LOCUS BE389161 506 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601285960F1 NIH\_MGC\_44 Homo sapiens CDNA clone IMAGE:3607719 5',  
mRNA sequence.  
ACCESSION BE389161  
VERSION BE389161.1 GI:9334526  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
1 (bases 1 to 506)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCM259 row: g column: 16  
High quality sequence stop: 504.  
Location/Qualifiers  
1. .506  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3607719"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; CDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-CDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 120 a 116 c 148 g 122 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 76.6 Length: 506  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 10 Gaps: 0  
US-09-214-836-1 (1-9) x BE389161 (1-506)  
Qy 1 Ly5ThrTTPGlyGlnTYTTPAlaVal 9  
|||

Db 454 AAGACCTGGGGCCAACTGCAAGT 480

# RESULT 6

BM707920

LOCUS BM707920 506 bp mRNA linear EST 28-FEB-2002  
 DEFINITION UI-E-C11-af1-a-17-0-UI.r1 UI-E-C11 Homo sapiens cDNA clone  
 UI-E-C11-af1-a-17-0-UI 5', mRNA sequence.

ACCESSION BM707920

VERSION BM707920.1 GI:19021178

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 506)

TITLE Normalization and subtraction: two approaches to facilitate gene

REFERENCE discovery

REFERENCE genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477

MEDLINE 8889548

COMMENT PubMed

CONTACT: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@iowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse

Location/Qualifiers

1..506

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-C11-af1-a-17-0-UI"

/tissue\_type="RPE and Choroid"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-C11"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-E-C11 is a normalized cDNA library containing the

following tissue(s): RPE and Choroid. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into pT73-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is ACCCA.

This library was created for the program, Gene Discovery

in the Visual System, supported by National Eye Institute

(NEI)."

BASE COUNT 93 a 151 c 138 g 124 t

ORIGIN

Alignment Scores:

Pred. No.: 76.6 Length: 506

Score: 53.00 Matches: 8

Percent Similarity: 88.89% Conservatve: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 91.38% Indels: 0

DB: 12 Gaps: 0

US-09-214-836-1 (1-9) x BM707920 (1-506)

Oy 1 LyeThrTPGlyGlnTYTTPAlaVal 9  
 Db 63 AAGACCTGGGGCCAACTGCAAGT 89

RESULT 7  
 BE407844  
 LOCUS BE407844 515 bp mRNA linear EST 21-JUL-2000  
 DEFINITION 601300882F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:365301 5',  
 mRNA sequence.

ACCESSION BE407844

VERSION BE407844.1 GI:9344294

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS 1 (bases 1 to 515)

TITLE NIH-MGC http://mgs.nci.nih.gov/

REFERENCE National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

CONTACT: Robert Strauberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov

Plate: LNCM31 row: d column: 22

High quality sequence stop: 503.

Location/Qualifiers

1..515

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:365301"

/tissue\_type="choriocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_21"

/note="Organ: placenta; Vector: pOT8; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 126 a 120 c 149 g 120 t

ORIGIN

Alignment Scores:

Pred. No.: 78.5 Length: 515

Score: 53.00 Matches: 8

Percent Similarity: 88.89% Conservatve: 0

Best Local Similarity: 88.89% Mismatches: 1

Query Match: 91.38% Indels: 0

DB: 10 Gaps: 0

US-09-214-836-1 (1-9) x BE407844 (1-515)

Oy 1 LyeThrTPGlyGlnTYTTPAlaVal 9

Db 462 AAGACCTGGGGCCAACTGCAAGT 488

RESULT 8

BE276871

LOCUS BE276871 523 bp mRNA linear EST 13-JUL-2000

DEFINITION 601178433F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3050793 5',  
 mRNA sequence.

ACCESSION BE276871

VERSION BE276871.1 GI:9151933

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 523)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
Plate: LNCM97 row: b column: 10  
High quality sequence stop: 523.  
Location/Qualifiers  
1..523  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3050793"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 20"  
/note="Organ: skin; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 124 a 117 c 158 g 124 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 80.3 Length: 523  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x BE276871 (1-523)  
QY 1 Ly5ThrTpgIyGInTyTTPaLaVal 9  
Db 454 AAGACCTGGGGCCAACTACTGGCAAGTT 480  
RESULT 9  
BE280517 531 bp mRNA linear EST 13-JUL-2000  
LOCUS 601155392P1 NIH\_MGC\_21 Homo sapiens CDNA clone IMAGE:3138863 5',  
DEFINITION mRNA sequence.  
ACCESSION BE280517  
VERSION BE280517.1 GI:9155522  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 531)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
Plate: LNCM104 row: g column: 24  
High quality sequence stop: 529.  
Location/Qualifiers  
1..531  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3138863"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 21"  
/note="Organ: placenta; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 102 a 170 c 143 g 116 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 82 Length: 531  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
Gaps: 0  
US-09-214-836-1 (1-9) x BE280517 (1-531)  
QY 1 Ly5ThrTpgIyGInTyTTPaLaVal 9  
Db 8 AAGACCTGGGGCCAACTACTGGCAAGTT 34  
RESULT 10  
BE408811 546 bp mRNA linear EST 21-JUL-2000  
LOCUS 60130333P1 NIH\_MGC\_21 Homo sapiens CDNA clone IMAGE:3637544 5',  
DEFINITION mRNA sequence.  
ACCESSION BE408811  
VERSION BE408811.1 GI:9345261  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 546)  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
Plate: LNCM37 row: b column: 09  
High quality sequence stop: 543.  
Location/Qualifiers  
1..546  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3637544"  
/tissue\_type="choriocarcinoma"

/lab host="DH10B (phage-resistant)"  
/clone lib="NIH MGC 21"  
/note="Organ: placenta; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming  
directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 98 a 170 c 145 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 85.3 Length: 546  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 10 Gaps: 0

US-09-214-836-1 (1-9) x BE408811 (1-546)

OY 1 LysHTTPGlyGlnTYTTPAlaVal 9  
Db 77 AAGACCTGGGGCCAACTACTGCGCAGTT 103

RESULT 11  
LOCUS CA397722 577 bp mRNA linear EST 06-NOV-2002  
DEFINITION cs94g12.y1 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs Homo sapiens CDNA clone cs94g12  
5', mRNA sequence.  
CA397722  
CA397722.1 GI:24735291

ACCESSION  
VERSION CA397722.1 GI:24735291  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 577)  
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
Touchman,D.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NIH Bank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
22103460  
12107410

JOURNAL MEDLINE  
PUBMED  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: greenehelix.nih.gov  
Plate: 94 row: 9 column: 12  
Seq primer: M13R1 reverse primer (ABI).  
Location/Qualifiers  
1..577  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="cs94g12"  
/tissue="cs94g12"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: pCMTS6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA

library in the pCMTS6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the Superscript  
Plasmid System (Invitrogen Corp).  
http://www.invitrogen.com/>. The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

BASE COUNT 121 a 161 c 160 g 135 t  
ORIGIN

Alignment Scores:  
Pred. No.: 92.3 Length: 577  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x CA397722 (1-577)

OY 1 LysHTTPGlyGlnTYTTPAlaVal 9  
Db 194 AAGACCTGGGGCCAACTACTGCGCAGTT 220

RESULT 12  
LOCUS BE281030 585 bp mRNA linear EST 13-JUL-2000  
DEFINITION 601156355F1 NIH\_MGC\_21 Homo sapiens CDNA clone IMAGE:3139788 5',  
mRNA sequence.  
BE281030  
BE281030.1 GI:9156043

ACCESSION  
VERSION BE281030.1 GI:9156043  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 585)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LNCM106 row: n column: 13.  
Location/Qualifiers  
1..585  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3139788"  
/tissue="IMAGE:3139788"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_21"  
/note="Organ: placenta; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 144 a 137 c 171 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 94.1 Length: 585

Score: 53.00 Matches: 8  
 Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 91.38% Indels: 0  
 DB: 10 Gaps: 0

US-09-214-836-1 (1-9) x BE281030 (1-585)

Qy 1 LyethrtpgylgintytrpAlaVal 9  
 Db 470 AAGACCTGGGCGCAATCTGCGCAAGTT 496

RESULT 13  
 CA392552 587 bp mRNA linear EST 06-NOV-2002  
 LOCUS ce78g10.y1 Human Retinal pigment epithelium/choroid cDNA  
 DEFINITION (un-normalized, unamplified): cs Homo sapiens cDNA clone ce78g10  
 5', mRNA sequence.

ACCESSION CA392552  
 VERSION CA392552.1 GI:24725382  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 587)  
 AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
 TITL Expresed sequence tag analysis of human RPE/choroid for the  
 NEIRBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants

JOURNAL Mol. Vis. 8 (4), 205-220 (2002)  
 MEDLINE 22103460  
 PUBMED 12107410

## COMMENT

Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 26 row: a column: 07  
 Seq primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers

## FEATURES

source

1..587  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="ce78g10"  
 /tissue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the SuperScript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>". The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

BASE COUNT 145 a 135 c 173 g 134 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 94.5  
 Score: 53.00

Length: 587  
 Matches: 8

Percent Similarity: 88.89% Conservative: 0  
 Best Local Similarity: 88.89% Mismatches: 1  
 Query Match: 91.38% Indels: 0  
 DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x CA392552 (1-587)

Qy 1 LyethrtpgylgintytrpAlaVal 9  
 Db 478 AAGACCTGGGCGCAATCTGCGCAAGTT 504

RESULT 14  
 CA396509 587 bp mRNA linear EST 06-NOV-2002  
 LOCUS ce78g10.y1 Human Retinal pigment epithelium/choroid cDNA  
 DEFINITION (un-normalized, unamplified): cs Homo sapiens cDNA clone ce78g10  
 5', mRNA sequence.

ACCESSION CA396509  
 VERSION CA396509.1 GI:24732961  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 587)  
 AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
 TITL Expresed sequence tag analysis of human RPE/choroid for the  
 NEIRBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants

JOURNAL Mol. Vis. 8 (4), 205-220 (2002)  
 MEDLINE 22103460  
 PUBMED 12107410

## COMMENT

Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 76 row: g column: 10  
 Seq primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers

## FEATURES

source

1..587  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="ce78g10"  
 /tissue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the SuperScript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>". The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

BASE COUNT 145 a 135 c 174 g 133 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 94.5  
 Score: 53.00

Length: 587  
 Matches: 8  
 Conservative: 0

Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x CA396509 (1-587)

Qy 1 LysThrTPGlyGlnTyrTPAlaVal 9  
Db 475 AAGACCTGGGGCAATCTGGCAAGTT 501

RESULT 15  
Bg762070 594 bp mRNA linear EST 15-MAY-2001  
LOCUS 602718443F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4858379 5',  
DEFINITION mRNA sequence.  
ACCESSION Bg762070.1 GI:14072723  
VERSION Bg762070  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 594)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1CM1712 row: F column: 12  
High quality sequence stop: 590.  
Location/Qualifiers  
1..594  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4858379"  
/tissue\_type="melanocytic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_49"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

BASE COUNT 145 a 141 c 175 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 96.1 Length: 594  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 12 Gaps: 0

US-09-214-836-1 (1-9) x Bg762070 (1-594)

Qy 1 LysThrTPGlyGlnTyrTPAlaVal 9  
Db 470 AAGACCTGGGGCAATCTGGCAAGTT 496

RESULT 16

BE743315  
LOCUS BE743315 595 bp mRNA linear EST 15-SEP-2000  
DEFINITION 601573227F1 NIH\_MGC\_9 Homo sapiens cDNA clone IMAGE:3834247 5',  
mRNA sequence.  
ACCESSION BE743315  
VERSION BE743315.1 GI:10157307  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 595)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
Plate: L1CM514 row: F column: 08  
High quality sequence stop: 595.  
Location/Qualifiers  
1..595  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3834247"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_9"  
/note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 142 a 140 c 177 g 136 t  
ORIGIN

Alignment Scores:  
Pred. No.: 96.4 Length: 595  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 10 Gaps: 0

US-09-214-836-1 (1-9) x BE743315 (1-595)

Qy 1 LysThrTPGlyGlnTyrTPAlaVal 9  
Db 461 AAGACCTGGGGCAATCTGGCAAGTT 487

RESULT 17  
Bg767860 603 bp mRNA linear EST 15-MAY-2001  
LOCUS 602741357F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4870925 5',  
mRNA sequence.  
ACCESSION Bg767860  
VERSION Bg767860.1 GI:14078513  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 603)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.



TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DRP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LNCM1745 row: a column: 16  
High quality sequence stop: 601.  
Location/Qualifiers  
1..603  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4870935"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 49"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

BASE COUNT 140 a 155 c 172 g 136 t  
ORIGIN

Alignment Scores:  
Pred. No.: 98.2 Length: 603  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 12 Gaps: 0

US-09-214-836-1 (1-9) x BG767860 (1-603)

Oy 1 [LyfThrTpGlyGIntYrTPAlaVal](#) 9  
Db 391 [AAGACCTGGGGCCAACTACTGGCAAGTT](#) 417

RESULT 18 BE384038 604 bp mRNA linear EST 21-JUN-2000  
LOCUS 601272829P1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3613927 5',  
DEFINITION mRNA sequence.  
ACCESSION BE384038  
VERSION BE384038.1 GI:3329403  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 604)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DRP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LNCM275 row: j column: 08

High quality sequence stop: 599.  
Location/Qualifiers  
1..604  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3613927"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 20"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 140 a 147 c 176 g 141 t  
ORIGIN

Alignment Scores:  
Pred. No.: 98.4 Length: 604  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 10 Gaps: 0

US-09-214-836-1 (1-9) x BE384038 (1-604)

Oy 1 [LyfThrTpGlyGIntYrTPAlaVal](#) 9  
Db 454 [AAGACCTGGGGCCAACTACTGGCAAGTT](#) 480

RESULT 19 BG761374 605 bp mRNA linear EST 15-MAY-2001  
LOCUS 602718257P1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4858262 5',  
DEFINITION mRNA sequence.  
ACCESSION BG761374  
VERSION BG761374.1 GI:14072027  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 605)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DRP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LNCM1712 row: a column: 15  
High quality sequence stop: 605.  
Location/Qualifiers  
1..605  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4858262"  
/tissue\_type="melanotic melanoma, high MDR (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 49"  
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:  
GGACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-CDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

BASE COUNT 139 a 154 c 173 g 139 t  
ORIGIN

Alignment Scores:  
Pred. No.: 98.7 Length: 605  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 12 Gaps: 0

US-09-214-836-1 (1-9) x BG761374 (1-605)

QY 1 LysThrTPGlyGlnTYrTPAlaVal 9  
DB 412 AAGACCTGGGGCCAACTGCAAGTT 438

RESULT 20 CA397065 605 bp mRNA linear EST 06-NOV-2002  
LOCUS CA397065  
DEFINITION c885f10.y2 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs Homo sapiens cDNA clone c885f10  
5', mRNA sequence.

ACCESSION CA397065  
VERSION CA397065.1 GI:24734031  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 605)  
AUTHORS Wiscow G., Bernstein, S.L., Wyal, M.K., Farris, R.N., Behal, A.,  
Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NEI/Bank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants

TITLE Mcl. Vis. 8 (4), 205-220 (2002)  
JOURNAL 22103460  
MEDLINE 12107410  
PUBMED

COMMENT Contact: Wiscow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: gscow@helix.nih.gov  
Plate: 85 row: F column: 10  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

FEATURES  
SOURCE

1. 605  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="c885f10"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMD10B"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: PCWVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the PCWVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript

Plasmid System (Invitrogen Corp.  
<http://www.invitrogen.com/>). The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

BASE COUNT 122 a 188 c 162 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 98.7 Length: 605  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x CA397065 (1-605)

QY 1 LysThrTPGlyGlnTYrTPAlaVal 9  
DB 30 AAGACCTGGGGCCAACTGCAAGTT 56

RESULT 21 BM722309 606 bp mRNA linear EST 01-MAR-2002  
LOCUS BM722309  
DEFINITION UI-E-E00-ahx-c-18-0-UI.r1 UI-E-E00 Homo sapiens cDNA clone  
UI-E-E00-ahx-c-18-0-UI 5', mRNA sequence.

ACCESSION BM722309  
VERSION BM722309.1 GI:19042795  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 606)  
AUTHORS Bonaldo, M.F., Lennon, G., and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery

TITLE Genome Res. 6 (9), 791-806 (1996)  
JOURNAL 97044477  
MEDLINE 8889548  
PUBMED

COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers

FEATURES  
SOURCE

1. 606  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-E00-ahx-c-18-0-UI"  
/tissue\_type="fetal eye"  
/dev\_stage="fetal"  
/lab\_host="UI-E-E00"  
/clone\_lib="UI-E-E00 (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-E-E00 is a cDNA library containing the following  
tissue(s): fetal eye. The library was constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (pT73 tail. The sequence tag for this library is GCGCATATCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 127 a 164 c 167 g 147 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 98.9 Length: 606  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 12 Gaps: 0

US-09-214-836-1 (1-9) x BW722309 (1-606)

Oy 1 LysThrTpgIyGlnTYTTPAlaVal 9  
Db 288 AAGACTGGGCGCAATCTGGCAAGTT 314

RESULT 22 CA397499 611 bp mRNA linear EST 06-NOV-2002  
LOCUS CA397499  
DEFINITION c991h07.y1 Human Retinal pigment epithelium/choroid cDNA c991h07 (Un-normalized, unamplified): cs Homo sapiens cDNA clone c991h07 5', mRNA sequence.

ACCESSION CA397499  
VERSION CA397499.1 GI:24734863  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 611)  
Wistow, G., Bernsteln, S. L., Wyal, M. K., Farris, R. N., Behal, A., Touchman, J. W., Bouffard, G., Smith, D. and Peterson, K.  
Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants

Mol. Vis. 8 (4), 205-220 (2002)  
22103460  
12107410

COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 91 row: h column: 07  
Seq primer: M13RP1 reverse primer (ABI).

FEATURES  
Location/Qualifiers  
1..611  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="c991h07"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp),

essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>". The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

BASE COUNT 144 a 146 c 178 g 143 t  
ORIGIN

Alignment Scores:  
Pred. No.: 100 Length: 611  
Score: 53.00 Matches: 8  
Percent Similarity: 88.89% Conservative: 0  
Best Local Similarity: 88.89% Mismatches: 1  
Query Match: 91.38% Indels: 0  
DB: 14 Gaps: 0

US-09-214-836-1 (1-9) x CA397499 (1-611)

Oy 1 LysThrTpgIyGlnTYTTPAlaVal 9  
Db 464 AAGACTGGGCGCAATCTGGCAAGTT 490

RESULT 23 BE389689 616 bp mRNA linear EST 21-JUL-2000  
LOCUS BE389689  
DEFINITION 601281927F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3603823 5', mRNA sequence.

ACCESSION BE389689  
VERSION BE389689.1 GI:9335054  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 616)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strauberg, Ph.D.  
Email: cgabs-1@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

COMMENT DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LCM249 row: e column: 08  
High quality sequence stop: 560.  
Location/Qualifiers  
1..616  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3603823"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7, site 1: XhoI, site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
Location/Qualifiers  
1..616  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3603823"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7, site 1: XhoI, site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 144 a 149 c 176 g 147 t  
ORIGIN

Alignment Scores:  
Pred. No.: 101 Length: 616  
Score: 53.00 Matches: 8

US-09-214-836-1 (1-9) x CA397499 (1-611)

Percent Similarity: 88.89%  
 Best Local Similarity: 88.89%  
 Query Match: 91.38%  
 DB: 10  
 Gaps: 0

US-09-214-836-1 (1-9) x BE389689 (1-616)

QY 1 LysThrTPGlyGlnTYTTPAlaVal 9  
 DB 454 AAGACCTGGGGCCCACTGCGCAAGTT 480

## RESULT 24

CA396195 619 bp mRNA linear EST 06-NOV-2002  
 LOCUS CA396195  
 DEFINITION c875b02.y1 Human Retinal pigment epithelium/choroid cDNA clone c875b02  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone c875b02  
 5', mRNA sequence.

ACCESSION CA396195  
 VERSION CA396195.1 GI:24732355

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 619)

Wistow,G., Bernstein,S.L., Wiatl,M.K., Faris,R.N., Behal,A.,  
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
 Expressed sequence tag analysis of human RPE/choroid for the  
 NEBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants

Mo1. Vis. 8 (4), 205-220 (2002)

JOURNAL MEDLINE  
 PUBMED

COMMENT

Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: gwieme@helix.nih.gov  
 Plate: 75 row: b column: 02  
 Seq primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers

## FEATURES

source

1..619  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="c875b02"  
 /tissue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMD10B"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the Superscript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>. The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

BASE COUNT 126 a 175 c 168 g 150 t

## ORIGIN

Alignment Scores: 102  
 Pred. No.: 53.00  
 Score: 53.00  
 Percent Similarity: 88.89%  
 Length: 619  
 Matches: 8  
 Conservative: 0

Best Local Similarity: 88.89%  
 Query Match: 91.38%  
 DB: 14  
 Gaps: 0

US-09-214-836-1 (1-9) x CA396195 (1-619)

QY 1 LysThrTPGlyGlnTYTTPAlaVal 9  
 DB 218 AAGACCTGGGGCCCACTGCGCAAGTT 244

## RESULT 25

BE384085 622 bp mRNA linear EST 21-JUL-2000  
 LOCUS BE384085  
 DEFINITION 601272888F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3614085 5',  
 mRNA sequence.

ACCESSION BE384085  
 VERSION BE384085.1 GI:9329450

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 622)

NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
 Plate: LNCM25 row: p column: 22  
 High quality sequence stop: 622.

Location/Qualifiers

## FEATURES

source

1..622  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3614085"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 20"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAAGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 145 a 151 c 180 g 146 t

## ORIGIN

Alignment Scores: 103  
 Pred. No.: 53.00  
 Score: 53.00  
 Percent Similarity: 88.89%  
 Best Local Similarity: 88.89%  
 Query Match: 91.38%  
 DB: 10  
 Gaps: 0

US-09-214-836-1 (1-9) x BE384085 (1-622)

QY 1 LysThrTPGlyGlnTYTTPAlaVal 9  
 DB 459 AAGACCTGGGGCCCACTGCGCAAGTT 485

Search completed: August 24, 2003, 03:57:09  
 Job time : 1903.5 secs

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:41 ; Search time 37 Seconds  
(without alignments)  
38.609 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGQYWAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	9	AAW45771	Melanoma associate
2	54	93.1	9	ABU57365	Gp100 peptide sequ
3	53	91.4	9	AAW78644	Immunogenic peptid
4	53	91.4	9	AAW77119	gp100/Pmel17 synth
5	53	91.4	9	AAW78850	PWEL 17 (Gp100) pr
6	53	91.4	9	AAW70010	Melanoma-associate
7	53	91.4	9	AAW54598	Peptide 3 from gp
8	53	91.4	9	AAW45777	Melanoma associate
9	53	91.4	9	AAW45770	Melanoma associate

10	53	91.4	9	20	AAV49663	Tumour antigenic p
11	53	91.4	9	20	AAV53524	Human melanoma Pme
12	53	91.4	9	20	AAV47616	Immunogenic peptid
13	53	91.4	9	20	AAV33172	Human gp100-Pmel11
14	53	91.4	9	20	AAV40211	Amino acid sequenc
15	53	91.4	9	20	AAV26867	Melanoma-derived 1
16	53	91.4	9	20	AAV01753	Exemplary antigen
17	53	91.4	9	20	AAV00715	Tumour antigen booc
18	53	91.4	9	21	AAV10449	HLA Class I motif
19	53	91.4	9	21	AAV33662	MHC class I associ
20	53	91.4	9	21	AAV3679	Cytotoxic T lympho
21	53	91.4	9	21	AAV08694	Antigenic peptide
22	53	91.4	9	21	AAV71520	Human gp100 Pmel11
23	53	91.4	9	21	AAV02622	Tumour associated
24	53	91.4	9	21	AAV08083	Human leukocyte an
25	53	91.4	9	21	AAV92299	gp100-Pmel117 anti
26	53	91.4	9	21	AAV84296	Tumour associated
27	53	91.4	9	21	AAV82979	gp100(Pmel117) tum
28	53	91.4	9	21	AAV56614	gp100-Pmel-117 gen
29	53	91.4	9	22	AAU71993	gp100 melanoma ant
30	53	91.4	9	22	AAU28928	gp100 immunogenic
31	53	91.4	9	22	AAE06841	Human gp100-Pmel11
32	53	91.4	9	22	AAE33758	Human Pmel 17 (Gp1
33	53	91.4	9	22	AAE02661	Human melanoma gp1
34	53	91.4	9	22	AAE02111	gp100 Pmel1 17 hum
35	53	91.4	9	22	AAE95908	MHC class-I associ
36	53	91.4	9	22	AAE00451	Human melanoma gp1
37	53	91.4	9	22	AAE31354	Exemplary antigen
38	53	91.4	9	23	AAE79994	Melanoma specific
39	53	91.4	9	23	AAE26789	Human gp100 (154-1
40	53	91.4	9	23	ABG79038	Human gp100 class
41	53	91.4	9	23	ABG80132	MHC class I molecu
42	53	91.4	9	23	AAO18864	Human gp100 protei
43	53	91.4	9	23	ABG66779	Tumour antigen Gp1
44	53	91.4	9	23	ABE76739	Tumour antigen epi
45	53	91.4	10	16	AAW78643	Immunogenic peptid

## ALIGNMENTS

RESULT 1	
AAW45771	standard; peptide: 9 AA.
AAW45771:	
22-JUN-1998	(first entry)
22-JUN-1998	Melanoma associated peptide analogue #2.
Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis; antigen; CTL; immunogenic; viral disease.	
Synthetic.	
OS Homo sapiens.	
W09802538-A1.	
22-JAN-1998.	
08-JUL-1997;	97W0-EP03712.
11-JUL-1996;	96EP-0201945.
(ALKU) AKZO NOBEL NV.	
Adema GJ, Figdor CG;	
WPI; 1998-110586/10.	
Melanoma associated peptide analogues - useful in vaccines against melanoma	

XX Claim 4; Figure 1; 47pp; English.  
PS  
CC This sequence represents a specifically claimed example of a novel  
CC peptide, which is immunogenic with lymphocytes directed against  
CC metastatic melanomas. It is characterised in that it comprises at least  
CC a part of the following sequence, where the amino acid at position 2 or 8  
CC is substituted: Lys-Thr-Trip-Gly-Gln-Tyr-Trip-Gln-Val. Vaccines comprising  
CC the peptide, or an epitope of the peptide, nucleotide sequence encoding the  
CC peptide, or an antigen presenting cell preloaded with the peptide or  
CC antibody as above, are useful for cancer, particularly melanoma,  
CC treatment. The peptides can also be used to generate antigen reactive  
CC tumour infiltrating lymphocytes, which can also be used in vaccines. The  
CC peptides can be exploited to elicit native epitope-reactive CTL. Usage  
CC of the peptides with improved immunogenicity may contribute to the  
CC development of CTL-epitope based vaccines in viral disease and cancer.

XX Sequence 9 AA;

Query Match 100.0%; Score 58; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
|||  
1 KTWGQYMAV 9

DB 1 KTWGQYMAV 9

RESULT 2  
ABUS7365  
ID ABUS7365 standard; Peptide; 9 AA.

AC ABUS7365;

DT 08-APR-2003 (first entry)

DE Gp100 peptide sequence.

XX MHC; major histocompatibility complex; human; cytostatic; anti-HIV;  
XX antiinflammatory; dermatological; antidiabetic; virucide;  
XX antileukosclerotic; antitumor; antineoplastic; antidiabetic; AIDS;  
XX antiproliferative; immunosuppressive; inflammatory; bowel disease; measles;  
XX Crohn's disease; ulcerative colitis; scleroderma; type 1 diabetes; pox;  
XX rheumatoid arthritis; psoriasis; atopic dermatitis; asthma; chicken pox;  
XX malignant melanoma; carcinoma; cancer; leukemia; lymphoma; hepatitis;  
XX rubella; herpes; human immunodeficiency virus.

OS Synthetic.

PN WO200272631-A2.

PD 19-SEP-2002.

PF 13-MAR-2002; 2002WO-DK00169.

PR 14-MAR-2001; 2001DK-0000435.

PR 14-MAR-2001; 2001DK-0000436.

PR 14-MAR-2001; 2001DK-0000441.

PR 14-MAR-2001; 2001US-275447P.

PR 14-MAR-2001; 2001US-275448P.

PR 14-MAR-2001; 2001US-275470P.

PA (DAKO-) DAKOCYTOMATION DENMARK AS.

PI (DYNA-) DYNAL BIOTECH ASA.

PI Winther L, Petersen LO, Buus S, Schoeller J, Raub E, Aamellem O;

DR WPI; 2002-759637/82.

XX New Major Histocompatibility Complex (MHC) molecule construct, useful

PT for treating, preventing, stabilizing or alleviating a disease

PT involving MHC recognizing cells e.g., cancer

XX

PS Example 1; Page 159; 304pp; English.

XX This invention relates to a new Major Histocompatibility Complex (MHC)  
CC molecule construct comprising a carrier molecule to which one or more  
CC MHC molecules are attached either directly or via one or more entities.  
CC The construct of the invention may have cytostatic, antineoplastic,  
CC dermatological, antidiabetic, antineoplastic, anti-HIV, virucide,  
CC antileukosclerotic, antitumor, antineoplastic, antidiabetic,  
CC antiproliferative and immunosuppressive activities and may be used in gene  
CC therapy. The MHC molecule construct is useful as a therapeutic  
CC composition in vivo or ex vivo therapy, for treating, preventing,  
CC stabilizing or alleviating a disease involving MHC recognizing cells,  
CC for monitoring MHC recognizing cells or establishing a prognosis of a  
CC disease or diagnosing a disease, or determining the status of a disease  
CC or the effectiveness of a medication against a disease, involving MHC  
CC recognising cells, e.g., chronic inflammatory bowel disease such as  
CC Crohn's disease or ulcerative colitis, scleroderma, type 1 diabetes,  
CC rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant  
CC melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the  
CC uterus, cervical cancer, prostate cancer, brain cancer, head and neck  
CC cancer, leukemia, cutaneous lymphoma, hepatic carcinoma, colorectal  
CC cancer, bladder cancer, rejection-related disease, graft-versus-host-  
CC related disease, or a viral disease associated with hepatitis, Acquired  
CC immunodeficiency Syndrome (AIDS), measles, pox, chicken pox, rubella or  
CC herpes. The MHC molecule construct is also useful for flow cytometry,  
CC histology or cytology. The present sequence represents a peptide  
CC used to create the MHC molecule construct of the invention.

XX Sequence 9 AA;

Query Match 93.1%; Score 54; DB 23; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
|||  
1 KTWGQYMAV 9

DB 1 KTWGQYMAV 9

RESULT 3  
AAR78644  
ID AAR78644 standard; Protein; 9 AA.

AC AAR78644;

DT 22-JAN-1996 (first entry)

DE Immunogenic peptide of melanoma associated antigen gp100.

XX Melanoma; antigen; vaccine; immunogen; primer; probe; detection;

XX identification; tumour; gp100.

OS Homo sapiens.

PN EP668350-A1.

PD 23-AUG-1995.

PF 14-FEB-1995; 95EP-0200348.

PR 21-DEC-1994; 94EP-0203709.

PR 16-FEB-1994; 94EP-0200337.

PA (ALKU) AKZO NOBEL NV.

PI Adema GJ, Figdor CG;

DR WPI; 1995-284790/38.

XX N-PSDB; AAQ96055.

XX Melanoma associated antigen gp100 - used in vaccines and for the

PT detection of tumours

XX



PS Claim 5, Page 31, 40pp; English.

CC Immunogenic peptides derived from the melanoma associated antigen  
 CC (See AAR7633-45) may be used in the production of vaccines.  
 CC Nucleotide sequences encoding the immunogenic peptides may be used  
 CC as primers and probes in the detection of melanoma cells. Tumour  
 CC infiltrating lymphocytes capable of binding to the melanoma  
 CC associated antigen can be cultured ex vivo and returned to melanoma  
 CC particles, and when radiolabelled, they may be used to identify  
 CC tumour deposits.

XX Sequence 9 AA;

SO Query Match 91.4%; Score 53; DB 16; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9  
 Db 1 KTWGQYMQV 9

RESULT 4  
 ID AAW77119 standard; peptide; 9 AA.  
 XX AAW77119;  
 AC AAW77119;  
 XX 16-NOV-1998 (first entry)  
 DT  
 DE gp100/Fmel17 synthetic peptide epitope 1.  
 XX  
 DE Tyrosinase; tyrosinase cytotoxic lymphocyte response;  
 KM cytotoxic T lymphocyte; cysteine-depleted; melanoma.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9833810-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 29-JAN-1998; 98WO-US01592.  
 XX  
 PR 30-JAN-1997; 97US-0037781.  
 XX  
 PA (UVVI-) UNIV VIRGINIA PATENT FOUND.  
 XX  
 PI Engelhard VH, Hunt DF, Kittlesen D, Slingluff CL;  
 DR WPI; 1998-437388/37.  
 XX  
 PT Disease specific immunogen - comprises disease specific cytotoxic T  
 PT lymphocyte epitope used to elicit melanoma specific CTL response  
 XX  
 PS Disclosure; Page 27; 93pp; English.

CC The peptide epitope AAW77119-W77138 were created for human  
 CC tumour-specific cytotoxic T lymphocyte response. These peptides are  
 CC cysteine-depleted mutants of a native disease-specific CTL epitope. The  
 CC cysteine-depleted CTL epitopes elicit a stronger or more specific CTL  
 CC response than the native epitope. The epitopes can be used in a  
 CC disease-specific immunogen to protect a mammal against disease in  
 CC particular melanomas. The peptides may also be used to screen a sample  
 CC for the presence of an antigen with the same epitope, or with a different  
 CC cross-reactive epitope.

XX Sequence 9 AA;

SO Query Match 91.4%; Score 53; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9  
 Db 1 KTWGQYMQV 9

Db 1 KTWGQYMQV 9

RESULT 5  
 ID AAW78850 standard; peptide; 9 AA.  
 XX AAW78850;  
 AC AAW78850;  
 XX 17-NOV-1998 (first entry)  
 DT  
 DE PML 17 (GP100) protein fragment 154-162.  
 XX  
 DE Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;  
 KM class II associated peptide; pathogen; gene therapy; genetic disease;  
 KM infection; downregulation; immune response.  
 XX  
 OS Homo sapiens.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9833398-A1.  
 XX  
 PD 23-JUL-1998.  
 XX  
 PF 22-JAN-1998; 98WO-US01499.  
 XX  
 PR 06-JAN-1998; 98US-0003253.  
 PR 22-JAN-1997; 97US-0787547.  
 XX  
 PA (PANG-) PANGAEA PHARM INC.  
 XX  
 PI Curley JM, Hedley ML, Langer RS, Lunsford LB;  
 DR WPI; 1998-427556/36.  
 XX  
 PT New preparations of microparticles - comprising a synthetic polymer  
 PT matrix and nucleic acid comprising an expression vector for use in  
 PT gene therapy  
 XX  
 PS Disclosure; Page 10; 101pp; English.

CC A microparticle preparation (MP) has been developed, consisting of  
 CC microparticles having a diameter of less than 100 mu m. The MP  
 CC comprises: (a) a polymeric matrix (PM) consisting of one or more  
 CC synthetic polymers having a solubility in water of less than 1 mg/l; and  
 CC (b) an expression vector selected from RNA molecules (at least 50% of  
 CC which are closed circles) or circular plasmid DNA (at least 50% of which  
 CC are supercoiled). Also described is a MP of at most 20 microns in  
 CC diameter, comprising: (a) a PM; and (b) a NAM comprising an expression  
 CC control sequence operatively linked to a coding sequence, where the  
 CC coding sequence encodes an expression product selected from: (1) a  
 CC polypeptide at least 7 amino acids in length, having a sequence identical  
 CC to the sequence of: (i) a fragment of a naturally-occurring mammalian  
 CC protein; or (ii) a fragment of a naturally-occurring protein from an  
 CC infectious agent which infects a mammal; (2) a peptide having a length  
 CC and sequence which permits it to bind to an MHC class I or II molecule;  
 CC and (3) the polypeptide or the peptide linked to a trafficking sequence.  
 CC AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for  
 CC use in the present invention. The MPs are highly effective vehicles for  
 CC the delivery of polynucleotides into phagocytic cells. They can be used  
 CC for gene therapy, e.g. for treating genetic diseases, infections or  
 CC tumours or for downregulating an immune response.

XX Sequence 9 AA;

SO Query Match 91.4%; Score 53; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9  
 Db 1 KTWGQYMQV 9

## RESULT 6

AAW70010

ID AAW70010 standard; peptide; 9 AA.

XX AAW70010;

DT 22-OCT-1998 (first entry)

DE Melanoma-associated antigen gp100 derived HLA-A2.1 binding peptide 1.

XX Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;  
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;  
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;  
 KW fungal infection; tuberculosis; melanoma; gp100.

XX Synthetic.

OS Homo sapiens.

XX MO983388-A1.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01959.

XX 31-JAN-1997; 97US-0036696.

XX (EPI-M-) EPIMUNE INC.

XX Cells E, Sette A, Sidney J, Southwood S, Teal V;

XX WPI; 1998-437445/37.

XX Production of antigen-specific cytotoxic T cells - by incubating  
 PT immunogenic peptide(s) from antigen that binds class I major  
 PT histocompatibility complex molecules with pre-created antigen  
 PT presenting cells

XX Example 4; Page 62; 104pp; English.

XX Sequences shown in AAW70010 to AAW70026 represent peptides derived from  
 CC melanoma-associated antigen gp100 that can bind to a human leukocyte  
 CC antigen (HLA), HLA-A2.1. The peptides are used to exemplify the method  
 CC of invention of producing antigen-specific cytotoxic T cells (CTLs) in  
 CC vitro. The method comprises contacting immunogenic peptides from an  
 CC antigen that binds class I major histocompatibility complex (MHC)  
 CC molecules with antigen presenting cells (APCs) pretreated with  
 CC pretreatment growth factors, and incubating the APCs with purified CD8  
 CC cells in the presence of at least 2 incubation growth factors, thereby  
 CC producing antigen-specific CTLs. A method for specifically killing  
 CC target cells in a human patient is also provided which comprises  
 CC obtaining a fluid sample containing CTLs from a patient, contacting the  
 CC cytotoxic T cells with APCs pretreated with pre-treatment growth  
 CC factors, where the APCs comprise class I MHC molecules. The pretreated  
 CC APCs are incubated with the cytotoxic growth factors, thereby producing  
 CC activated CTLs which are contacted with a carrier to form a composition.  
 CC The composition can then be administered to the patient. The activated  
 CC CTLs can be used for treating cancers, immune disorders, viral  
 CC infections, AIDS, hepatitis, bacterial infection, fungal infection,  
 CC malaria or tuberculosis.

XX Sequence 9 AA;

XX Query Match 91.4%; Score 53; DB 19; Length 9;

XX Best Local Similarity 88.9%; Pred. No. 9.3e+05;

XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9

Db 1 KTWGQYMAV 9

## RESULT 7

AAW54598

ID AAW54598 standard; peptide; 9 AA.

XX AAW54598;

DT 25-SEP-1998 (first entry)

DE Peptide 3 from gp 100/Pmel-17.

XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
 KW vaccine; treatment.

XX Synthetic.

XX MO9813378-A1.

XX 02-APR-1998.

XX 25-SEP-1997; 97WO-NL00536.

XX 26-SEP-1996; 96EP-0202701.

XX (UYLE-) RIJXSUNIV LEIDEN.

XX Drijfhout JW, Konig F;

XX WPI; 1998-230631/20.

XX Increasing uptake and presentation of antigen(s) - by adding mannose  
 PT residue(s) to antigen for increasing T cell response, useful in,  
 PT e.g. vaccines against viral infection(s)

XX Disclosure; Page 24; 47pp; English.

XX The peptides AAW54598-W54809 are examples of peptides to which at least  
 CC 1 (preferably 2) mannose can be attached to increase their uptake as  
 CC antigens by antigen-presenting cells. Uptake of agonist mannosylated  
 CC peptides will increase the T cell response, whereas uptake of antagonist  
 CC peptides blocks the T cell response. Blocking binding of immunogenic  
 CC autoantigens can be used in treatment of type I diabetes, rheumatoid  
 CC arthritis, graft rejection etc., also to induce T-cell non-  
 CC responsiveness. Vaccines containing mannosylated antigen are used to  
 CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths  
 CC and parasites.

XX Sequence 9 AA;

XX Query Match 91.4%; Score 53; DB 19; Length 9;

XX Best Local Similarity 88.9%; Pred. No. 9.3e+05; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9

Db 1 KTWGQYMAV 9

## RESULT 8

AAW5777

ID AAW5777 standard; peptide; 9 AA.

XX AAW5777;

XX 22-JUN-1998 (first entry)

DE Melanoma associated peptide analogue #8.

KW Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;  
 KW antigen; CTL; immunogenic; viral disease.

XX Synthetic.

OS Homo sapiens.

XX WO9802538-A1.  
 XX 22-JAN-1998.  
 PD  
 XX 08-JUL-1997; 97WO-EP03712.  
 PF  
 XX 11-JUL-1996; 96EP-0201945.  
 PR  
 XX (ALKU ) AKZO NOBEL NV.  
 PA  
 XX Adema GJ, Figdor CG;  
 XX WPI; 1998-110586/10.  
 DR  
 XX Melanoma associated peptide analogues - useful in vaccines against  
 PT melanoma  
 PT  
 XX Claim 4; Page 35; 47pp; English.  
 PS  
 XX This sequence represents a specifically claimed example of a novel  
 CC peptide, which is immunogenic with lymphocytes directed against  
 CC metastatic melanoma. It is characterised in that it comprises at least  
 CC a part of the following sequence, where the amino acid at position 2 or 8  
 CC is substituted: Lys-Thr-Tip-Gly-Gln-Tyr-Tip-Gln-Val. Vaccines comprising  
 CC the peptide, an epitope of the peptide, nucleotide sequence encoding the  
 CC peptide, or an antigen presenting cell preloaded with the peptide or  
 CC antibody as above, are useful for cancer, particularly melanoma.  
 CC treatment. The peptides can also be used to generate antigen reactive  
 CC tumour infiltrating lymphocytes, which can also be used in vaccines. The  
 CC peptides can be exploited to elicit native epitope-reactive CTL. Usage  
 CC of the peptides with improved immunogenicity may contribute to the  
 CC development of CTL-epitope based vaccines in viral disease and cancer.  
 XX  
 SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
 |||||  
 Db 1 KTWGQYMAV 9

RESULT 9  
 AAM45770  
 ID AAM45770 standard; peptide; 9 AA.  
 XX  
 AC AAM45770;  
 XX  
 DT 22-JUN-1998 (first entry)  
 XX  
 DE Melanoma associated peptide analogue #1.  
 XX  
 KW Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis;  
 KW antigen; CTL; immunogenic; viral disease.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9802538-A1.  
 PN  
 PD 22-JAN-1998.  
 PD  
 XX 08-JUL-1997; 97WO-EP03712.  
 PF  
 XX 11-JUL-1996; 96EP-0201945.  
 PR  
 XX (ALKU ) AKZO NOBEL NV.  
 PA  
 XX Adema GJ, Figdor CG;  
 XX

DR WPI; 1998-110586/10.  
 XX  
 XX Melanoma associated peptide analogues - useful in vaccines against  
 PT melanoma  
 PT  
 XX Claim 1; Figure 1; 47pp; English.  
 PS  
 XX This sequence represents a specifically claimed example of a novel  
 CC peptide, which is immunogenic with lymphocytes directed against  
 CC metastatic melanoma. It is characterised in that it comprises at least  
 CC a part of the following sequence, where the amino acid at position 2 or 8  
 CC is substituted: Lys-Thr-Tip-Gly-Gln-Tyr-Tip-Gln-Val. Vaccines comprising  
 CC the peptide, an epitope of the peptide, nucleotide sequence encoding the  
 CC peptide, or an antigen presenting cell preloaded with the peptide or  
 CC antibody as above, are useful for cancer, particularly melanoma.  
 CC treatment. The peptides can also be used to generate antigen reactive  
 CC tumour infiltrating lymphocytes, which can also be used in vaccines. The  
 CC peptides can be exploited to elicit native epitope-reactive CTL. Usage  
 CC of the peptides with improved immunogenicity may contribute to the  
 CC development of CTL-epitope based vaccines in viral disease and cancer.  
 XX  
 SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
 |||||  
 Db 1 KTWGQYMAV 9

RESULT 10  
 AAY49663  
 ID AAY49663 standard; peptide; 9 AA.  
 XX  
 AC AAY49663;  
 XX  
 DT 14-JAN-2000 (first entry)  
 XX  
 DE Tumour antigenic peptide SEQ ID NO:30.  
 XX  
 DE Human; scdp3.10; SAGE; scdp3.8; HAGE; scdp3.5; TRAP; sarcoma;  
 KW tumour rejection antigen precursor; tumour associated nucleic acid;  
 KW carcinoma; cancer; immune response; diagnosis.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9953061-A2.  
 PN  
 PD 21-OCT-1999.  
 PD  
 XX 14-APR-1999; 99WO-US08163.  
 PF  
 XX 15-APR-1998; 98US-0060706.  
 PR  
 XX 27-JUL-1998; 98US-0122989.  
 PR  
 XX 30-OCT-1998; 98US-0183706.  
 PR  
 XX 30-OCT-1998; 98US-0183789.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PA Martelange V, De Smet C, Boon-Falleur T;  
 XX  
 DR WPI; 1999-620430/53.  
 DR  
 XX New nucleic acid encoding sarcoma-associated gene products, useful for  
 XX diagnosing, e.g. treating and preventing cancer  
 PT  
 XX Disclosure; Page 25; 93pp; English.  
 PS  
 XX The present invention describes sarcoma-associated gene products (I).  
 CC Agents, specifically sarcoma associated nucleic acids (II) or their  
 CC expression products that are tumour rejection antigens (TRA), that

CC selectively increase formation of HLA (human leucocyte antigen)/(I)  
 CC complexes are used for treating cancer, especially sarcoma and  
 CC carcinoma, in humans and other animals. Compositions containing  
 CC autologous cytolytic T cells (CTL), specific for the HLA(I) complex,  
 CC are similarly useful, also transformed cells that stimulate such CTL  
 CC in vivo. (II) are also used: (i) as source of therapeutic antisense  
 CC sequences that reduce expression of (II); (ii) for recombinant  
 CC production of (I); (iii) particularly its fragments, as primers and  
 CC probes in usual hybridisation and amplification assays, for diagnosis,  
 CC prognosis and monitoring of tumours, or for measuring binding  
 CC specificity of HLA molecules or CTL clones; (iv) to identify related  
 CC sequences; and (v) for generating transgenic animals, e.g. for studying  
 CC cancer and immune responses to it. (I) are used to raise specific  
 CC antibodies (Ab) and therapeutically. Ab are used to diagnose tumours in  
 CC immunosays, also for delivering drugs, toxins, imaging agents etc. to  
 CC (I)-expressing cells. AAY49637 to AAY49670 represent exemplary tumour  
 CC antigenic peptides given in the present invention.

XX SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
 |||||  
 1 KTWGQYMQV 9

RESULT 11  
 AAY53524  
 ID AAY53524 standard; Protein; 9 AA.

XX AC AAY53524;

XX DT 18-JAN-2000 (first entry)

XX DE Human melanoma Pmel17 (gp100) (aa 154-162) binds HLA-A2.

XX KM Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;  
 XX electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;  
 XX human immunodeficiency virus; hepatitis B virus; papilloma virus;  
 XX melanoma; malaria; parasite.

XX OS Synthetic.  
 XX Homo sapiens.

XX PN FR2776926-A1.

XX PD 08-OCT-1999.

XX PF 07-APR-1998; 98FR-0004323.

XX PR 07-APR-1998; 98FR-0004323.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PA (INSP) INST PASTEUR LILLE.

XX PI Le Gal PA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;

XX DR WPI; 1999-583113/50.

XX PT New lipopeptide containing lipid regions and two epitopes, all  
 XX separated by peptide spacers that impart hydrophilicity, useful in  
 XX vaccines -  
 XX PS Disclosure; Page 24; 35pp; French.

XX CC The invention relates to the generation of a lipopeptide comprising at  
 CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)  
 CC epitope and at least one lipid residue with (i) the epitopes and lipid  
 CC portion and (ii) the epitopes, being separated independently by peptide

CC spacers. These spacers comprise sequences of amino acids which carry an  
 CC overall electrical charge in neutral media to ensure that the  
 CC lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents  
 CC examples of peptide epitopes used to generate the lipopeptides. These are  
 CC used in therapeutic or prophylactic compositions and vaccines to induce  
 CC specific immune responses against human immunodeficiency, hepatitis B or  
 CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
 |||||  
 1 KTWGQYMQV 9

RESULT 12  
 AAY47616  
 ID AAY47616 standard; Peptide; 9 AA.

XX AC AAY47616;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2227.

XX KM Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 XX immune response; T cell activation; major histocompatibility complex;  
 XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 XX vaccine; immunisation.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9945954-A1.

XX PD 16-SEP-1999.

XX PF 13-MAR-1998; 98WO-US05039.

XX PR 13-MAR-1998; 98WO-US05039.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX DR WPI; 1999-551214/46.

XX PT New immunogenic peptides with HLA binding motif, useful in treatment  
 XX and diagnosis of cancers and viral diseases -  
 XX PS Claim 1; Page 116; 150pp; English.

XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also

CC useful diagnostically, and can be used to induce a cytotoxic T cell  
CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
CC produce CTLs ex vivo for infusion back into a patient. The  
CC polynucleotides encoding the immunogenic peptides are also useful  
CC therapeutically and for immunisation as above.

XX Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMQV 9

RESULT 13

AAV33172  
ID AAV33172 standard; peptide; 9 AA.

XX AAV33172;

XX 17-NOV-1999 (first entry)

XX Human gp100-Pmel117 peptide #1.

XX Human; protein delivery; Yersinia sp.; effector gene; mutant; antigen;

XX immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;

XX pathological disorder; gp100-Pmel117.

XX Homo sapiens.

XX WO9945098-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-1B00587.

XX 06-MAR-1998; 98US-0036582.

XX (YBRU/) VAN DER BRUGGEN P B.

XX (CORN/) CORNELIS G R.

XX (BOLA/) BOLAND A M.

XX (BOON/) BOON-FALLEUR T R.

XX Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Falleur TR;

XX WPI; 1999-540840/45.

XX New mutant Yersinia strains useful for treating a pathological disorder

XX Example 1; Page 71, 80pp; English.

XX This invention describes a novel mutant Yersinia (Y1) strain, comprising

XX mutation(s) in effector-encoding gene(s) and deficient in the production

XX of functional effector protein(s). The invention describes (1) a

XX quintuple mutant Yersinia strain, having the designation Yersinia

XX enterocolitica yopEHOMP or Yersinia pseudotuberculosis yopEHAOU; (2) an

XX expression vector (EV1) for delivering a heterologous protein into a

XX eukaryotic cell, comprising in the 5'-3' direction; (3) a Yersinia or

XX mutant Yersinia strain for delivering a heterologous protein into a

XX eukaryotic cell, comprising contacting the cell with a Y1 transformed

XX with the above vector (Y1-EV1); (4) a method for delivering a

XX heterologous protein into a eukaryotic cell, comprising contacting the

XX cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method

XX for inducing an immune response specific for a heterologous protein; (6)

XX a method for inducing a cytotoxic T-lymphocyte (CTL) response specific

XX for a heterologous protein; (7) a method for determining the efficacy of

XX an antigen vaccination regimen in a subject. Y1 is used to treat a

XX pathological disorder, by providing recombinant Yersinia for the safe

XX delivery of proteins into eukaryotic cells. AAV33147-Y33178 are

XX human-derived peptides used to illustrate the method of the invention.

XX Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMQV 9

RESULT 14

AAV40211  
ID AAV40211 standard; Peptide; 9 AA.

XX AAV40211;

XX 19-NOV-1999 (first entry)

XX Amino acid sequence of a human melanoma epitope.

XX Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;

XX CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;

XX vaccine; tumor; infection; immune response; cytokine profile;

XX acquired immune deficiency syndrome; papilloma; cancer; hepatitis;

XX autoimmune disease.

XX Homo sapiens.

XX FR2774687-A1.

XX 13-AUG-1999.

XX 06-FEB-1998; 98FR-0001439.

XX 06-FEB-1998; 98FR-0001439.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX (INSP) INST PASTEUR LILLE.

XX Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Ieing E;

XX WPI; 1999-510734/43.

XX New lipopeptide comprising C-terminal interferon-gamma fragment with

XX attached lipophilic groups, used as interferon mimic, e.g. for treating

XX cancer or virus infection

XX Disclosure; Page 35; 53pp; French.

XX AA40123-Y40379 represent epitopes that are able to activate cytotoxic

XX T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or

XX B epitopes recognized by corresponding antibodies. The epitopes may be

XX used in the composition of the invention. The specification describes a

XX lipopeptide that has a peptide part derived from mammalian interferon

XX gamma (IFNg) and one or more lipophilic parts comprising a linear or

XX branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The

XX lipopeptide mimics the activity of IFNg. Compositions comprising the

XX lipopeptide are used to treat or prevent any condition that responds

XX to IFNg, and as adjuvant for vaccines (particularly those directed

XX against tumors, viral or parasitic infections), to stimulate or

XX (re)orient the immune response between types 1 and 2 cytokine profiles.

XX Particular applications are treatment of infections (particularly

XX viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and

XX hepatitis, but also bacterial, fungal, parasitic or helminth); cancers

XX (particularly of kidney, cutaneous T cells or ovary, chronic

XX myelogenous leukemia or mesothelioma), allergy; and autoimmune

XX diseases.

XX Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTWGQYNAV 9  
| | | | |  
Db 1 KTWGQYMQV 9

## RESULT 15

AAV26867 standard; peptide; 9 AA.

XX AAV26867;

DT 14-SEP-1999 (first entry)

DE Melanoma-derived lipopeptide epitope #8 for mixed micelles.

XX Micelle; microaggregate; induction; immune response; lipopeptide; CTL;

KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;

KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;

XX melanoma; Plasmodium falciparum; malaria.

XX Synthetic.

OS Homo sapiens.

XX FR2771640-A1.

PD 04-JUN-1999.

XX 03-DEC-1997; 97FR-0015246.

PR 03-DEC-1997; 97FR-0015246.

XX 03-DEC-1997; 97FR-0015246.

PA (CNRS ) CNRS CENT NAT RECH SCI.

PA (INSM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP ) INST PASTEUR LILLE.

PI Bousset M, Bourguet VI, Gras-Masse H, Guillet JG, Lippens G;

PI Tartar A, Wieruszski JM;

DR WPI; 1999-349509/30.

XX Immunogenic lipopeptide micelles - comprising lipopeptides

XX containing cytotoxic and helper T-lymphocyte epitopes

XX Disclosure; Page 37; 60pp; French.

XX The invention relates to the generation of mixed micelles or

CC microaggregates for inducing an immune response comprising: (a) a first

CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope

CC and at least one lipid unit; and (b) a second lipopeptide comprising at

CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit

CC different from that of the first lipopeptide. This peptide represents

CC an example of a lipopeptide epitope used in the invention and is derived

CC from a human melanoma protein. The immunogenic lipopeptide micelles

CC are used in vaccines, especially against HIV, hepatitis B virus (HBV),

CC papilloma viruses, p53, melanoma or Plasmodium falciparum malaria.

XX SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTWGQYNAV 9  
| | | | |  
Db 1 KTWGQYMQV 9

## RESULT 16

AAV01753 standard; Peptide; 9 AA.

XX AAV01753;

XX 25-JUN-1999 (first entry)

DT Exemplary antigenic peptide derived from gp100(Pmel117).

XX MAGE-3; tumour associated gene; human leucocyte antigen Class II;

KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;

KW osteosarcoma; leukemia; carcinoma.

XX Homo sapiens.

OS WO9914326-A1.

XX 25-MAR-1999.

PD 04-SEP-1998; 98WO-US18601.

XX 12-SEP-1997; 97US-0928615.

PR (LUDM-) LUDMIG INST CANCER RES.

PA (UYVR-) UNIV VRIJE BRUSSEL.

XX Boon-Falleur T, Chaux P, Cortals J, Heirman G;

PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;

XX WPI; 1999-244031/20.

DR Isolated peptides that bind to human leucocyte antigen class II

XX molecules

XX Disclosure; Page 29; 88pp; English.

XX The present sequence represents an exemplary tumour associated peptide

CC antigen. The specification describes a MAGE-3 tumour associated gene.

CC Peptides (AAV01721-25) that bind human leucocyte antigen (HLA) Class II

CC molecules can be derived from the MAGE-3 protein. These peptides and

CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide

CC and HLA Class II, are used to treat MAGE-3 related diseases.

CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and

CC various forms of carcinoma). The peptides are also used to produce

CC specific antibodies. Detection of of the peptides, e.g. in binding

CC assays, particularly with antibodies, is used for diagnosis of such

XX diseases.

XX SQ Sequence 9 AA;

Query Match 91.4%; Score 53; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTWGQYNAV 9  
| | | | |  
Db 1 KTWGQYMQV 9

## RESULT 17

AAV00715 standard; peptide; 9 AA.

XX AAV00715;

XX 12-MAY-1999 (first entry)

DT Tumour antigen booster peptide gp100Pmel117 HLA-A2 #1.

XX Tumour antigen; booster peptide; immune response modulation; allergy;

KW immune response enhancer; tumour cell; tumour rejection antigen;

KW leukocyte antigen-presenting molecule; autoimmune disease;

KW allograft rejection.

XX Homo sapiens.



XX  
CO

CONFERENCE

100



Query Match 91.4%; Score 53; DB 21; Length 9;  
Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
DB 1 KTWGQYMAV 9

## RESULT 22

AA71520  
ID AA71520 standard; peptide; 9 AA.

AA71520;

12-OCT-2000 (first entry)

Human gp100 Pmel17 nonapeptide-1.

gp100 Pmel17; human; Tumour Rejection Antigen; TRA; tumour; cancer;  
HLA; Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;  
cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;  
diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.

Homo sapiens.

WO200032769-A2.

08-JUN-2000.

26-NOV-1999; 99WO-IB02018.

27-NOV-1998; 98GB-0026143.

(LUDW-) LUDWIG INST CANCER RES.

Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;

WPI; 2000-412317/35.

Novel polypeptides expressed in tumor cells useful for treating cancers  
have an ability to complex with a major histocompatibility complex  
molecule and comprises a specific undbroken amino acid sequence -  
Disclosure; Page 20; 80pp; English.

The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and  
decapeptide sequences, that function as tumour rejection antigens  
(TRAs). These peptides are capable of forming a complex with major  
histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte  
Antigen), that are recognised by T-lymphocytes and elicit an immune  
response from cytolytic T-lymphocytes (CTL). They function as an immune  
response stimulator. Tumour rejection antigens are useful in prophylaxis,  
therapy and diagnosis of tumours and are effective in controlling or  
preventing tumour growth. The present sequence is the human gp100 Pmel17  
nonapeptide-1, that corresponds to residues 154-162 of the tumour  
associated gene, gp100 Pmel17 encoding protein. It can be administered  
to induce or enhance an immune response and is presented by HLA-A2  
complex. This peptide can serve as a tumour rejection antigen (TRA) and  
in combination with adjuvants, can produce vaccines useful for treating  
a variety of tumours.

Sequence 9 AA;

Query Match 91.4%; Score 53; DB 21; Length 9;

Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
DB 1 KTWGQYMAV 9

RESULT 23  
AAB02622  
ID AAB02622 standard; peptide; 9 AA.

AAB02622;

18-AUG-2000 (first entry)

Tumour associated peptide antigen from gp100 #2.

MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
cancer; human; tumour; tumour associated gene product.

Homo sapiens.

WO2000020581-A1.

13-APR-2000.

15-SEP-1999; 99WO-US21230.

05-OCT-1998; 98US-0166448.

(LUDW-) LUDWIG INST CANCER RES.

(UYVR-) UNIV VRIJE BRUSSEL.

Chaux P, Stroobant V, Boon-Pallieur T, Van Der Bruggen P;

Schultz ES, Van Snick J, Lethe B, Thielemans K, Cortalais J;

Heitman C;

WPI; 2000-317713/27.

New MAGE-A3 class II binding peptides, useful to diagnose and treat  
tumours, are fragments of MAGE-A3 which bind to and are presented to T  
lymphocytes by human leukocyte antigen class II molecules -  
Disclosure; Page 33; 119pp; English.

The present invention relates to MAGE-A3 (tumour associated gene  
product) human leukocyte antigen (HLA) class II-binding peptides (see  
AAB02566-B02585, and AAB02633-B02637). These peptides are presented to T  
cells in the context of HLA class II molecules. The peptides stimulate  
the activity and proliferation of CD4+ T lymphocytes. The invention also  
includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928  
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used  
to create antibodies against the MAGE-A3 peptides, the antibodies, the  
peptides and nucleotide sequences can be used to create a vaccine. The  
peptides are used to diagnose or treat a disorder characterized by  
expression of MAGE-3, particularly cancer. The methods can also be used  
in the diagnosis of disorders associated with MAGE-3 expression. Included  
in the invention are other human tumour antigens (see AAB02596-B02637)  
and PCR primers used in the course of the invention (see AAA37929-A37937  
and AAA37941-A37942).

Sequence 9 AA;

Query Match 91.4%; Score 53; DB 21; Length 9;

Best Local Similarity 88.9%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
DB 1 KTWGQYMAV 9

## RESULT 24

AA90803  
ID AA90803 standard; peptide; 9 AA.

AA90803;

25-AUG-2000 (first entry)

```

DE Human leukocyte antigen A2 gp100-Pmel117 peptide SEQ ID NO:32.
XX
XX Human leukocyte antigen; HLA-B35; binding; recognition; lysis;
KM cytolytic T cell; tyrosinase; immune response; diagnosis;
XX identification; human.
XX
OS Homo sapiens.
XX
PN WO200021551-A1.
XX
PD 20-APR-2000.
XX
PF 04-OCT-1999; 99WO-US23038.
XX
PR 09-OCT-1998; 98US-0169717.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Ooms A, De Giovanni G, Morel S, Van Den Eynde B, Boon-Falleur T;
XX
PI WPI; 2000-317842/27.
XX
DR WPI; 2000-317842/27.
XX
XX Isolated peptides, sometimes derived from tyrosinase, which bind to
PT HLA-B35 leading to recognition and lysis of the resulting complexes by
PT cytolytic T cells -
XX
PS Example 3; Page 9; 20pp; English.
XX
XX The present invention describes isolated peptides which bind to human
CC leukocyte antigen (HLA)-B35 molecules leading to recognition and lysis
CC of the resulting complexes by cytolytic T cells. The isolated peptides
CC are sometimes derived from tyrosinase. Compositions comprising the
CC peptides of the invention can be used to generate immune responses,
CC preferably in humans, but also in non-human animals to generated immune
CC components which can then be used to treat humans or diagnostically.
CC Therapeutically, the peptides are useful in generation of cytolytic T
CC cells either in vitro or in vivo which specifically lyse pathogenic
CC cells. The peptides can also be used to identify HLA-B35 positive
CC cells, or to remove HLA-B25 positive cells from mixtures containing
CC such cells. Nucleic acid molecules encoding the peptides can be used
CC inter alia as probes to identify cells which are expressing tyrosinase.
CC The present sequence represents an HLA binding peptide used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;

```

```

Query Match 91.4%; Score 53; DB 21; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 KTWGQYMAV 9
Db 1 KTWGQYMOV 9

```

```

RESULT 25
AA92229
ID AA92229 standard; peptide; 9 AA.
XX
XX AA92229;
AC
XX
XX 10-AUG-2000 (first entry)
DT
XX
XX gp100-Pmel17 antigenic peptide epitope (residues 154-162).
DE
XX
XX gp100-Pmel17; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;
KM human leukocyte antigen; HLA.
XX
XX Homo sapiens.
OS
XX
XX WO200020445-A2.
PN
XX
XX 13-APR-2000.
PD

```

```

XX
XX 15-SEP-1999; 99WO-IB01664.
PF
XX
XX 02-OCT-1998; 98US-0165863.
PR
XX
XX 09-APR-1999; 99US-0289350.
XX
XX (CHAU/) CHAUD P.
PA
XX (LUIT/) LUITEN R.
PA
XX (DEMO/) DEMOTTE N.
PA
XX (DUFF/) DUFFOUR M.
PA
XX (LURQ/) LURQUIN C.
PA
XX (TRAV/) TRAVERSARI C.
PA
XX (STRO/) STROOBANT V.
PA
XX (COEN/) CORNELIS G R.
PA
XX (BOON/) BOON-FALLEUR T.
PA
XX (VERU/) VAN DER BRUGEN P.
XX
XX Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;
PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;
PI Schultz E, Warner G;
XX
XX WPI; 2000-303739/26.
XX
XX Isolation of cytotoxic T-lymphocytes clones by successive steps of
PT stimulation and testing of lymphocytes with antigen presenting cells
PT which present antigens derived from different expression systems
XX
XX Disclosure; Page 22; 99pp; English.
XX
XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
CC comprises successive steps of stimulation and testing of lymphocytes
CC with antigen presenting cells (APCs) which present antigens derived
CC from different expression systems. The CTL clones isolated recognize
CC specific antigenic peptides of proteins, preferably of the MAGS family.
CC The APC is autologous and each expression system is different from at
CC least one of the other expression systems, therefore isolating a
CC cytotoxic T cell clone specific for the protein. The method can also be
CC used to identify an antigenic peptide epitope. Isolated CTL clones
CC specific for a peptide/human leukocyte antigen (HLA) complex are claimed.
CC The CTL cells specific for the complexes, peptides or cells which present
CC the complexes on the cell surface are useful for treating pathological
CC conditions characterized by abnormal expression of the complexes.
XX
SQ Sequence 9 AA;

```

```

Query Match 91.4%; Score 53; DB 21; Length 9;
Best Local Similarity 88.9%; Pred. No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 KTWGQYMAV 9
Db 1 KTWGQYMOV 9

```

```

Search completed: August 14, 2003, 09:11:30
Job time : 39 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 20.5 seconds

(without alignments)  
18.575 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGQYWAY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_Aa.\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/1aa/backfltest.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	91.4	9	1	US-08-787-547-61
2	53	91.4	9	2	US-08-417-174-46
3	53	91.4	9	2	US-08-902-516-29
4	53	91.4	9	2	US-09-036-582-26
5	53	91.4	9	3	US-09-183-706-30
6	53	91.4	9	3	US-09-267-439-46
7	53	91.4	9	3	US-09-166-448-71
8	53	91.4	9	3	US-09-567-995-30
9	53	91.4	9	4	US-09-165-863-26
10	53	91.4	9	4	US-09-697-884-71
11	53	91.4	9	4	US-09-847-185-29
12	53	91.4	9	4	US-08-388-852B-22
13	53	91.4	9	4	US-09-289-350-26
14	53	91.4	9	4	US-09-073-138-46
15	53	91.4	9	4	US-09-574-749B-27
16	53	91.4	9	4	US-09-341-982-82
17	53	91.4	10	2	US-08-417-174-47
18	53	91.4	10	3	US-09-267-439-47
19	53	91.4	10	4	US-08-388-852B-21
20	53	91.4	10	4	US-09-073-138-47
21	53	91.4	11	4	US-08-388-852B-20
22	53	91.4	12	4	US-08-388-852B-10
23	53	91.4	661	3	US-08-417-174-121
24	53	91.4	661	3	US-09-267-439-121
25	53	91.4	661	4	US-08-388-852B-2
26	53	91.4	661	4	US-09-073-138-121
27	53	91.4	668	1	US-07-891-942G-6

28	50	86.2	661	2	US-08-417-174-27	Sequence 27, Appl
29	50	86.2	661	2	US-08-231-565A-27	Sequence 27, Appl
30	50	86.2	661	2	US-09-007-961-27	Sequence 27, Appl
31	50	86.2	661	3	US-09-267-439-27	Sequence 27, Appl
32	50	86.2	661	4	US-09-073-138-27	Sequence 27, Appl
33	48	82.8	8	4	US-08-388-852B-8	Sequence 8, Appl
34	48	82.8	9	2	US-08-417-174-71	Sequence 72, Appl
35	48	82.8	9	2	US-08-417-174-72	Sequence 72, Appl
36	48	82.8	9	2	US-08-417-174-73	Sequence 74, Appl
37	48	82.8	9	2	US-08-417-174-74	Sequence 75, Appl
38	48	82.8	9	2	US-08-417-174-75	Sequence 71, Appl
39	48	82.8	9	3	US-09-267-439-71	Sequence 72, Appl
40	48	82.8	9	3	US-09-267-439-72	Sequence 73, Appl
41	48	82.8	9	3	US-09-267-439-73	Sequence 74, Appl
42	48	82.8	9	3	US-09-267-439-74	Sequence 75, Appl
43	48	82.8	9	3	US-09-267-439-75	Sequence 73, Appl
44	48	82.8	9	4	US-08-388-852B-23	Sequence 71, Appl
45	48	82.8	9	4	US-09-073-138-71	Sequence 72, Appl

## ALIGNMENTS

RESULT 1  
US-08-787-547-61  
Sequence 61, Application US/08787547  
Patent No. 5783567  
GENERAL INFORMATION:  
APPLICANT: Hedley, Mary Lynne  
APPLICANT: Curley, Joanne M.  
APPLICANT: Langer, Robert S.  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY  
TITLE OF INVENTION: OF NUCLEIC ACID  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: PastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/787,547  
FILING DATE: 22-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-787-547-61

Query Match 91.4%; Score 53; DB 1; Length 9;  
Best Local Similarity 86.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0;



APPLICANT: De Smet, Charles  
APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
FILE REFERENCE: 10461/7054  
CURRENT APPLICATION NUMBER: US/09/183,706  
CURRENT FILING DATE: 1998-10-30  
EARLIER APPLICATION NUMBER: 09/122,989  
EARLIER FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 43  
SEQ ID NO 30  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-183-706-30

Query Match 91.4%; Score 53; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 6  
US-09-267-439-46

Sequence 46, Application US/09267439  
Patent No. 6270778

GENERAL INFORMATION:

APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE

CITY: NEW YORK  
STATE: NEW YORK

COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439

FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPE

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9  
TYPE: amino acid

STRANDEDNESS: Unknown  
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide  
US-09-267-439-46

Query Match 91.4%; Score 53; DB 3; Length 9;

Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 7  
US-09-166-448-71

Sequence 71, Application US/09166448  
Patent No. 6291430

GENERAL INFORMATION:

APPLICANT: Chaux, Pascal  
APPLICANT: Vanlomme, Valrie

APPLICANT: Stroobant, Vincent  
APPLICANT: Boon-Falleur, Thierry

APPLICANT: Van der Bruggen, Pierre  
APPLICANT: Thielemans, Kris

APPLICANT: Corhals, Jurgen  
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES

FILE REFERENCE: 10461/7052

CURRENT APPLICATION NUMBER: US/09/166,448

CURRENT FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 81

SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 71

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-166-448-71

Query Match 91.4%; Score 53; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 8  
US-09-567-995-30

Sequence 30, Application US/09567995  
Patent No. 6303756

GENERAL INFORMATION:

APPLICANT: Martelange, Valrie  
APPLICANT: De Smet, Charles

APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR

FILE REFERENCE: 10461/7054

CURRENT APPLICATION NUMBER: US/09/567,995

CURRENT FILING DATE: 2000-05-10

PRIOR APPLICATION NUMBER: 09/183,706

PRIOR FILING DATE: 1998-10-30

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 30

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-567-995-30

Query Match 91.4%; Score 53; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 9  
US-09-165-863-26

US-09-165-863-26

```
; Sequence 26, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Dufour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chaux, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 11727
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human gp100Pmel117 peptide
US-09-165-863-26

Query Match          91.4%; Score 53; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KTWGQYMAV 9
    |||||
    1 KTWGQYMAV 9
```

```
RESULT 10
US-09-697-884-71
```

```
; Sequence 71, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vanomme, Val'rie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-697-884-71
```

```
Query Match          91.4%; Score 53; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KTWGQYMAV 9
    |||||
    1 KTWGQYMAV 9
```

```
RESULT 11
US-09-847-185-29
; Sequence 29, Application US/09847185
; Patent No. 6482407
```

```
; GENERAL INFORMATION:
; APPLICANT: Soc Hoc, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1M 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-847-185-29

Query Match          91.4%; Score 53; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KTWGQYMAV 9
    |||||
    1 KTWGQYMAV 9
```

```
RESULT 12
US-08-388-852B-22
```

```
; Sequence 22, Application US/08388852B
; Patent No. 6500919
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide,
; comprising thereof and vaccine against melanoma.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav
; STREET: Philips van Leydenlaan 25
; CITY: Nijmegen
; STATE: Brabant
; COUNTRY: the Netherlands
; ZIP: 6525 EX
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,852B
```

;; FILING DATE: February 15, 1995  
;; INFORMATION FOR SEQ ID NO: 22:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
US-08-388-852B-22

Query Match 91.4%; Score 53; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMOV 9

RESULT 13  
US-09-289-350-26  
; Sequence 26, Application US/09289350  
; Patent No. 6531451  
; GENERAL INFORMATION:  
; APPLICANT: Chauv, Pascal  
; APPLICANT: Luitien, Rosalie  
; APPLICANT: Defout, Marie-Therese  
; APPLICANT: Lurquin, Christophe  
; APPLICANT: Traversari, Catia  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Cornelis, Guy R.  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: Van Der Bruggen, Pierre  
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
; TITLE OF INVENTION: PROCEDURE  
; FILE REFERENCE: 117272  
; CURRENT APPLICATION NUMBER: US/09/289,350  
; CURRENT FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 09/165,863  
; PRIOR FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human GP100Pmel117 peptide  
US-09-289-350-26

Query Match 91.4%; Score 53; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMOV 9

RESULT 14  
US-09-073-138-46  
; Sequence 46, Application US/09073138  
; Patent No. 6537560  
; GENERAL INFORMATION:  
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
; APPLICANT: STEVEN A.  
; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 126  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: MORGAN & PINNEGAN, L.L.P.

;; STREET: 345 PARK AVENUE  
;; CITY: NEW YORK  
;; STATE: NEW YORK  
;; COUNTRY: USA  
;; ZIP: 10154

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: FLOPPY DISK  
;; COMPUTER: IBM PC COMPATIBLE  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: ASCII  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/073,138  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/417,174  
;; FILING DATE: 05-APR-1995

;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CAROL M. GRUPE  
;; REGISTRATION NUMBER: 37,341  
;; REFERENCE/DOCKET NUMBER: 2026-4124US1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 758-4800  
;; TELEFAX: (212) 751-6849  
;; TELE: 421792

;; INFORMATION FOR SEQ ID NO: 46:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9  
;; TYPE: amino acid  
;; STRANDEDNESS: Unknown  
;; TOPOLOGY: Unknown  
;; MOLECULE TYPE: Peptide  
US-09-073-138-46

Query Match 91.4%; Score 53; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMOV 9

RESULT 15  
US-09-574-749B-27  
; Sequence 27, Application US/09574749B  
; Patent No. 6548299  
; GENERAL INFORMATION:  
; APPLICANT: ROSENZWEIG, Michael  
; APPLICANT: PYKETT, Mark J.  
; APPLICANT: SCADDEN, David T.  
; APPLICANT: POZNANSKY, Mark C.  
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
; TITLE OF INVENTION: DEVICES  
; FILE REFERENCE: C1005/7012/KA/ERG  
; CURRENT APPLICATION NUMBER: US/09/574,749B  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: PCT/US99/26795  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/524,749  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo Sapiens source  
US-09-574-749B-27

Query Match 91.4%; Score 53; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
|||||  
1 KTWGQYMOV 9

RESULT 16  
US-09-341-982-82

; Sequence 82, Application US/09341982  
; Patent No. 6558671  
; GENERAL INFORMATION:

; APPLICANT: SLINGLUFF, Craig L.

; APPLICANT: HUNT, Donald F.

; APPLICANT: ENGELHARD, Victor H.

; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR

; FILE REFERENCE: SLINGLUFF-3B

; CURRENT APPLICATION NUMBER: US/09/341,982

; CURRENT FILING DATE: 1999-09-20

; EARLIER APPLICATION NUMBER: PCT/US98/01592

; EARLIER FILING DATE: 1998-01-29

; EARLIER APPLICATION NUMBER: 60/037,781

; EARLIER FILING DATE: 1997-01-31

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 82

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Description of Artificial Sequence: Fragment of

; OTHER INFORMATION: human protein

US-09-341-982-82

Query Match 91.4%; Score 53; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
|||||  
1 KTWGQYMOV 9

RESULT 17  
US-08-417-174-47

; Sequence 47, Application US/08417174  
; Patent No. 5844075  
; GENERAL INFORMATION:

; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

; APPLICANT: STEVEN A.

; TITLE OF INVENTION: MELANOMA ANTIGENS AND

; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 126

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/417,174

; FILING DATE: 05-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/231,565  
; FILING DATE: 22-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

; NAME: CAROL M. GRUPPI

; REGISTRATION NUMBER: 37,341

; REFERENCE/DOCKET NUMBER: 2026-4124US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10

; TYPE: amino acid

; STRANDEDNESS: Unknown

; TOPOLOGY: Unknown

; MOLECULE TYPE: Peptide

US-08-417-174-47

Query Match 91.4%; Score 53; DB 2; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.021;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
|||||  
1 KTWGQYMOV 9

RESULT 18  
US-09-267-439-47

; Sequence 47, Application US/09267439  
; Patent No. 6270778  
; GENERAL INFORMATION:

; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

; APPLICANT: STEVEN A.

; TITLE OF INVENTION: MELANOMA ANTIGENS AND

; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 126

; CORRESPONDENCE ADDRESS: 126

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/267,439

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/417,174

; FILING DATE: 05-APR-1995

; APPLICATION NUMBER: US/08/231,565

; FILING DATE: 22-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: CAROL M. GRUPPI

; REGISTRATION NUMBER: 37,341

; REFERENCE/DOCKET NUMBER: 2026-4124US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10



TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-09-267-439-47

Query Match 91.4% Score 53; DB 3; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.021;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 19  
US-08-388-852B-21  
Sequence 21, Application US/08388852B  
Patent No. 6500919

GENERAL INFORMATION:  
APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.  
TITLE OF INVENTION: Melanoma associated antigenic polypeptide.  
TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav  
STREET: Philips van Leydenlaan 25  
CITY: Nijmegen  
STATE: Brabant  
COUNTRY: the Netherlands  
ZIP: 6525 EX  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,852B  
FILING DATE: February 15, 1995  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-388-852B-21

Query Match 91.4% Score 53; DB 4; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.021;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 20  
US-09-073-138-47  
Sequence 47, Application US/09073138  
Patent No. 6537560  
GENERAL INFORMATION:  
APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE

CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,138  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPT  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
US-09-073-138-47

Query Match 91.4% Score 53; DB 4; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.021;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 21  
US-08-388-852B-20  
Sequence 20, Application US/08388852B  
Patent No. 6500919  
GENERAL INFORMATION:  
APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.  
TITLE OF INVENTION: Melanoma associated antigenic polypeptide,  
TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav  
STREET: Philips van Leydenlaan 25  
CITY: Nijmegen  
STATE: Brabant  
COUNTRY: the Netherlands  
ZIP: 6525 EX  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,852B  
FILING DATE: February 15, 1995  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-388-852B-20

Query Match 91.4%; Score 53; DB 4; Length 11;  
Best Local Similarity 88.9%; Pred. No. 0.025;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
Db 3 KTWGQYMOV 11

## RESULT 22

US-08-388-852B-10  
Sequence 10, Application US/06388852B  
Patent No. 6500919  
GENERAL INFORMATION:  
APPLICANT: Adema, Gosse Jan, Figdor, Carl Gustav.  
TITLE OF INVENTION: Melanoma associated antigenic polypeptide,  
TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Adema, Gosse Jan, Figdor, Carl Gustav  
STREET: Philips van Leydenlaan 25  
CITY: Nijmegen  
STATE: Brabant  
COUNTRY: the Netherlands  
ZIP: 6525 EX  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,852B  
FILING DATE: February 15, 1995  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-388-852B-10

Query Match 91.4%; Score 53; DB 4; Length 12;  
Best Local Similarity 88.9%; Pred. No. 0.025;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
Db 3 KTWGQYMOV 11

## RESULT 23

US-08-417-174-121  
Sequence 121, Application US/08417174  
Patent No. 3844075  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA

ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 661  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Protein  
US-08-417-174-121

Query Match 91.4%; Score 53; DB 2; Length 661;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
Db 154 KTWGQYMOV 162

## RESULT 24

US-09-267-439-121  
Sequence 121, Application US/09267439  
Patent No. 6270778  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
APPLICANT: STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-4800  
 TELEFAX: (212) 751-6849  
 TELEX: 423792  
 INFORMATION FOR SEQ ID NO: 121:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 661  
 TYPE: amino acid  
 STRANDEDNESS: Unknown  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: Protein  
 US-09-267-439-121

Query Match 91.4%; Score 53; DB 3; Length 661;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
 |||||  
 154 KTWGQYMOV 162

RESULT 25  
 US-08-388-852B-2  
 Sequence 2, Application US/0838852B  
 Patent No. 6500919  
 GENERAL INFORMATION:  
 APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.  
 TITLE OF INVENTION: Melanoma associated antigenic polypeptide,  
 TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Adema, Gosse Jan, Figdor, Carl Gustav  
 STREET: Philips van Leydenlaan 25  
 CITY: Nijmegen  
 STATE: Brabant  
 COUNTRY: the Netherlands  
 ZIP: 6525 EX  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/388,852B  
 FILING DATE: February 15, 1995  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 661 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-388-852B-2

Query Match 91.4%; Score 53; DB 4; Length 661;  
 Best Local Similarity 88.9%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
 |||||  
 154 KTWGQYMOV 162

Search completed: August 14, 2003, 09:08:00  
 Job time : 21.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:07:19 ; Search time 153 Seconds  
(without alignments)  
7.706 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTMQYNAV 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PTCT\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	91.4	9	US-09-847-185-29	Sequence 29, Appl
2	53	91.4	9	US-09-923-831-30	Sequence 30, Appl
3	53	91.4	9	US-09-766-889A-42	Sequence 42, Appl
4	53	91.4	9	US-09-909-460-61	Sequence 61, Appl
5	53	91.4	9	US-09-898-860-46	Sequence 46, Appl
6	53	91.4	9	US-10-106-487-2	Sequence 2, Appl
7	53	91.4	9	US-10-047-539-5	Sequence 5, Appl
8	53	91.4	9	US-10-080-013-5	Sequence 5, Appl
9	53	91.4	9	US-10-161-097-27	Sequence 27, Appl
10	53	91.4	9	US-10-224-286-29	Sequence 29, Appl
11	53	91.4	10	US-09-898-860-47	Sequence 47, Appl
12	53	91.4	92	US-10-106-487-24	Sequence 2, Appl
13	53	91.4	661	US-09-862-260A-2	Sequence 2, Appl
14	53	91.4	661	US-09-812-238B-2	Sequence 2, Appl
15	53	91.4	661	US-09-898-860-121	Sequence 121, App

16	53	91.4	661	15	US-10-207-655-77	Sequence 77, Appl
17	53	91.4	668	14 <td>US-10-047-539-4</td> <td>Sequence 4, Appl</td>	US-10-047-539-4	Sequence 4, Appl
18	50	86.2	661	12 <td>US-09-898-860-27</td> <td>Sequence 27, Appl</td>	US-09-898-860-27	Sequence 27, Appl
19	49	84.5	9	14 <td>US-10-047-539-2</td> <td>Sequence 8, Appl</td>	US-10-047-539-2	Sequence 8, Appl
20	49	84.5	626	14 <td>US-10-047-539-2</td> <td>Sequence 2, Appl</td>	US-10-047-539-2	Sequence 2, Appl
21	48	82.8	9	12 <td>US-09-898-860-71</td> <td>Sequence 71, Appl</td>	US-09-898-860-71	Sequence 71, Appl
22	48	82.8	9	12 <td>US-09-898-860-72</td> <td>Sequence 72, Appl</td>	US-09-898-860-72	Sequence 72, Appl
23	48	82.8	9	12 <td>US-09-898-860-73</td> <td>Sequence 73, Appl</td>	US-09-898-860-73	Sequence 73, Appl
24	48	82.8	9	12 <td>US-09-898-860-74</td> <td>Sequence 74, Appl</td>	US-09-898-860-74	Sequence 74, Appl
25	48	82.8	9	12 <td>US-09-898-860-75</td> <td>Sequence 75, Appl</td>	US-09-898-860-75	Sequence 75, Appl
26	47	81.0	9	12 <td>US-09-898-860-68</td> <td>Sequence 68, Appl</td>	US-09-898-860-68	Sequence 68, Appl
27	47	81.0	9	12 <td>US-09-898-860-69</td> <td>Sequence 69, Appl</td>	US-09-898-860-69	Sequence 69, Appl
28	47	81.0	9	12 <td>US-09-898-860-70</td> <td>Sequence 70, Appl</td>	US-09-898-860-70	Sequence 70, Appl
29	44	75.9	9	12 <td>US-09-898-860-77</td> <td>Sequence 77, Appl</td>	US-09-898-860-77	Sequence 77, Appl
30	43	74.1	9	12 <td>US-09-898-860-76</td> <td>Sequence 76, Appl</td>	US-09-898-860-76	Sequence 76, Appl
31	43	74.1	9	12 <td>US-09-898-860-78</td> <td>Sequence 78, Appl</td>	US-09-898-860-78	Sequence 78, Appl
32	43	74.1	9	12 <td>US-09-898-860-79</td> <td>Sequence 79, Appl</td>	US-09-898-860-79	Sequence 79, Appl
33	43	74.1	9	12 <td>US-09-898-860-80</td> <td>Sequence 80, Appl</td>	US-09-898-860-80	Sequence 80, Appl
34	43	74.1	9	12 <td>US-09-898-860-81</td> <td>Sequence 81, Appl</td>	US-09-898-860-81	Sequence 81, Appl
35	43	74.1	9	12 <td>US-09-898-860-82</td> <td>Sequence 82, Appl</td>	US-09-898-860-82	Sequence 82, Appl
36	40	69.0	136	9	US-09-864-761-39224	Sequence 39224, A
37	39	67.2	133	9	US-09-925-297-581	Sequence 581, App
38	39	67.2	432	12 <td>US-10-105-733-67</td> <td>Sequence 67, Appl</td>	US-10-105-733-67	Sequence 67, Appl
39	39	67.2	432	15 <td>US-10-081-872-76</td> <td>Sequence 76, Appl</td>	US-10-081-872-76	Sequence 76, Appl
40	39	67.2	432	15 <td>US-10-081-872-78</td> <td>Sequence 78, Appl</td>	US-10-081-872-78	Sequence 78, Appl
41	39	67.2	432	15 <td>US-10-081-872-84</td> <td>Sequence 84, Appl</td>	US-10-081-872-84	Sequence 84, Appl
42	39	67.2	432	15 <td>US-10-081-872-86</td> <td>Sequence 86, Appl</td>	US-10-081-872-86	Sequence 86, Appl
43	39	67.2	436	12 <td>US-10-105-733-2</td> <td>Sequence 2, Appl</td>	US-10-105-733-2	Sequence 2, Appl
44	39	67.2	436	12 <td>US-10-228-063-1</td> <td>Sequence 1, Appl</td>	US-10-228-063-1	Sequence 1, Appl
45	39	67.2	436	15 <td>US-10-146-662-2</td> <td>Sequence 2, Appl</td>	US-10-146-662-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1

US-09-847-185-29

Sequence 29, Application US/09847185

Patent No. US20020076392A1

GENERAL INFORMATION:

APPLICANT: SCO HO, William

TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS

COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE

RESPONSE USING SAME

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMPBELL & FLORES, LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/847,185

FILING DATE: 01-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/201,931

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IM 2442

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)535-9001

TELEFAX: (619)535-8949

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-847-185-29

Query Match 91.4%; Score 53; DB 9; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 2  
US-09-923-831-30

Sequence 30, Application US/09923831  
Patent No. US20020115142A1  
GENERAL INFORMATION:

APPLICANT: Martelange, Val,rie  
APPLICANT: De Smet, Charles  
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
FILE REFERENCE: L0461/7054  
CURRENT APPLICATION NUMBER: US/09/923,831  
PRIOR FILING DATE: 2001-08-07  
PRIOR APPLICATION NUMBER: 09/183,706  
PRIOR FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 43  
SEQ ID NO 30

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-923-831-30

Query Match 91.4%; Score 53; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 3  
US-09-766-889A-42

Sequence 42, Application US/09766889A  
Patent No. US20020164654A1  
GENERAL INFORMATION:

APPLICANT: Luiten, Rosalie  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: van der Bruggen, Pierre  
APPLICANT: Stroobant, Vincent  
APPLICANT: Demotte, Nathalie  
APPLICANT: Schultze, Erwin  
TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B\*35 AND HLA-B\*44  
FILE REFERENCE: L0461/7104  
CURRENT APPLICATION NUMBER: US/09/766,889A  
CURRENT FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 60/177,242  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: US 60/243,212  
PRIOR FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 42  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-766-889A-42

Query Match 91.4%; Score 53; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 4  
US-09-909-460-61

Sequence 61, Application US/09909460  
Publication No. US20020182258A1  
GENERAL INFORMATION:

APPLICANT: Lunsford, Lynn B.  
APPLICANT: Putnam, David  
APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC  
FILE REFERENCE: 08191/014001  
CURRENT APPLICATION NUMBER: US/09/909,460  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-909-460-61

Query Match 91.4%; Score 53; DB 10; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

RESULT 5  
US-09-898-860-46

Sequence 46, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:

APPLICANT: KAKAKAMI, YUTAKA; ROSENBERG, STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-898-860-46

Query Match 91.4%; Score 53; DB 12; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYAV 9  
Db 1 KTWGQYQV 9

RESULT 6  
US-10-106-487-2  
Sequence 2, Application US/10106487  
Publication No. US20020164721A1  
GENERAL INFORMATION:  
APPLICANT: FIRAT, HUSEYIN  
APPLICANT: LEMONNIER, FRANCOIS  
APPLICANT: LANGLADE-DEMOYEN, PIERRE  
APPLICANT: MICHEL, MARIE-LOUISE  
TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION  
TITLE OF INVENTION: OF  
TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING  
FILE REFERENCE: 03495.0196 SEQUENCE LISTING  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: US/10/106,487  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/158,356  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-106-487-2

Query Match 91.4%; Score 53; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYAV 9  
Db 1 KTWGQYQV 9

RESULT 7  
US-10-047-539-5  
Sequence 5, Application US/10047539  
Publication No. US20020177547A1  
GENERAL INFORMATION:  
APPLICANT: MOLLING, KARIN  
APPLICANT: PAVLOVIC, JOVAN  
APPLICANT: NAVRATH, MICHAEL

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING  
FILE REFERENCE: VOS-27  
CURRENT APPLICATION NUMBER: US/10/047,539  
CURRENT FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
PRIOR FILING DATE: 2001-01-16  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-047-539-5

Query Match 91.4%; Score 53; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYAV 9  
Db 1 KTWGQYQV 9

RESULT 8  
US-10-080-013-5  
Sequence 5, Application US/10080013  
Publication No. US20030077248A1  
GENERAL INFORMATION:  
APPLICANT: Moriarty, Ann  
APPLICANT: Leturcq, Didier  
APPLICANT: Degraw, Juli  
APPLICANT: Heiskala, Marja  
APPLICANT: Peterson, Per  
APPLICANT: Jackson, Michael  
TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS  
FILE REFERENCE: ORT-1557  
CURRENT APPLICATION NUMBER: US/10/080,013  
CURRENT FILING DATE: 2002-02-19  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-080-013-5

Query Match 91.4%; Score 53; DB 15; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYAV 9  
Db 1 KTWGQYQV 9

RESULT 9  
US-10-161-097-27  
Sequence 27, Application US/10161097  
Publication No. US20030096404A1  
GENERAL INFORMATION:  
APPLICANT: ROSENZWEIG, Michael  
APPLICANT: PYKETT, Mark J.  
APPLICANT: SCADDEN, David T.  
APPLICANT: POZNANSKY, Mark C.  
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
FILE REFERENCE: CI005/7012/KA/ERG  
CURRENT APPLICATION NUMBER: US/10/161,097  
CURRENT FILING DATE: 2002-05-31  
PRIOR APPLICATION NUMBER: US/09/574,749  
PRIOR FILING DATE: 2002-05-31

PRIOR APPLICATION NUMBER: US 60/107,972  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: PCT/US99/26795  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 09/524,749  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 27  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Homo Sapiens source  
US-10-097-27

Query Match 91.4%; Score 53; DB 15; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

## RESULT 10

US-10-224-286-29  
Sequence 29, Application US/10224286  
Publication No. US20030108517A1  
GENERAL INFORMATION:  
APPLICANT: Soo Hoo, William  
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
RESPONSE USING SAME

NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92121

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/224,286  
FILING DATE: 19-Aug-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,516  
FILING DATE: 29-JUL-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-1M 2442  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)535-9001  
TELEFAX: (619)535-8949

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-10-224-286-29

Query Match 91.4%; Score 53; DB 15; Length 9;  
Best Local Similarity 88.9%; Pred. No. 4.4e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

## RESULT 11

US-09-898-860-47  
Sequence 47, Application US/09898860  
Publication No. US2003014482A1  
GENERAL INFORMATION:  
APPLICANT: KAMAKAMI, YUTAKA, ROSENBERG,  
STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS

NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPEL

REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792

INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: amino acid  
STRANDEDNESS: Unknown

MOLECULE TYPE: Unknown  
TOPOLOGY: Unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
US-09-898-860-47

Query Match 91.4%; Score 53; DB 12; Length 10;  
Best Local Similarity 88.9%; Pred. No. 0.082; 1; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
Db 1 KTWGQYMAV 9

## RESULT 12

US-10-106-487-24  
Sequence 24, Application US/10106487  
Publication No. US20020164721A1  
GENERAL INFORMATION:  
APPLICANT: FIRAT, HUSEYIN  
APPLICANT: LEMONNIER, FRANCOIS



APPLICANT: LANGADE-DEMOYEN, PIERRE  
APPLICANT: MICHEL, MARIE-LOUISE  
TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION  
TITLE OF INVENTION: OF  
TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING  
TITLE OF INVENTION: HHD MICE  
FILE REFERENCE: 03495.0196 SEQUENCE LISTING  
CURRENT FILING DATE: 2002-03-27  
PRIOR FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: 09/675,673  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/158,356  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-106-487-24

Query Match 91.4%; Score 53; DB 14; Length 92;  
Best Local Similarity 88.9%; Pred. No. 0.53;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9  
Db 38 KTWGQYMOV 46

RESULT 13  
US-09-862-260A-2  
Sequence 2, Application US/09862260A  
Patent No. US20020082217A1  
GENERAL INFORMATION:  
APPLICANT: Nicolette, Charles A.  
TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
FILE REFERENCE: 126881210200  
CURRENT FILING DATE: 2001-05-21  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/208,955  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/267,877  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 661  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-862-260A-2

Query Match 91.4%; Score 53; DB 9; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9  
Db 154 KTWGQYMOV 162

RESULT 14  
US-09-812-238B-2  
Sequence 2, Application US/09812238B  
Patent No. US20020169132A1  
GENERAL INFORMATION:  
APPLICANT: Nicolette, Charles  
TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS  
FILE REFERENCE: GZ 2094.00  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2  
LENGTH: 661  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-812-238B-2

Query Match 91.4%; Score 53; DB 10; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9  
Db 154 KTWGQYMOV 162

RESULT 15  
US-09-898-860-121  
Sequence 121, Application US/09898860  
Patent No. US2003014482A1  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 661  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 121:  
US-09-898-860-121

Query Match 91.4%; Score 53; DB 12; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYNAV 9  
Db 154 KTWGQYMOV 162

RESULT 16  
US-10-207-655-77  
; Sequence 77, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069,401C1  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 77  
; LENGTH: 661  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-655-77

Query Match 91.4%; Score 53; DB 15; Length 661;  
Best Local Similarity 88.9%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
|||  
Db 154 KTWGQYMOV 162

RESULT 17  
US-10-047-539-4  
; Sequence 4, Application US/10047539  
; Publication No. US20020177547A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLLING, KARIN  
; APPLICANT: PAVLOVIC, JOVAN  
; APPLICANT: NAMRATH, MICHAEL  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: VOS-27  
; CURRENT APPLICATION NUMBER: US/10/047,539  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
; PRIOR FILING DATE: 2001-01-16  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 668  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-047-539-4

Query Match 91.4%; Score 53; DB 14; Length 668;  
Best Local Similarity 88.9%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYMAV 9  
|||  
Db 154 KTWGQYMOV 162

RESULT 18  
US-09-898-860-27  
; Sequence 27, Application US/09898860  
; Publication No. US20030144482A1  
; GENERAL INFORMATION:  
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
; STEVEN A.  
; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS  
; NUMBER OF SEQUENCES: 126

## CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

## COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898, 860  
FILING DATE: 03-Jul-2001

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994

## ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:

LENGTH: 661

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-898-860-27

Query Match 86.2%; Score 50; DB 12; Length 661;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWGQYV 7  
|||  
Db 154 KTWGQYV 160

RESULT 19  
US-10-047-539-8  
; Sequence 8, Application US/10047539  
; Publication No. US20020177547A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLLING, KARIN  
; APPLICANT: PAVLOVIC, JOVAN  
; APPLICANT: NAMRATH, MICHAEL  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: VOS-27  
; CURRENT APPLICATION NUMBER: US/10/047,539  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
; PRIOR FILING DATE: 2001-01-16  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-047-539-8

Query Match 84.5%; Score 49; DB 14; Length 9;

Best Local Similarity 77.8%; Pred. No. 4.4e+05;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYNAV 9  
|||:|  
Db 1 KTWGKYMOV 9

## RESULT 20

US-10-047-539-2  
; Sequence 2, Application US/10047539  
; Publication No. US20020177547A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLLING, KARIN  
; APPLICANT: PAVLOVIC, JOVAN  
; APPLICANT: NAMRATH, MICHAEL  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: VOS-27  
; CURRENT APPLICATION NUMBER: US/10/047,539  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: EP 01 10 0914.9  
; PRIOR FILING DATE: 2001-01-16  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 626  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-047-539-2

Query Match 84.5%; Score 49; DB 14; Length 626;  
Best Local Similarity 77.8%; Pred. No. 10;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYNAV 9  
|||:|  
Db 154 KTWGKYMOV 162

## RESULT 21

US-09-898-860-71  
; Sequence 71, Application US/09898860  
; Publication No. US20030144482A1  
; GENERAL INFORMATION:  
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS  
; NUMBER OF SEQUENCES: 126  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/898,860  
; FILING DATE: 03-Jul-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/267,439  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US/08/417,174  
; FILING DATE: 05-APR-1995  
; APPLICATION NUMBER: US/08/231,565  
; FILING DATE: 22-APR-1994

## ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 71:  
US-09-898-860-71

Query Match 82.8%; Score 48; DB 12; Length 9;  
Best Local Similarity 87.5%; Pred. No. 4.4e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TWGQYNAV 9  
|||:|  
Db 2 TWGQYMOV 9

## RESULT 22

US-09-898-860-72  
; Sequence 72, Application US/09898860  
; Publication No. US20030144482A1  
; GENERAL INFORMATION:  
; APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,  
; STEVEN A.  
; TITLE OF INVENTION: MELANOMA ANTIGENS AND  
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
; METHODS  
; NUMBER OF SEQUENCES: 126  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/898,860  
; FILING DATE: 03-Jul-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/267,439  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US/08/417,174  
; FILING DATE: 05-APR-1995  
; APPLICATION NUMBER: US/08/231,565  
; FILING DATE: 22-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CAROL M. GRUPPI  
; REGISTRATION NUMBER: 37,341  
; REFERENCE/DOCKET NUMBER: 2026-4124US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; TELEX: 421792  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: amino acid  
; STRANDEDNESS: Unknown

TOPOLOGY: Unknown  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-898-860-72

Query Match 82.8%; Score 48; DB 12; Length 9;  
Best Local Similarity 87.5%; Pred. No. 4.4e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYAV 9  
DB 2 TWGQYQV 9

RESULT 23  
US-09-898-860-73  
Sequence 73, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-898-860-73

Query Match 82.8%; Score 48; DB 12; Length 9;  
Best Local Similarity 87.5%; Pred. No. 4.4e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYAV 9  
DB 2 TWGQYQV 9

RESULT 24  
US-09-898-860-74  
Sequence 74, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,860  
FILING DATE: 03-Jul-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/267,439  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/417,174  
FILING DATE: 05-APR-1995  
APPLICATION NUMBER: US/08/231,565  
FILING DATE: 22-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4124US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-898-860-74

Query Match 82.8%; Score 48; DB 12; Length 9;  
Best Local Similarity 87.5%; Pred. No. 4.4e+05;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYAV 9  
DB 2 TWGQYQV 9

RESULT 25  
US-09-898-860-75  
Sequence 75, Application US/09898860  
Publication No. US20030144482A1  
GENERAL INFORMATION:  
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,  
STEVEN A.  
TITLE OF INVENTION: MELANOMA ANTIGENS AND  
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC  
METHODS  
NUMBER OF SEQUENCES: 126  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/898,860  
 FILING DATE: 03-Jul-2001  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/267,439  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US/08/417,174  
 FILING DATE: 05-APR-1995  
 APPLICATION NUMBER: US/08/231,565  
 FILING DATE: 22-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CAROL M. GRUPPI  
 REGISTRATION NUMBER: 37,341  
 REFERENCE/DOCKET NUMBER: 2026-4124US1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-4800  
 TELEFAX: (212) 751-6849  
 TELE: 421792  
 INFORMATION FOR SEQ ID NO: 75:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9  
 TYPE: amino acid  
 STRANDEDNESS: Unknown  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: Peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
 US-09-898-860-75

Query Match 82.8% Score 48; DB 12; Length 9;  
 Best Local Similarity 87.5% Pred. No. 4.4e+05;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 TWGQYMAV 9  
 |||||  
 Db 2 TWGQYMAV 9

Search completed: August 14, 2003, 09:25:45  
 Job time : 154 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 24 Seconds

(without alignments)  
36.063 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGQYMAV 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	91.4	662	2	melanoma-associated
2	53	91.4	662	2	melanocyte-specific
3	49	84.5	626	2	Pmel 17 protein -
4	42	72.4	290	2	4-hydroxybenzoate
5	42	72.4	305	2	spore cortex-lytic
6	42	72.4	315	2	cytochrome c-type
7	42	72.4	608	2	conserved hypochet
8	40	69.0	264	2	hypothetical prote
9	40	69.0	264	2	hypothetical prote
10	40	69.0	276	2	probable lactose t
11	40	69.0	281	2	conserved hypochet
12	40	69.0	305	1	hypothetical prote
13	40	69.0	13	2	hypothetical prote
14	40	69.0	549	2	hypothetical prote
15	40	69.0	807	2	ycds protein precu
16	40	69.0	807	2	probable outer mem
17	40	69.0	807	2	probable outer mem
18	40	69.0	1870	2	protein P20H1.2 [
19	39	67.2	208	2	fucoxanthin chloro
20	39	67.2	236	2	cytochrome c-type
21	39	67.2	256	2	hypothetical prote
22	39	67.2	335	1	protein-tyrosine-p
23	39	67.2	545	2	probable peptide/a
24	39	67.2	568	2	hypothetical prote
25	39	67.2	585	2	histidine transport
26	39	67.2	586	2	probable membrane
27	39	67.2	1081	2	hypothetical prote
28	38	65.5	209	2	sulfate/thiosulfat
29	38	65.5	277	1	ORECST

30	38	65.5	277	2	G91040	sulfate transport
31	38	65.5	277	2	AF0366	sulfate transport
32	38	65.5	277	2	B85885	sulfate transport
33	38	65.5	290	2	G91256	4-hydroxybenzoate-
34	38	65.5	290	2	C86097	4-hydroxybenzoate-
35	38	65.5	290	2	JC2316	4-hydroxybenzoate-
36	38	65.5	562	2	T22928	hypothetical prote
37	38	65.5	622	2	H64447	hypothetical prote
38	38	65.5	936	2	B64567	cytochrome c bioge
39	38	65.5	936	2	H71862	probable cytochrom
40	37	63.8	240	1	J50591	endo-1,4-beta-xylo
41	37	63.8	241	2	T37005	endo-1,4-beta-xylo
42	37	63.8	277	2	AH0811	sulphate transport
43	37	63.8	293	2	T11969	cytochrome c-type
44	37	63.8	301	2	D82040	cytochrome c-type
45	37	63.8	306	1	S25309	cytochrome c-type

## ALIGNMENTS

RESULT 1  
138400 melanoma-associated ME20 antigen (me20m) - human  
N:Alternate names: melanoma antigen 25  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence revision 01-Nov-1996 #text\_change 01-Dec-2000  
C:Accession: 138400; A53668; A55753  
R:Marsh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.; Ma  
DNA Cell Biol. 13, 87-95, 1994  
A>Title: Cloning and expression of the gene for the Melanoma-Associated ME20 Antigen.  
A:Reference number: 138400; PMID:94235155; PMID:8179825  
A:Accession: 138400  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-662 <RBS>  
A:Cross-references: EMBL:U01874; NID:9494939; PIDN:AAA18479.1; PID:9494940  
R:Adema, G.J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.  
J. Biol. Chem. 269, 20126-20133, 1994  
A>Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.  
A:Reference number: A53668; PMID:94327568; PMID:7519602  
A:Accession: A53668  
A:Molecule type: mRNA  
A:Residues: 1-592,594-662 <ADE>  
A:Cross-references: GB:S73003; NID:9639589; PIDN:AA060634.1; PID:9639590  
R:Kwakami, Y.; Blyahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E.; Ye  
Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994  
A>Title: Identification of a human melanoma antigen recognized by tumor-infiltrating lymph  
A:Reference number: A55753; PMID:94294401; PMID:8022805  
A:Accession: A55753  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-161, 'P', 163-592,594-662 <KAW>  
C:Keywords: glycoprotein

Query Match 91.4%; Score 53; DB 2; Length 662;  
Best Local Similarity 88.9%; Pred. No. 1.2;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
DB 154 KTWGQYMAV 162

RESULT 2  
A11234 melanocyte-specific protein Pmel-17 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 30-Sep-1993  
C:Accession: A11234  
R:Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.;  
Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991  
A>Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on mc

A:Reference number: A41234; MUID:92021023; PMID:1924386  
 A:Accession: A41234  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-668 <KMO>  
 A:Cross-references: GB:M77348

Query Match 91.4%; Score 53; DB 2; Length 668;  
 Best Local Similarity 88.9%; Pred. No. 1.2;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
 |||||  
 DB 154 KTWGQYMAV 162

RESULT 3  
 S53871  
 Pmel 17 protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 05-Nov-1999  
 C:Accession: S53871  
 R:Kwon, B.S.; Halaan, R.; Ponnahaan, S.; Kim, K.; Chintamani, C.; Bennett, D.; Pick  
 Nucleic Acids Res. 23, 154-158, 1995  
 A>Title: Mouse silver mutation is caused by a single base insertion in the putative cyto  
 A:Reference number: S53871; MUID:95175358; PMID:7870580  
 A:Accession: S53871  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-626 <KMO>  
 A:Cross-references: GB:U14133; NID:9887940; PIDN:AAA69538.1; PID:9887941

Query Match 84.5%; Score 49; DB 2; Length 626;  
 Best Local Similarity 77.8%; Pred. No. 4.4;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYMAV 9  
 |||||  
 DB 154 KTWGQYMAV 162

RESULT 4  
 A11014  
 4-hydroxybenzoate octaprenyl transferase [imported] - Salmonella enterica subsp. enteric  
 C:Species: Salmonella enterica subsp. enterica serovar Typh  
 A>Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: A11014  
 R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,  
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: A11014  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-290 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD09218.1; PID:916505222; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STY4430  
 C:Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 72.4%; Score 42; DB 2; Length 290;  
 Best Local Similarity 85.7%; Pred. No. 25;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMAV 9  
 |||||  
 DB 237 WGOYMAV 243

RESULT 5  
 C69708  
 spore cortex-lytic enzyme prepeptide [imported] - Bacillus subtilis

C:Species: Bacillus subtilis  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 21-Jul-2000  
 C:Accession: C69708; 144770  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertek  
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert  
 lech, U.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,  
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Tosato, V.; Uchiyama,  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: C69708  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-305 <KUN>  
 A:Cross-references: GB:299115; GB:299116; GB:AL009126; NID:92634723; PIDN:CAB14225.1; PII  
 A:Experimental source: strain 168

R:Moriyama, R.; Hattori, A.; Miyata, S.; Kudoh, S.; Makino, S.  
 J. Bacteriol. 178, 6059-6063, 1996  
 A>Title: A gene (slab) encoding a spore cortex-lytic enzyme from Bacillus subtilis and r  
 A:Reference number: Z22836; MUID:96427343; PMID:8830707

A:Accession: T44770  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-305 <MOR>  
 A:Cross-references: EMBL:D79978; NID:91688021; PIDN:BA11473.1; PID:91688023  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: slab

Query Match 72.4%; Score 42; DB 2; Length 305;  
 Best Local Similarity 85.7%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMAV 9  
 |||||  
 DB 67 WGOYMAV 73

RESULT 6  
 T07314  
 cytochrome c-type synthesis protein homolog - Chlorella vulgaris chloroplast

C:Species: Chlorella vulgaris  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000  
 C:Accession: T07314  
 R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas  
 Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997  
 A>Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo  
 A:Reference number: Z15985; MUID:97303241; PMID:9158184

A:Accession: T07314  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-315 <MAK>  
 A:Cross-references: EMBL:AB001684; NID:92224352; PIDN:BA57962.1; PID:92224478  
 C:Genetics:  
 A:Gene: yci5  
 A:Genome: chloroplast  
 C:Superfamily: cytochrome c-type synthesis protein  
 C:Keywords: chloroplast

Query Match 72.4%; Score 42; DB 2; Length 315;  
 Best Local Similarity 62.5%; Pred. No. 27;



Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 KTWGQYWA 8  
:|||||:  
Db 243 ETWGNWYS 250

RESULT 7  
H90530  
Conserved hypothetical protein MYPU\_1520 [imported] - Mycoplasma pulmonis (strain UAB CT  
C/Species: Mycoplasma pulmonis  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
C/Accession: H90530  
R/Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul  
A/Reference number: A99512; MUID:21267165; PMID:11353084  
A/Accession: H90530  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-608 <KUR>  
A/Cross-references: GB:AL45566; PID:914089565; PIDN:CAK13325.1; GSPDB:GN00153  
A/Experimental source: strain UAB CTIP  
C/Genetics:  
A/Gene: MYPU\_1520  
A/Genetic code: SGC3

Query Match 72.4%; Score 42; DB 2; Length 608;  
Best Local Similarity 83.3%; Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 TWGQYW 7  
:|||||:  
Db 349 TWGQYW 354

RESULT 8  
F91017  
hypothetical protein EC63110 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C/Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C/Accession: F91017  
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasaway, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
A/Reference number: A99629; MUID:21156231; PMID:11258796  
A/Accession: F91017  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-264 <HAY>  
A/Cross-references: GB:BA000007; PIDN:BA06533.1; PID:913362579; GSPDB:GN00154  
A/Experimental source: strain O157:H7, substrain RMD 0509952  
C/Genetics:  
A/Gene: EC63110

Query Match 69.0%; Score 40; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 WQGYW 7  
:|||||:  
Db 125 WQGYW 129

RESULT 9  
H85861  
hypothetical protein Z3480 [imported] - Escherichia coli (strain O157:H7, substrain EDL8  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C/Accession: H85861  
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: H85861  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-264 <STO>  
A/Cross-references: GB:AB005174; NID:912516559; PIDN:AAG57356.1; GSPDB:GN00145; UWGP:Z34  
A/Experimental source: strain O157:H7, substrain EDL933  
C/Genetics:  
A/Gene: Z3480

Query Match 69.0%; Score 40; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 WQGYW 7  
:|||||:  
Db 125 WQGYW 129

RESULT 10  
A72451  
probable lactose transport system permease protein APE2253 - Aeropyrum pernix (strain KI  
C/Species: Aeropyrum pernix  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C/Accession: A72451  
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah  
awa, H.; Takamaya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ko  
DNA Res. 6, 83-101, 1999  
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr  
A/Reference number: A72450; MUID:99310339; PMID:10382966  
A/Accession: A72451  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-276 <KAW>  
A/Cross-references: DDBJ:AP000064; NID:95105945; PIDN:BA081265.1; PID:95105954  
A/Experimental source: strain KI  
C/Genetics:  
A/Gene: APE2253  
C/Superfamily: inner membrane protein ugpa

Query Match 69.0%; Score 40; DB 2; Length 276;  
Best Local Similarity 55.6%; Pred. No. 47;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 KTWGQYWA 9  
:|||||:  
Db 215 RTWGQWWSL 223

RESULT 11  
A82104  
conserved hypothetical protein VC2229 [imported] - Vibrio cholerae (strain N16961 serogro  
C/Species: Vibrio cholerae  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C/Accession: A82104  
R/Heidelberg, U.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
charlson, D.; Elnelave, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A/Reference number: A82035; MUID:20406833; PMID:10952501  
A/Accession: A82104  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-281 <HRI>  
A/Cross-references: GB:AE004294; GB:AE003852; NID:99656774; PIDN:AAF95373.1; GSPDB:GN00121  
A/Experimental source: serogroup O1, strain N16961, biotype El Tor  
C/Genetics:  
A/Gene: VC2229  
A/Map position: 1  
C/Superfamily: hypothetical protein H11037

Query Match 69.0%; Score 40; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYW 7  
|||||  
DB 99 WGOYW 103

## RESULT 12

S52775

hypothetical protein 2 - Chloroflexus aurantiacus

C:Species: Chloroflexus aurantiacus

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C:Accession: S52775

R.Niedemeier, G.; Shiozawa, J.A.; Lottspeich, F.; Feick, R.G.

FEBS Lett. 342, 61-65, 1994

A:Title: The primary structure of two chlorosome proteins from Chloroflexus aurantiacus.

A:Reference number: S43678; PMID:94192803; PMID:7511541

A:Accession: S52775

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-305 &lt;NIB&gt;

A:Cross-references: EMBL:Z34000; NID:9496485; PIDN:CAA83969.1; PID:9496488

A:Note: only a part of the coding sequence is given in this paper

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein M2079

Query Match 69.0%; Score 40; DB 1; Length 305;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYW 7  
|||||  
DB 246 WGOYW 250

## RESULT 13

S76446

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999

C:Accession: S76446

R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

s.

A:Reference number: S74322; PMID:97061201; PMID:8905231

A:Accession: S76446

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-400 &lt;KAN&gt;

A:Cross-references: EMBL:D90915; GB:AB001339; NID:91653604; PIDN:BA18575.1; PID:4101930

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 69.0%; Score 40; DB 2; Length 400;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYW 7  
|||||  
DB 335 WGOYW 339

## RESULT 14

H64992

hypothetical protein b2226 - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002

C:Accession: H64992

R.Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

.A.; Rose, D.J.; Mau, B.; Sha, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; PMID:97426617; PMID:9278503

A:Accession: H64992

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-549 <BLAT>

A:Cross-references: GB:AE000312; GB:U00096; NID:91788555; PIDN:AACT5286.1; PID:91788557;

A:Experimental source: strain K-12, substrain MG1655

C:Superfamily: Escherichia coli hypothetical protein b2226

Query Match 69.0%; Score 40; DB 2; Length 549;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYW 7  
|||||  
DB 125 WGOYW 129

## RESULT 15

F64844

ydcS protein precursor - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002

C:Accession: F64844

R.Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

.A.; Rose, D.J.; Mau, B.; Sha, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; PMID:97426617; PMID:9278503

A:Accession: F64844

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-807 <BLAT>

A:Cross-references: GB:AE000204; GB:U00096; NID:91787256; PIDN:AACT4109.1; PID:91787261;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: ydcS

C:Superfamily: Escherichia coli ydcS protein

F.1-26/Domains: signal sequence #status predicted <SIG>

F.27-807/Product: ydcS protein #status predicted <MAT>

Query Match 69.0%; Score 40; DB 2; Length 807;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYW 7  
|||||  
DB 314 WGOYW 318

## RESULT 16

F90787

probable outer membrane protein Eca1270 [imported] - Escherichia coli (strain O157:H7, su

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001

C:Accession: F90787

R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A:Reference number: A99629; PMID:21156231; PMID:11528796

A:Accession: F90787

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-807 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA834693.1; PID:913360730; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RIMD 0509552

C:Genetics:

A:Gene: Eca1270

## C:Superfamily: Escherichia coli ycds protein

Query Match 69.0%; Score 40; DB 2; Length 807;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WGOYX 7  
|||  
Db 314 WGOYX 318

## RESULT 17

F85647 probable outer membrane protein ycds [imported] - Escherichia coli (strain O157:H7, sub

C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: F85647  
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamowski, K.; Apodaca,  
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85647  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-807 <STD>

A:Cross-references: GB:AE005174; NID:G12514389; PIDN:AA655642.1; GSPDB:GN00145; UWGP:Z15  
C:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:  
A:Gene: ycds

C:Superfamily: Escherichia coli ycds protein

Query Match 69.0%; Score 40; DB 2; Length 807;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WGOYX 7  
|||  
Db 314 WGOYX 318

## RESULT 18

D88486 protein F20H11.2 (imported) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C:Accession: D88486  
R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: A platform for investigating biolog  
A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: D88486  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-1870 <STD>

A:Cross-references: GB:chr\_III; PIDN:AA53984.1; PID:G2076895; GSPDB:GN00021; CESP:F20H1  
C:Genetics:  
A:Gene: F20H11.2

A:Map position: 3

Query Match 69.0%; Score 40; DB 2; Length 1870;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WGOYX 8  
|||  
Db 991 WGOYX 996

## RESULT 19

S46301

fucoxanthin chlorophyll a/c-binding light-harvesting protein - Isochrysis galbana

N:Alternate names: FCP protein  
C:Species: Isochrysis galbana

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 05-Nov-1999

C:Accession: S46301  
R:Lancone, J.; Henry, D.; Wyman, K.; Sukenik, A.; Falkowski, P.

Plant Mol. Biol. 25, 355-368, 1994  
A:Title: Cloning and nucleotide sequence of a cDNA encoding a major fucoxanthin-, chloro  
e family.

A:Reference number: S46301; MUID:94325461; PMID:8049362

A:Accession: S46301  
A:Molecule type: mRNA

A:Residues: 1-208 <LNR>  
A:Cross-references: EMBL:X77333; NID:9535080; PIDN:CAA54547.1; PID:9535081

A:Experimental source: cultivar DUN  
C:Keywords: light-harvesting complex

Query Match 67.2%; Score 39; DB 2; Length 208;  
Best Local Similarity 83.3%; Pred. No. 52;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TWGOYX 7  
|||  
Db 198 TWGOYX 203

## RESULT 20

A75530 cytochrome c-type biogenesis protein, heme exporter protein C - Deinococcus radiodurans

C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C:Accession: A75530  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; H

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75530  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-236 <WHI>

A:Cross-references: GB:AE001895; GB:AE000513; NID:96458024; PIDN:AAF09930.1; PID:96458024

A:Experimental source: strain R1  
C:Genetics:

A:Gene: DR0348  
A:Map position: 1

C:Superfamily: hclC protein

Query Match 67.2%; Score 39; DB 2; Length 236;  
Best Local Similarity 83.3%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TWGOYX 7  
|||  
Db 101 TWGOYX 106

## RESULT 21

B70750 hypothetical protein Rv0090 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 28-Jul-2000

C:Accession: B70750  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: B70750  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA  
A.Residues: 1-256 <COL>  
A.Cross-references: GB:Z74410; GB:AL123456; NID:G3261600; PIDN:CAA98926.1; PID:e249404;  
A.Experimental source: strain H37Rv  
C.Genetics:  
A.Gene: RV0090  
C.Superfamily: Mycobacterium tuberculosis hypothetical protein RV0090

Query Match 67.2%; Score 39; DB 2; Length 256;  
Best Local Similarity 66.7%; Pred. No. 63;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMGOYMW 9  
DB 177 KRMGEYPAV 185

RESULT 22  
A39862  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - yeast (Saccharomyces cerevisiae)  
C.Species: Saccharomyces cerevisiae  
C.Date: 30-Dec-1991 #sequence\_revision 08-Mar-1996 #text\_change 21-Jul-2000  
C.Accession: A39862; S67793  
J.Guan, K.; Deschenes, R.J.; Qiu, H.; Dixon, J.E.  
J. Biol. Chem. 266, 12964-12970, 1991  
A.Title: Cloning and expression of a yeast protein tyrosine phosphatase.  
A.Reference number: A39862; MUID:91302312; PMID:1649172  
A.Accession: A39862  
A.Molecule type: DNA  
A.Residues: 1-335 <GUA>  
A.Cross-references: GB:M64062; NID:G172295; PIDN:AAA34923.1; PID:G172296  
R.Rasmussen, S.W.  
Submitted to the Protein Sequence Database, July 1996  
A.Reference number: S67778  
A.Accession: S67793  
A.Molecule type: DNA  
A.Residues: 1-335 <RAS>  
A.Cross-references: EMBL:Z74278; NID:G1431387; PIDN:CAA98809.1; PID:G1431388; GSPDB:GN00  
A.Experimental source: strain S288C  
C.Genetics:  
A.Gene: SGD:PTP1; MIPS:YDL230W  
A.Cross-references: SGD:S0002389; MIPS:YDL230W  
A.Map position: 4L  
C.Superfamily: Saccharomyces protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphatase, phosphoric monoester hydrolase; tyrosine-specific phosphatase  
C.Keywords: phosphoprotein; protein-tyrosine-phosphatase homology <PTP>  
F:52-303/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:252/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:258/Binding site: substrate phosphate (Arg) #status predicted

Query Match 67.2%; Score 39; DB 1; Length 335;  
Best Local Similarity 71.4%; Pred. No. 80;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMGOYMW 7  
DB 108 KTMDOFW 114

RESULT 23  
A84432  
probable peptide/amino acid transporter [imported] - Arabidopsis thaliana  
C.Species: Arabidopsis thaliana (mouse-ear cress)  
C.Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C.Accession: A84432  
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A.Reference number: A84432; MUID:20083487; PMID:10617197  
A.Accession: A84432  
A.Status: preliminary

A.Molecule type: DNA  
A.Residues: 1-545 <STO>  
A.Cross-references: GB:AE002093; NID:G4406784; PIDN:AAD20094.1; GSPDB:GN00139  
C.Genetics:  
A.Gene: AC2802020  
A.Map position: 2

Query Match 67.2%; Score 39; DB 2; Length 545;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMW 9  
DB 111 WGRYWTI 117

RESULT 24  
E96648  
hypothetical protein F19K23.13 [imported] - Arabidopsis thaliana  
C.Species: Arabidopsis thaliana (mouse-ear cress)  
C.Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C.Accession: E96648  
R.Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso, C.; W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzilli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.ber, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A.Reference number: A86411; MUID:21016719; PMID:11130712  
A.Accession: E96648  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-568 <STO>  
A.Cross-references: GB:AE005173; NID:G2160144; PIDN:AAB60766.1; GSPDB:GN00141  
C.Genetics:  
A.Gene: F19K23.13  
A.Map position: 1

Query Match 67.2%; Score 39; DB 2; Length 568;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYMW 9  
DB 106 WGRYWTI 112

RESULT 25  
C84432  
histidine transport protein (PTR2-B) [imported] - Arabidopsis thaliana  
C.Species: Arabidopsis thaliana (mouse-ear cress)  
C.Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C.Accession: C84432  
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A.Reference number: A84420; MUID:20083487; PMID:10617197  
A.Accession: C84432  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-585 <STO>  
A.Cross-references: GB:AE002093; NID:G4406786; PIDN:AAD20096.1; GSPDB:GN00139  
C.Genetics:  
A.Gene: AC2802040  
A.Map position: 2

Query Match 67.2%; Score 39; DB 2; Length 585;

Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WGOYWAV 9  
|||:  
Db 110 WGRYWTI 116

Search completed: August 14, 2003, 09:07:13  
Job time : 26 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 13.5 seconds

(without alignments)  
31.351 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGQYWAV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	91.4	661	PM17_HUMAN	P40967 homo sapien
2	49	84.5	626	PM17_MOUSE	Q60696 mus musculu
3	44	75.9	762	P115_CHICK	Q98917 gallus gall
4	42	72.4	305	SLB8_BACSU	P50739 bacillus su
5	42	72.4	315	CCSA_CHIYU	P56315 chlorella v
6	42	72.4	902	NRFI_WOLSU	Q98164 wolinsella s
7	41	70.7	328	CCSA_ARATH	P56770 arabidopsis
8	40	69.0	549	YFAQ_ECOLI	P75463 escherichia
9	40	69.0	807	YCD5_ECOLI	P75907 escherichia
10	39	67.2	208	PCP_ISOGA	Q39709 isochrysis
11	39	67.2	256	Y090_MYCTU	Q10887 mycobacteri
12	39	67.2	259	SLB8_BACCR	P70874 bacillus ce
13	39	67.2	276	SLB8_OCEIH	P53105 oceanobacil
14	39	67.2	281	NPS2_MOUSE	O55126 mus musculu
15	39	67.2	286	NPS2_HUMAN	O75323 mus sapien
16	39	67.2	288	NPS2_BRABR	Q99588 brachydanio
17	39	67.2	335	PTP1_YEAST	P25054 saccharomyc
18	39	67.2	585	PT2B_ARATH	P40032 arabidopsis
19	38	65.5	277	CYST_ECOLI	P16701 escherichia
20	38	65.5	290	UB1A_ECOLI	P26601 escherichia
21	38	65.5	312	EX24_ARATH	Q98176 arabidopsis
22	37	63.8	240	XYNC_STRLI	P26220 streptomyce
23	37	63.8	256	RM09_MOUSE	O99994 mus musculu
24	37	63.8	267	RM09_HUMAN	Q99994 mus sapien
25	37	63.8	277	CYST_SALTY	P41032 salmoneilla
26	37	63.8	293	CCSA_CYACA	O19901 cyanidium c
27	37	63.8	306	CCSA_GALASU	P31564 galatieria s
28	37	63.8	312	CCSA_ODOSI	P45523 odontella s
29	37	63.8	316	MANA_STRMU	O59935 streptococc
30	37	63.8	319	CCSA_PORPU	P51369 porphyra pu
31	37	63.8	320	CCSA_PINTH	P41650 pinus thunb
32	37	63.8	322	CCSA_CYAPA	P48257 cyanophora
33	37	63.8	353	CCSA_CHLRE	P48269 chlamydomon

34	37	63.8	373	1	SMF_HAEIN	P43862 haemophilus
35	37	63.8	739	1	YGIQ_ECOLI	Q46861 escherichia
36	37	63.8	756	1	IKKB_HUMAN	O14920 homo sapien
37	37	63.8	757	1	IKKB_MOUSE	O88351 mus musculu
38	37	63.8	757	1	IKKB_RAT	O9978 ratius norv
39	37	63.8	802	1	XYND_RUMFL	Q53317 rumiococcu
40	37	63.8	1009	1	YE68_METVA	Q58863 methanococc
41	36	62.1	133	1	PA2B_BUNMU	Q91647 bungarus mu
42	36	62.1	137	1	PA25_BUNMU	P59018 bungarus mu
43	36	62.1	137	1	PA26_BUNMU	O90251 bungarus mu
44	36	62.1	137	1	PA27_BUNMU	O99997 bungarus mu
45	36	62.1	138	1	PA2A_BUNMU	Q91647 bungarus mu

## ALIGNMENTS

```

RESULT 1
ID PM17_HUMAN STANDARD; PRT; 661 AA.
AC P40967; Q12763; Q14448; Q14817; Q16565;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanocyte protein Pmel 17 precursor (Melanocyte lineage-specific
DE antigen GP100) (Melanoma-associated ME20 antigen) (ME20W/ME20S)
DE (ME20-W/ME20-S) (95 kDa melanocyte-specific secreted glycoprotein).
GN SLIV OR PWE117 OR D125S53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92021023; PubMed=1924386;
RA Kwon B.S., Chintamani C., Kozak C.A., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Barton D., Francke U., Kobayashi Y.,
RA Kim K.-K.;
RT "A melanocyte-specific gene, Pmel 17, maps near the silver coat color
RT locus on mouse chromosome 10 and is in a syntenic region on human
RT chromosome 12."
RT Proc. Natl. Acad. Sci. U.S.A. 88:9228-9232(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94327568; PubMed=7519602;
RA Adema G.J., de Boer A.J., Vogel A.M., Loenen W.A., Figdor C.G.;
RT "Molecular characterization of the melanocyte lineage-specific
RT antigen gp100."
RT J. Biol. Chem. 269:20126-20133(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96154052; PubMed=8592076;
RA Ballin T., Lee S.T., Spritz R.A.;
RT "Genomic organization and sequence of D12S53E (Pmel 17), the human
RT homologue of the mouse silver (sl) locus."
RT J. Invest. Dermatol. 106:24-27(1996).
RN [4]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 25-53.
RX MEDLINE=94235165; PubMed=8179825;
RA Marsh G.A., Marken J.S., Neuber M., Aruffo A., Hellstrom I.,
RA Hellstrom K.E., Marguardt H.;
RT "Cloning and expression of the gene for the melanoma-associated ME20
RT antigen."
RT DNA Cell Biol. 13:87-95(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX Kwon B.S., Kim K., Heng H.H., Shi X.M., Teui L., Lee Z.H.,
RA Youn B., Pickard R.T.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX Vogel A.;
RT Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.

```





```
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 170 170 S -> L (IN SILVER).
FT VARIANT 175 175 R -> G (IN SILVER).
FT VARIANT 373 373 D -> N (IN SILVER).
FT VARIANT 471 471 F -> S (IN SILVER).
FT VARIANT 603 626 AAPAGGLARGLGENSPILSGQOV -> SSASLRSSRPWP
SEQUENCE 626 AA; 65980 MW; 7AB941D2E3FB1044 CRC64;

Query Match 84.5%; Score 49; DB 1; Length 626;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTWGQYMAV 9
Db 154 KTWGKTMQV 162

RESULT 3
P15_CHICK STANDARD; PRT; 762 AA.
AC Q98917;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 115 kDa melanosomal matrix protein precursor.
GN MPM15.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Retinal pigment epithelium;
RX MEDLINE=9202067; PubMed=1924173;
RA Mochizuki M., Agata K., Eguchi G.;
RT "Expression of gene coding for a melanosomal matrix protein
transcriptionally regulated in the transdifferentiation of chick
embryo pigmented epithelial cells.";
RL Cell Differ. 24:67-74(1988).
CC -1- FUNCTION: MIGHT BE REQUIRED FOR POLYMERIZATION OF MELANIN ONTO THE
CORE STRUCTURE OF MELANOSOMES WITH ENZYMIC FUNCTION OF TYROSINASE.
CC -1- SUBCELLULAR LOCATION: ON THE FIBROUS MATRIX STRUCTURE OF THE
PREMELANOSOME.
CC -1- TISSUE SPECIFICITY: SPECIFIC TO PIGMENTED EPITHELIAL CELLS AND
MELANOCYTES. NOT EXPRESSED IN LENS, NEURAL RETINA, BRAIN, HEART,
GIZZARD OR LIVER.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE REDIFFERENTIATION OF
PIGMENTED EPITHELIAL CELLS (PEC).
CC -1- PTM: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE PML-17/NMB FAMILY.
CC -1- SIMILARITY: Contains 1 PKD domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; D88348; BAA13589.1; -
```

```
DR InterPro; IPR000601; PKD_domain.
DR Pfam; PF00801; PKD; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS50093; PKD; 1.
KW Signal; Glycoprotein; Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 762 115 KDA MELANOSOMAL MATRIX PROTEIN.
FT DOMAIN 223 323 PKD.
FT DOMAIN 441 532 4 X 20-24 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 441 464 1.
FT REPEAT 465 488 2.
FT REPEAT 489 508 3.
FT REPEAT 509 532 4.
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 659 659 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 762 AA; 77356 MW; 172C8DB4FDC67C6 CRC64;

Query Match 75.9%; Score 44; DB 1; Length 762;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TWGQYMAV 9
Db 161 TWGRYMV 168

RESULT 4
SLEB_BACSU STANDARD; PRT; 305 AA.
ID SLEB_BACSU
AC P50739;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Spore cortex-lytic enzyme precursor (SCLP).
GN SLEB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96427343; PubMed=8830707;
RA Moriyama R., Hattori A., Miyata S., Kudoh S.;
RT "A gene (SleB) encoding a spore cortex-lytic enzyme from Bacillus
subtilis and response of the enzyme to L-alanine-mediated
germination.";
RL J. Bacteriol. 178:6059-6063(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / Matburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
the serA and kds loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Besieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.U., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghm S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
```

RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Ilanhard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,  
 RA Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Pirescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan B., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seior S.J., Seior P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tognoni A.,  
 RA Tosoato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambut R., Wedler E., Wedler H., Weitzenecker T.,  
 RA Winers P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zimstein E., Yoshikawa H., Danchin A.,  
 RA "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT subtilis".  
 RT Nature 390:249-256 (1997).  
 RL Nature 390:249-256 (1997).  
 RP CHARACTERIZATION.  
 RC STRAIN=168;  
 RX MEDLINE=99214084; PubMed=10197998;  
 RA Moriyama R., Fukuko H., Miyata S., Kudoh S., Hattori A., Kozuka S.,  
 RA Yasuda Y., Tochikubo K., Makino S.;  
 RT "Expression of a germination-specific amidase, SleB, of *Bacilli* in the  
 RT forespore compartment of sporulating cells and its localization on  
 RT the exterior side of the cortex in dormant spores".  
 RL J. Bacteriol. 181:2373-2378 (1999).  
 RN [5]  
 RP CHARACTERIZATION.  
 RC STRAIN=168;  
 RX MEDLINE=20121739; PubMed=10658652;  
 RA Boland F.M., Arith A., Chitrakal H., Foster S.J., Moir A.;  
 RT "Complete spore-cortex hydrolysis during germination of *Bacillus*  
 RT subtilis 168 requires SleB and YpeB".  
 RL Microbiology 146:57-64 (2000).  
 CC -1- FUNCTION: Could be a lytic transglycosylase. Required for spore  
 CC cortex hydrolysis during germination. Interacts strongly but  
 CC noncovalently with spore components.  
 CC -1- SUBCELLULAR LOCATION: Expressed in the forespore. SleB is then  
 CC transported across the inner forespore membrane and deposited on  
 CC the outside of the cortex.  
 CC -1- DEVELOPMENTAL STAGE: Expressed during sporulation and active  
 CC during germination. Exists as mature but inactive form in the  
 CC dormant spore.  
 CC -1- INDUCTION: Expression is sigma G-dependent.  
 CC -1- MISCELLANEOUS: B. subtilis sleB could not be detected with anti-  
 CC B. cereus sleB antiserum and vice versa.  
 CC -1- SIMILARITY: BELONGS TO THE SLB FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL, D79978; BAA11473.1; -;  
 CC DR EMBL, L47648; AAC83957.1; -;  
 CC DR EMBL, Z99115; CAB14209.1; -;  
 CC DR EMBL, Z99116; CAB14225.1; -;  
 CC DR PIR, C69708; C69708.  
 CC DR Subtilast; BG11439; sleB.  
 CC InterPro: IPR002477; PG binding.  
 CC Pfam: PF01471; PG binding\_1; 1  
 CC Hydrolase, Sporulation; Germination; Cell wall; Signal;  
 CC Complete proteome.  
 KW SIGNAL  
 FT CHAIN 1 29 POTENTIAL.  
 FT 30 305 SPORE CORTEX-LYTIC ENZYME.

SEQ SEQUENCE 305 AA; 34001 MW; 9DF1305975F5BE16 CRC64;  
 Query Match 72.4%; Score 42; DB 1; Length 305;  
 Best Local Similarity 85.7%; Pred. No. 7.8;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 WGYWAV 9  
 DB 67 WGYWAV 73  
 RESULT 5  
 ID\_CCSA\_CHLVU STANDARD; PRT; 315 AA.  
 AC P56315;  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE Cytochrome c biogenesis protein ccsa.  
 GN CCSA.  
 OS Chlorella vulgaris.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;  
 OC Chlorellaceae; Chlorella.  
 OX NCBI\_TaxID=3077;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IAM C-27 / Tamiya;  
 RX MEDLINE=97303241; PubMed=9159184;  
 RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,  
 RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,  
 RA Inamura A., Yoshinaga K., Sugita M.;  
 RT "Complete nucleotide sequence of the chloroplast genome from the  
 RT green alga *Chlorella vulgaris*: the existence of genes possibly  
 RT involved in chloroplast division".  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972 (1997).  
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF  
 CC HEME ATTACHMENT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL, AB001684; BAA57962.1; -;  
 CC DR PIR, T07314; T07314.  
 CC InterPro: IPR002541; CytoC. asm.  
 CC Pfam, PF01578; CytoC. asm. 1.  
 CC Cytochrome c-type biogenesis; Chloroplast.  
 KW SEQUENCE 315 AA; 35471 MW; 502038854FE4F10 CRC64;  
 SQ  
 Query Match 72.4%; Score 42; DB 1; Length 315;  
 Best Local Similarity 62.5%; Pred. No. 8.1;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KTWGQYWA 8  
 DB 243 KTWGQYWA 250  
 RESULT 6  
 ID\_NRF1\_WOLSTU STANDARD; PRT; 902 AA.  
 AC O951B4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Nrf1 protein.  
 GN NRF1.

OS Wolinella succinogenes.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Helicobacteriaceae; Wolinella.  
 RX NCBI\_TaxID=844;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 EX MEDLINE=20138370; PubMed=10672190;  
 RA Simon J., Gross R., Emsle O., Kroneck P.M.H., Kroeger A.,  
 RA Klimek O.;  
 RT "A Napc/Nit-type cytochrome c (Nrfh) is the mediator between the  
 RT quinone pool and the cytochrome c nitrite reductase of Wolinella  
 RT succinogenes.";  
 RL Mol. Microbiol. 35:686-696(2000).  
 CC -1- FUNCTION: May play a role in cytochrome c biogenesis and may be  
 CC required for maturation of the nrfA protein.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: IN THE C-TERMINUS, BELONGS TO THE  
 CC CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AJ245540; CAB53161.1; -  
 DR GO: GO:0016021; C:Integral to membrane; NAS  
 DR GO: GO:0017004; P:Cytochrome biogenesis; NAS.  
 DR InterPro: IPR002541; Cytc\_asm.  
 DR Pfam: PF01578; Cytc\_asm; 1.  
 KW Cytochrome c-type biogenesis; Transmembrane.  
 FT TRANSMEM 9 29 POTENTIAL.  
 FT TRANSMEM 75 95 POTENTIAL.  
 FT TRANSMEM 300 320 POTENTIAL.  
 FT TRANSMEM 335 355 POTENTIAL.  
 FT TRANSMEM 602 622 POTENTIAL.  
 FT TRANSMEM 659 679 POTENTIAL.  
 FT TRANSMEM 731 751 POTENTIAL.  
 FT TRANSMEM 772 792 POTENTIAL.  
 FT TRANSMEM 832 852 POTENTIAL.  
 FT TRANSMEM 868 888 POTENTIAL.  
 SQ SEQUENCE 902 AA; 102016 MW; D2621BF042288380 CRC64;  
 Query Match 72.4%; Score 42; DB 1; Length 902;  
 Best Local Similarity 62.5%; Pred. No. 22;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 KTWGQYWA 8  
 Db 794 ESMGRYWA 801  
 RESULT 7  
 CCSA\_ARATH STANDARD; PRT; 328 AA.  
 ID CCSA\_ARATH  
 AC P56770;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c biogenesis protein ccsa.  
 DE CCSA OR ATCG01040.  
 GN Arabidopsis thaliana (Mouse-ear cress).  
 OS Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eustosids II; Brassicales; Brassicaceae; Arabidopsids.  
 RX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20039611; PubMed=10574454;

RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;  
 RT "Complete structure of the chloroplast genome of Arabidopsis  
 RT thaliana.";  
 RL DNA Res. 6:283-290(1999).  
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF  
 CC HEME ATTACHMENT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AP000423; BAB84436.1; -  
 DR InterPro: IPR002541; Cytc\_asm.  
 DR Pfam: PF01578; Cytc\_asm; 1.  
 KW Cytochrome c-type biogenesis; Chloroplast.  
 SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;  
 Query Match 70.7%; Score 41; DB 1; Length 328;  
 Best Local Similarity 71.4%; Pred. No. 12;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 KTWGQYWA 7  
 Db 255 ETWGSYWA 261  
 RESULT 8  
 YFAO\_ECOLI STANDARD; PRT; 549 AA.  
 ID YFAO\_ECOLI  
 AC P76463;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein yfaQ precursor.  
 GN YFAO OR B2226.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 RX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Bernal N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AB000312; AAC75286.1; -  
 DR PIR: H64992; H64992.  
 DR Ecogene; EG14079; yfaQ.  
 KW Hypothetical protein; Signal; Complete proteome.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 549 HYPOTHETICAL PROTEIN YFAQ.  
 SQ SEQUENCE 549 AA; 61475 MW; 72C26716D953C9D1 CRC64;  
 Query Match 69.0%; Score 40; DB 1; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 28;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYV 7  
 |||||  
 Db 125 WGOYV 129

RESULT 9  
 YCDS\_ECOLI STANDARD; PRT; 807 AA.

AC P75307;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein ycds precursor.  
 GN YCDS OR B1024 OR Z1526 OR ECS1270.  
 OS Escherichia coli, and  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxId=562, 83334;

RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474 (1997).

RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Alta H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,  
 RA Sanei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano W., Horiiuchi T.;  
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155 (1996).

RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobbeck E.J., Davis N.W., Lim A., Dinalanta E.T., Pocanousis K.,  
 RA Apodaca J., Antcharavan T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
 RL Nature 409:529-533 (2001).

RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takahashi H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 RA Kubura S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22 (2001).

CC -1- SUBCELLULAR LOCATION: Outer membrane (Potential).  
 CC -1- SIMILARITY: STRONG, TO Y.PESTIS HEMIN-BINDING PROTEIN HMSH.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announce/>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC -----  
 CC DR EMBL; AB000204; AAC74109.1; -;  
 CC DR EMBL; D90739; BAA35806.1; -;  
 CC DR EMBL; D90740; BAA35809.1; -;  
 CC DR EMBL; AB005302; AAC55642.1; -;  
 CC DR EMBL; AP002554; BAB34693.1; -;  
 CC DR PIR; F64844; F64844.  
 CC DR PIR; F90787; F90787.  
 CC DR EcoGene; EG13865; ycds.  
 CC DR InterPro; IPR01440; TPR.  
 CC DR Pfam; PF00515; TPR; 1.  
 CC KW Hypothetical protein; Outer membrane; Signal; Complete proteome.  
 CC FT SIGNAL  
 CC FT CHAIN 1..26  
 CC FT POTENTIAL.  
 CC FT CHAIN 27..807  
 CC FT HYPOTHETICAL PROTEIN YCDS.  
 CC SQ SEQUENCE 807 AA; 92207 MW; B20067C3D41723BD CRC64;

Query Match 69.0%; Score 40; DB 1; Length 807;  
 Best local Similarity 100.0%; Pred. No. 40;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYV 7  
 |||||  
 Db 314 WGOYV 318

RESULT 10  
 FCP\_ISOGA STANDARD; PRT; 208 AA.

AC Q39709;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Fucosanthin-chlorophyll A-C binding protein, chloroplast precursor  
 DE (FCP).  
 GN FCP.  
 OS Isochrysis galbana.  
 OC Eukaryota; Haptophyceae; Isochrysidales; Isochrysis.  
 OX NCBI\_TaxId=37099;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=DUN;  
 RX MEDLINE=94325461; PubMed=8049362;  
 RA Laroche J., Henry D., Wyman K., Sukenik A., Falkowski P.;  
 RT "Cloning and nucleotide sequence of a cDNA encoding a major  
 RT fucosanthin-chlorophyll a/c-containing protein from the chrysophyte  
 RT Isochrysis galbana: implications for evolution of the cab gene  
 RT family.";  
 RL Plant Mol. Biol. 25:335-368 (1994).

CC -1- FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT  
 CC RECEPTOR, IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS  
 CC WITH WHICH IT IS CLOSELY ASSOCIATED. ENERGY IS TRANSFERRED FROM  
 CC THE CAROTENOID AND CHL C (OR B) TO CHL A AND THE PHOTOSYNTHETIC  
 CC REACTION CENTERS WHERE IT IS USED TO SYNTHESIZE ATP AND REDUCING  
 CC POWER.  
 CC -1- SUBUNIT: THE LHC COMPLEX OF CHROMOPHYTIC ALGAE IS COMPOSED OF  
 CC P680XANTHIN, CHLOROPHYLL A AND C BOUND NON-COVALENTLY BY  
 CC PIGMENTS IN LHC, P680XANTHIN: CHLOROPHYLL C: CHLOROPHYLL A IS  
 CC (0.6-1): (0.1-0.3): (1).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE. FCPs ARE  
 CC PROBABLY TRANSPORTED ACROSS THE ENDOPLASMIC RETICULUM MEMBRANES  
 CC THAT SURROUND THE PLASTID VIA A SIGNAL PEPTIDE, FOLLOWED BY  
 CC TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE VIA A TRANSIT PEPTIDE.  
 CC -1- INDUCTION: EXPRESSION IS INCREASED 5-FOLD UNDER CONDITIONS OF  
 CC LOW LIGHT.  
 CC -1- SIMILARITY: BELONGS TO THE FCP FAMILY OF LIGHT-HARVESTING  
 CC PROTEINS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----  
CC EMBL; X77333; CAA54547.1; -  
DR PIR; S46301.  
DR InterPro; IPR001344; Chloro\_Abbind.  
DR Pfam; PF00504; chloro\_a\_bind.1.  
DR ProDom; PD000275; Chloro\_Abbind.1.  
KW Light-harvesting polypeptide; Chloroplast; Photosynthesis;  
KW Photosystem II; Multigene family; Chlorophyll; Transmembrane;  
KW Thylakoid; Transit peptide.  
FT TRANSLIT 1 31 CHLOROPLAST (PROBABLE).  
FT CHAIN 32 208 FUCOKANTHIN-CHLOROPHYLL A-C BINDING  
FT TRANSMEM 102 118 POTENTIAL.  
SQ SEQUENCE 208 AA; 22471 MW; 21A36700137A0F1B CRC64;

Query Match 67.2%; Score 39; DB 1; Length 208;  
Best Local Similarity 83.3%; Pred. No. 16;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TWGQYV 7  
Db 198 TWGTYW 203

RESULT 11  
ID Y090 MYCTU STANDARD; PRT; 256 AA.  
AC 010887;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein RV0090.  
GN RV0090 OR MT0099 OR MTCY251.08.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37Rv;  
RX MEDLINE=96295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sultun J.E., Taylor K., Whitehead S., Barrell B.G.;  
RA "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence."  
RL Nature 393:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 1551 / Oshkosh;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----  
CC EMBL; Z74410; CAA98926.1; -  
DR PIR; B70750; B70750.  
DR TIGR; MT0099; -  
DR Tuberculist; RV0090; -  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 155 175 POTENTIAL.  
FT TRANSMEM 203 223 POTENTIAL.  
SQ SEQUENCE 256 AA; 27837 MW; 01033C21199DEC51 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 256;  
Best Local Similarity 66.7%; Pred. No. 19;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTWGQYVAV 9  
Db 177 KRWGEYFV 185

RESULT 12  
ID SLEB\_BACCR STANDARD; PRT; 259 AA.  
AC P70874;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Spore cortex-lytic enzyme precursor (Germination-specific amidase)  
DE (SCLB).  
GN SLEB OR BC2753.  
OS Bacillus cereus (strain ATCC 14579 / DSM 31), and  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=226900, 1396;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14579 / DSM 31;  
RX MEDLINE=22608415; PubMed=12721630;  
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,  
RA Kapratel V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,  
RA Chu L., Mazur M., Gotsman E., Larsen N., D'Souza M., Malinas T.,  
RA Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Enllich S.D.,  
RA Overbeek R., Kyripides N.;  
RT "Genome sequence of Bacillus cereus and comparative analysis with  
RL Bacillus anthracis."  
RN Nature 423:87-91(2003).  
[2]  
RP SEQUENCE FROM N.A., SEQUENCE OF 33-52; 64-80; 83-94 AND 215-234, AND  
RC MUTAGENESIS OF CYS-258.  
RP STRAIN=IFO 13597;  
RX MEDLINE=96359394; PubMed=8752358;  
RA Moriyama R., Kudoh S., Miyata S., Nonobe S., Hattori A., Makino S.;  
RT "A germination-specific spore cortex-lytic enzyme from Bacillus cereus  
RT spores: cloning and sequencing of the gene and molecular  
RT characterization of the enzyme."  
RL J. Bacteriol. 178:5330-5332(1996).  
RN [3]  
RP SEQUENCE OF 33-51.  
RC STRAIN=IFO 13597;  
RX MEDLINE=94362905; PubMed=8081503;  
RA Makino S., Ito N., Inoue T., Miyata S., Moriyama R.;  
RT "A spore-lytic enzyme released from Bacillus cereus spores during  
RT germination."  
RL Microbiology 140:1403-1410(1994).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=99214084; PubMed=10157998;  
RA Moriyama R., Fukuoka H., Miyata S., Kudoh S., Hattori A., Kozuka S.,  
RA Yasuda Y., Tochikubo K., Makino S.;

RT "Expression of a germination-specific amidase, Sleb, of Bacilli in the  
 RT forespore compartment of sporulating cells and its localization on  
 RT the exterior of the cortex in dormant spores.";  
 RL J. Bacteriol. 181:2373-2378(1999).  
 CC -1- FUNCTION: Probable N-acetylmuramyl-L-alanine amidase. Required for  
 CC spore cortex hydrolysis during germination. May form a complex  
 CC with some hydrophobic spore component, leading to a stabilization  
 CC of the enzyme in a spore-bound form.  
 CC -1- ENZYME REGULATION: Inhibited by HgCl(2). Activity is recovered by  
 CC the addition of 2-mercaptoethanol.  
 CC -1- SUBCELLULAR LOCATION: Expressed in the forespore. Sleb is then  
 CC transported across the inner forespore membrane and deposited on  
 CC the outside of the cortex.  
 CC -1- DEVELOPMENTAL STAGE: Expressed during sporulation and active  
 CC during germination. Exists as mature but inactive form in the  
 CC dormant spore.  
 CC -1- INDUCTION: Expression is sigma G-dependent.  
 CC -1- MISCELLANEOUS: B.cereus sleb could not be detected with anti-  
 CC B.subtilis sleb antiserum and vice versa.  
 CC -1- SIMILARITY: BELONGS TO THE SLEB FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AE017007; AAP09706.1; -  
 DR EMBL; D63645; BAA09800.1; -  
 DR InterPro; IPR002477; PG\_binding\_1; 1.  
 DR Pfam; PF01471; PG\_binding\_1; 1.  
 KW Hydrolyase, Sporulation; Germination; Cell wall; Signal.  
 FT SIGNAL 1 32  
 FT CHAIN 33 259  
 FT MUTAGEN 258 C->G: STRONG DECREASE IN ACTIVITY.  
 FT CONFLICT 46 46 D -> K (IN REF. 3).  
 FT SEQUENCE 259 AA; 28257 MW; 36F266D32EDA54E CRC64;  
 SQ  
 Query Match 67.2%; Score 39; DB 1; Length 259;  
 Best Local Similarity 71.4%; Pred. No. 20;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 3 WGYWAV 9  
 Db 70 WGYWAVL 76  
 RESULT 13  
 SLEB\_OCEIH STANDARD; PRT; 276 AA.  
 ID SLEB\_OCEIH STANDARD; PRT; 276 AA.  
 AC P59105;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Spore cortex-lytic enzyme precursor (SCLF).  
 CN SLEB OR OBI806.  
 OS Oceanobacillus thelyensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.  
 OC NCBI\_TaxID=182710;  
 RX MEDLINE=22220767; PubMed=12235376;  
 RA Takami H., Takaki Y., Uchiyama I.;  
 RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya  
 RT Ridge and its unexpected adaptive capabilities to extreme  
 RT environments";  
 RT Nucleic Acids Res. 30:3927-3935(2002).  
 CC -1- FUNCTION: Required for spore cortex hydrolysis during germination  
 CC (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SLEB FAMILY.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AP004599; BAC13762.1; -  
 DR InterPro; IPR002477; PG\_binding\_1; 1.  
 DR Pfam; PF01471; PG\_binding\_1; 1.  
 KW Hydrolyase, Sporulation; Germination; Cell wall; Signal;  
 KW Complete proteome.  
 FT SIGNAL 1 25  
 FT CHAIN 26 276  
 FT SEQUENCE 276 AA; 30363 MW; DB1D640BBE83CF6 CRC64;  
 SQ  
 Query Match 67.2%; Score 39; DB 1; Length 276;  
 Best Local Similarity 71.4%; Pred. No. 21;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 3 WGYWAV 9  
 Db 70 WGYWAVL 76  
 RESULT 14  
 NPS2\_MOUSE STANDARD; PRT; 281 AA.  
 ID NPS2\_MOUSE STANDARD; PRT; 281 AA.  
 AC O55126;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NIPSNAP2 protein (Glioblastoma amplified sequence).  
 DE NIPSNAP2 protein (Glioblastoma amplified sequence).  
 GN GBAS OR NIPSNAP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CN NCBI\_TaxID=10090;  
 RX MEDLINE=96326305; PubMed=9661659;  
 RA Serousel E., Pan H.Q., Kedra D., Roe B.A., Dumanaki J.P.;  
 RT "Characterization of the human NIPSNAP1 gene from 22q12: a member of a  
 RT novel gene family";  
 RL Gene 212:13-20(1998).  
 CC -1- SIMILARITY: BELONGS TO THE NIPSNAP FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AJ001261; CAA04635.1; -  
 DR MGP; MGI:1278343; Gbaf.  
 DR SEQUENCE 281 AA; 32932 MW; 260D52675BF1CA7E CRC64;  
 SQ  
 Query Match 67.2%; Score 39; DB 1; Length 281;  
 Best Local Similarity 83.3%; Pred. No. 21;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 3 WGYWYA 8  
 Db 197 WGYWYA 202  
 RESULT 15  
 NPS2\_HUMAN STANDARD; PRT; 286 AA.  
 ID NPS2\_HUMAN STANDARD; PRT; 286 AA.

AC 075323; 043801;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE NipSnap2 protein (Glybiolastoma amplified sequence).  
 GN GBAS OR NIPSNAP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277458; PubMed=9615231;  
 RA Wang X.-Y., Smith D.I., Liu W., James C.D.;  
 RT "GBAS, a novel gene encoding a protein with tyrosine phosphorylation  
 sites and a transmembrane domain, is co-amplified with EGFR.";  
 RL Genomics 49:448-451(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98326305; PubMed=9661659;  
 RA Serousai E., Pan H.-O., Kedra D., Roe B.A., Dumaneki J.P.;  
 RT "Characterization of the human NIPSNAP1 gene from 22q12: a member of a  
 novel gene family";  
 RL Gene 212:13-20(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Colon;  
 MEDLINE=22386257; PubMed=12477932;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,  
 RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalski U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- TISSUE SPECIFICITY: Widely expressed. Most abundant in heart and  
 skeletal muscle.  
 CC -1- SIMILARITY: BELONGS TO THE NIPSNAP FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF029786; AAC29002.1; -;  
 DR EMBL; AJ001259; CA04633.1; -;  
 DR EMBL; BC001837; AA01837.1; -;  
 DR EMBL; BC000732; AA00732.1; -;  
 DR GeneW; HGNC:4179; GBAS.  
 DR MIM; 603004; -;  
 FT CONFLICT 9  
 SQ SEQUENCE 286 AA; 33742 MW; 7ED85297E4DC9D08 CRC64;  
 RGAAGAGG -> AEAAGRR (IN REF. 2).  
 Query Match 67.2%; Score 39; DB 1; Length 286;  
 Best Local Similarity 83.3%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WGYTWA 8  
 Db 202 WGYTWA 207  
 RESULT 16  
 NPS2\_BRARE STANDARD; PRT; 288 AA.  
 AC 09P058;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NipSnap2 protein (Fragment).  
 GN NIPSNAP2.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kedra D., Dumaneki J.P.;  
 RT "Cloning of NIPSNAP gene orthologues in Danio rerio and Drosophila  
 melanogaster";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE NIPSNAP FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AJ249797; CAB56702.1; -;  
 DR ZFIN; ZDB-GENE-991008-18; nipsnap2.  
 FT NON\_TSR 1  
 SQ SEQUENCE 288 AA; 33667 MW; 66EDDB045C6288C CRC64;  
 Query Match 67.2%; Score 39; DB 1; Length 288;  
 Best Local Similarity 83.3%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 3 WGYTWA 8  
 Db 204 WGYTWA 209  
 RESULT 17  
 PTP1\_YEAST STANDARD; PRT; 335 AA.  
 ID PTP1\_YEAST  
 AC P25044;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Protein-tyrosine phosphatase 1 (EC 3.1.3.48) (PTPase 1).  
 GN PTP1 OR YD1230W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OC NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91302312; PubMed=1649172;  
 RA Guan K., Deschenes R.J., Qiu H., Dixon J.E.;  
 RT "Cloning and expression of a yeast protein tyrosine phosphatase";  
 RL J. Biol. Chem. 266:12964-12970(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rasmussen S.W.;  
 RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IS NOT REQUIRED FOR VEGETATIVE GROWTH.

```

CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: M64062; AAA34923.1; -
CC EMBL: 274278; CAA98809.1; -
CC PIR: A39862; A39862.
CC HSSP: P29350; 1GM2.
CC SGD: S0002389; PTP1.
CC GO: GO:0006470; P:protein amino acid dephosphorylation; IDA.
CC InterPro: IPR000387; TYR_phosphatase.
CC InterPro: IPR000242; Tyr_PP.
CC Pfam: PF00102; Y_phosphatase; 1.
CC PRINTS: PR00700; PRTYPHPTASE.
CC SMART: SM00194; PTPc; 1.
CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
CC Hydrolase.
CC ACT_SITE
CC SEQUENCE 335 AA; 3868 MM; 15PFI5E0694B562 CRC64;
SQ
Query Match 67.2%; Score 39; DB 1; Length 335;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KTWQGYW 7
Db 108 KTWQDFW 114
-----
RESULT 18
ID PT2B_ARATH STANDARD; PRT; 585 AA.
AC P46032;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide transporter PTR2-B (Histidine transporting protein).
GN PTR2-B OR NTR1 OR AT2G02040 OR F14H20.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosida II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
OX 111
RN RA SEQUENCE FROM N.A.
RP STRAIN=cv. Landsberg erecta;
RA Song W., Steiner H.-Y., Zhang L., Naider F., Stacey G.,
RA Becker J.M.;
RL Submitted (XXX-1995) to the EMBL/GenBank/DDA databases.
[2]
RN RP SEQUENCE FROM N.A.
RP STRAIN=cv. C24;
RA MEDLINE=94307379; PubMed=8033999;
RA Frommer W.B., Hummel S., Rentsch D.;
RT "Cloning of an Arabidopsis histidine transporting protein related to
RL nitrate and peptide transporters.";
RL FEBS Lett. 347:185-189(1994).
[3]
RN RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;

```

```

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RL thaliana.";
RL Nature 402:761-768(1999).
CC -1- FUNCTION: PEPTIDE TRANSPORT. HIGH AFFINITY, LOW CAPACITY
CC TRANSPORTER. CAN ALSO TRANSPORT HISTIDINE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL: L39082; AAB00858.1; -
CC EMBL: X77503; CAA54634.1; -
CC EMBL: AC006532; AAD20096.1; -
CC PIR: C84432; C84432.
CC PIR: S46236; S46236.
CC InterPro: IPR001059; PTR2.
CC Pfam: PF00854; PTR2; 1.
CC PROSITE: PS01022; PTR2_1; 1.
CC PROSITE: PS01023; PTR2_2; 1.
CC Peptide transporter; Transport; Transmembrane.
CC TRANSMEM 91 111
CC TRANSMEM 116 136 POTENTIAL.
CC TRANSMEM 154 174 POTENTIAL.
CC TRANSMEM 200 220 POTENTIAL.
CC TRANSMEM 228 248 POTENTIAL.
CC TRANSMEM 351 371 POTENTIAL.
CC TRANSMEM 387 407 POTENTIAL.
CC TRANSMEM 431 451 POTENTIAL.
CC TRANSMEM 472 492 POTENTIAL.
CC TRANSMEM 511 531 POTENTIAL.
CC TRANSMEM 556 576 POTENTIAL.
CC CONFLICT 334 334 R -> ED (IN REF. 2).
SQ SEQUENCE 585 AA; 64421 MM; C58P8194776E2D97 CRC64;
QY 3 WGYWAV 9
Db 110 WGYWTI 116
-----
RESULT 19
ID CYST_ECOLI STANDARD; PRT; 277 AA.
AC P16701;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sulfate transport system permease protein cyst.
GN CYSU OR CYST OR B2424.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
OX 111
RN RP SEQUENCE FROM N.A.
RP STRAIN=KL2;

```



RX MEDLINE=90264334; PubMed=2188958;  
RA Sisko A., Hryniewicz M.M., Hulanicka D.M., Boeck A.;  
RT "Sulfate and thiosulfate transport in *Escherichia coli* K-12:  
RL J. Bacteriol. 172:3351-3357(1990).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12 / MG1655;  
RC MEDLINE=97426617; PubMed=9278503;  
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirpatrick H.A., Goeden W.A., Rose D.J.,  
RA Mau B., Siao Y.;  
RT "The complete genome sequence of *Escherichia coli* K-12.";  
RL Science 277:1453-1474(1997).  
[3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12;  
RC MEDLINE=97349980; PubMed=9205837;  
RA Yamamoto Y., Alba H., Baba T., Hayaishi K., Inada T., Isono K.,  
RA Itoh T., Kimura S., Kitegawa M., Makino K., Miki T., Mitsuhashi N.,  
RA Mitsuhashi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,  
RA Oshima T., Oyama S., Saito N., Sato Y., Sivasubramanian S.,  
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
RA Yamagata S., Horikuchi T.;  
RT "Construction of a contiguous 874-kb sequence of the *Escherichia coli*  
RT K-12 genome corresponding to 50.0-68.8 min on the linkage map and  
RT analysis of its sequence features.";  
RL DNA Res. 4:91-113(1997).  
CC -1- FUNCTION: Part of the ABC transporter complex *cysAMP* (TC  
CC 3.A.1.6.1) involved in sulfate/thiosulfate import. Probably  
CC responsible for the translocation of the substrate across the  
CC membrane.  
CC -1- SUBUNIT: The complex is composed of two ATP-binding proteins  
CC (*cysA*), two transmembrane proteins (*cysT* and *cysW*) and a solute-  
CC binding protein (*cysP*) (Probable).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
CC (Probable).  
CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT  
CC SYSTEM PERMEASE FAMILY. CYSTM SUBFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M32101; AAA23637.1; -;  
DR EMBL; AE000330; AAC75477.1; -;  
DR EMBL; D90871; BAA16298.1; -;  
DR EMBL; D90872; BAA16307.1; -;  
DR PIR; A35402; QRECSL;  
DR Ecocyc; EG10197; *cysU*.  
DR InterPro; IPR000515; BPD transp.  
DR InterPro; IPR005667; Sulph transp2.  
DR Pfam; PF00528; BPD transp.1.  
DR TIGRfams; TIGR00969; 3a0106s02.1.  
DR PROSITE; PS00402; BPD\_TRANSP\_INN\_MEMBER; 1.  
KW Transp; Sulfate transp; Membrane; Inner membrane; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 17 37 POTENTIAL.  
FT TRANSMEM 64 84 POTENTIAL.  
FT TRANSMEM 99 119 POTENTIAL.  
FT TRANSMEM 136 156 POTENTIAL.  
FT TRANSMEM 185 205 POTENTIAL.  
FT TRANSMEM 215 235 POTENTIAL.  
FT TRANSMEM 243 263 POTENTIAL.  
SQ SEQUENCE 277 AA; 30291 MW; 1392821BDE24459 CRC64;  
Query Match 65.5%; Score 38; DB 1; Length 277;  
Best Local Similarity 62.5%; Pred. No. 30;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Cy 2 TWGQYNAV 9  
Db 43 SMOYREV 50  
RESULT 20  
ID UBIA\_ECOLI  
AC P26601; STANDARD; PRT; 290 AA.  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 4-Hydroxybenzoate octaprenyltransferase (EC 2.5.1.-) (4-HB  
DE polyprenyltransferase)  
GN UBIA OR CYR OR B4040 OR C5010 OR Z5639 OR ECSS023.  
OS *Escherichia coli*,  
OS *Escherichia coli* O6, and  
OC *Escherichia coli* O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Escherichia*.  
CX NCBI\_TaxID=562, 217992, 83334;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12;  
RC MEDLINE=92355505; PubMed=1644758;  
RA Nichols B.P., Green J.M.;  
RT "Cloning and sequencing of *Escherichia coli* *ubiC* and purification of  
RT chorismate lyase.";  
RL J. Bacteriol. 174:5309-5316(1992).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12 / MC4100;  
RC MEDLINE=92354744; PubMed=1644192;  
RA Siebert M., Bechtold A., Melzer M., May U., Berger U., Schroeder G.,  
RA Schroeder J., Severin K., Heide L.;  
RT "Ubiquinone biosynthesis. Cloning of the genes coding for chorismate  
RT pyruvate-lyase and 4-hydroxybenzoate octaprenyl transferase from  
RT *Escherichia coli*.";  
RL FEBS Lett. 307:347-350(1992).  
[3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12 / W3110;  
RC MEDLINE=92380960; PubMed=1512213;  
RA Nishimura K., Nakahigashi K., Inokuchi H.;  
RT "Location of the *ubiA* gene on the physical map of *Escherichia coli*.";  
RL J. Bacteriol. 174:5762-5762(1992).  
[4]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12;  
RC Wolter F.P.;  
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.  
[5]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12 / MG1655;  
RC MEDLINE=94089392; PubMed=8265357;  
RA Blatter F.R., Burland V.D., Plunkett G. III, Sofia H.J.,  
RA Daniels D.L.;  
RT "Analysis of the *Escherichia coli* genome. IV. DNA sequence of the  
RT region from 89.2 to 92.8 minutes.";  
RL Nucleic Acids Res. 21:5408-5417(1993).  
[6]  
RN SEQUENCE FROM N.A.  
RP STRAIN=O6:H1 / CFT073 / ATCC 700928;  
RC MEDLINE=22388234; PubMed=12471157;  
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosch P.,  
RA Raeko D., Buckles E.L., Ikon S.-R., Boutin A., Hackett J., Stroud D.,  
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
RA Mobley H.L.T., Domeneberg M.S., Blatter F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
RT of uropathogenic *Escherichia coli*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

```

RN [7]
EMBL: M93136; AAA24712.1; -
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamotis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kubara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [9]
RP SEQUENCE OF 1-80 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=94014977; PubMed=8409922;
RA Wu G., Williams H.D., Gibson F., Foote R.K.;
RT "Mutants of Escherichia coli affected in respiration: the cloning and
RT nucleotide sequence of ubiA, encoding the membrane-bound p-
RT hydroxybenzoate:octaprenyltransferase.";
RL J. Gen. Microbiol. 139:1795-1805(1993).
RN [10]
RP CHARACTERIZATION.
RX MEDLINE=94207029; PubMed=8155731;
RA Weizer M., Heide L.;
RT "Characterization of polyprenyl:di-phosphate:4-hydroxybenzoate
RT polyprenyltransferase from Escherichia coli.";
RL Biochim. Biophys. Acta 1212:93-102(1994).
RN [11]
RP CHARACTERIZATION.
RX MEDLINE=95072311; PubMed=7765507;
RA Suzuki K., Ueda M., Yuasa M., Nakagawa T., Kawamukai M., Matsuda H.;
RT "Evidence that Escherichia coli ubiA product is a functional homolog
RT of yeast COQ2, and the regulation of ubiA gene expression.";
RL Biosci. Biotechnol. Biochem. 58:1814-1819(1994).
CC -1- FUNCTION: SYNTHESIS OF 3-OCTAPRENYL-4-HYDROXYBENZOATE.
CC -1- CATALYTIC ACTIVITY: 4-hydroxybenzoate + farnesylfarnesylgeraniol
CC = 3-octaprenyl-4-hydroxybenzoate.
CC -1- COFACTOR: Magnesium.
CC -1- PATHWAY: Ubiquinone biosynthesis; second step.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE UBIA PRENYLTRANSFERASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL: M93136; AAA24712.1; -
CC EMBL: M93413; AAA24717.1; -
CC EMBL: X66619; CAA47182.1; -
CC EMBL: X57434; CAA40682.1; -
CC EMBL: X69522; CAA49270.1; -
CC EMBL: U00006; AAC3134.1; -
CC EMBL: AE004777; AAC7010.1; -
CC EMBL: AE016770; AAN83436.1; -
CC EMBL: AB005637; AAG59239.1; -
CC EMBL: AP002568; BAB38446.1; -
CC EMBL: M96268; AAA17028.1; -

```

```

DR EMBL: X63407; CAA45003.1; -
DR PIR: G91256; G91256.
DR PIR: JC2316; JC2316.
DR EcGene; EG13370; ubiA.
DR InterPro; IPR000537; UbiA.
DR InterPro; IPR006370; UbiA_proteo.
DR Pfam; PF01040; UbiA_1.
DR TIGRfam; TIGR01474; ubiA_proteo; 1.
DR PROSITE; PS00943; UbiA_1.
KW Ubiquinone biosynthesis; Transferase; Transmembrane; Inner membrane;
KW Magnesium; Complete proteome.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT TRANSMEM 234 254 POTENTIAL.
FT TRANSMEM 268 288 POTENTIAL.
SQ SEQUENCE 290 AA; 32511 MW; P10FED1D7A30E115 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 290;
Best Local Similarity 57.1%; Pred. No. 31;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGYWAV 9
Db 237 WGYTMSI 243

RESULT 21
EX24 ARATH STANDARD; PRT; 312 AA.
ID EX24 ARATH
AC O9FL76;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative alpha-expansin 24 precursor (At-EXP24) (Ath-
DE ExpAlpha-1.19).
GN EXP24 OR AT5G39310 OR K3K3.22 OR K3K3.160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eupsidia II; Brassicales; Brassicaceae; Arabidopsids.
CX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=96344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Cosgrove D.J.;
RL Unpublished observations (DEC-2001).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; AB010694; BAB09386.1; ALT SEQ.  
DR InterPro; IPR007112; Expan\_endogl.  
DR InterPro; IPR007118; Expan\_lo1\_pi.  
DR InterPro; IPR007117; Expan\_lo1\_pi\_C.  
DR Pfam; PF01357; Pollen\_allergen; 1.  
DR PRINTS; PR01225; EXPANSIN\_FAMLY.  
DR PRODOM; PD002179; Expan\_lo1\_pi\_C; 1.  
DR PROSITE; PS50843; EXPANSIN\_CBD; 1.  
DR PROSITE; PS50842; EXPANSIN\_EG45; 1.  
KM Hypothetical protein; Cell wall; Signal; Repeat; Multigene family.  
FT SIGNAL 1 27  
FT CHAIN 28 312  
FT DOMAIN 42 77  
FT REPEAT 42 47  
FT REPEAT 48 53  
FT REPEAT 54 59  
FT REPEAT 60 65  
FT REPEAT 66 71  
FT REPEAT 72 77  
FT DOMAIN 108 218  
FT DOMAIN 228 307  
SQ SEQUENCE 312 AA; 33775 MW; FB3C64A2D529644B CRC64;

Query Match 65.5%; Score 38; DB 1; Length 312;  
Best Local Similarity 62.5%; Pred. No. 33;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTWGQYVA 8  
Db 260 KMWQIWS 267

RESULT 22  
XINC STRLI STANDARD; PRT; 240 AA.  
AC P26220;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (xylanase C)  
DE (1,4-beta-D-xylan xylanohydrolase C).  
GN XLNC.  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OC NCBI\_TaxID=1916;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.  
RC STRAIN=66 / 1326;  
RX MEDLINE=92077439; PubMed=1743521;  
RA Sharek P., Roy C., Yasuchi M., Morosoli R., Kluepfel D.;  
RT "Sequences of three genes specifying xylanases in Streptomyces  
RT lividans.";  
RL Gene 107:75-82(1991).  
CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major  
CC component of plant cell walls.  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylonic  
CC linkages in xylans.  
CC -1- PATHWAY: Xylan degradation.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; M64553; AAA26836.1; -;  
DR EMBL; A25307; CAA01768.1; -;  
DR PIR; J50591; J50591.  
DR HSPB; P09850; 1XNB.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR InterPro; IPR006311; Tat.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLYDRLASE11.  
DR TIGRFAMs; TIGR01409; Tat\_signal\_seg; 1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12; 1.  
KM Xylan degradation; Hydrolase; Glycosidase; Signal.  
FT SIGNAL 1 49  
FT CHAIN 50 240  
FT ACT\_SITE 134 134  
FT ACT\_SITE 226 226  
SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match 63.8%; Score 37; DB 1; Length 240;  
Best Local Similarity 66.7%; Pred. No. 37;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYVA 9  
Db 178 KTFQQWVS 186

RESULT 23  
RM09 MOUSE STANDARD; PRT; 256 AA.  
AC Q99N94;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 60S ribosomal protein L9, mitochondrial precursor (L9mc) (Fragment).  
GN MRPL9.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21293042; PubMed=11279069;  
RA Suzuki T., Terasaki M., Takemoto-Hori C., Hanada T., Wada A.,  
RA Matanabe K.;  
RT "Structural compensation for the deficit of rRNA with proteins in the  
RT mammalian mitochondrial ribosome. Systematic analysis of protein  
RT components of the large ribosomal subunit from mammalian  
RT mitochondria.";  
RL J. Biol. Chem. 276:21724-21736(2001).  
CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
CC -1- SIMILARITY: BELONGS TO THE L9P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; AB049637; BAB40842.1; -;  
DR MGD; MGI:2137211; Mrpl9.  
DR InterPro; IPR000244; Ribosomal\_L9.  
DR Pfam; PF01281; Ribosomal\_L9\_N; 1.  
KM Ribosomal protein; Mitochondrion; Transit peptide.  
FT NON\_TER 1 1  
FT TRANSIT <1 ? MITOCHONDRION (POTENTIAL).  
FT -----

FT CHAIN ? 256 60S RIBOSOMAL PROTEIN L9.  
 SQ SEQUENCE 256 AA; 29460 MW; FE22A2F8D1A1CB46 CRC64;  
 Query Match 63.8%; Score 37; DB 1; Length 256;  
 Best Local Similarity 80.0%; Pred. No. 40;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 GC 3 WGYW 7  
 Db 204 WGEYW 208  
 RESULT 24  
 RM09 HUMAN STANDARD; PRT; 267 AA.  
 AC Q9BYD2; Q9BSW8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE 60S ribosomal protein L9, mitochondrial precursor (L9mt).  
 GN MRPL9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21293042; PubMed=11279069;  
 RA Suzuki T., Terasaki M., Takemoto-Hori C., Hanada T., Ueda T., Wada A.,  
 RA Watanabe K.;  
 RT "Structural compensation for the deficit of rRNA with proteins in the  
 RT mammalian mitochondrial ribosome. Systematic analysis of protein  
 RT components of the large ribosomal subunit from mammalian  
 RT mitochondria.";  
 RL J. Biol. Chem. 276:21724-21736(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Bilesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Human and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE L9P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AB049636; BAB40841.1; -;  
 CC EMBL; BC004517; AA04517.1; -;  
 CC Genew; HGNC:14277; MRPL9.

DR InterPro; IPR00244; Ribosomal L9.  
 DR Pfam; PFO1281; Ribosomal L9 N; 1.  
 KW Ribosomal protein; Mitochondrion; Transic peptide.  
 FT TRANSIT 1  
 FT CHAIN ? 267 MITOCHONDRION (POTENTIAL).  
 FT CONFLICT 210 210 A -> E (IN REF. 2).  
 SQ SEQUENCE 267 AA; 30185 MW; 346C25420FFD1B4 CRC64;  
 Query Match 63.8%; Score 37; DB 1; Length 267;  
 Best Local Similarity 80.0%; Pred. No. 41;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 GC 3 WGYW 7  
 Db 216 WGEYW 220  
 RESULT 25  
 CYST SALTY STANDARD; PRT; 277 AA.  
 AC P41032;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Sulfate transport system permease protein cyst.  
 GN CYSU OR CYST OR STM2443.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Lt2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 RT Lt2.";  
 RL Nature 413:852-856(2001).  
 RN [2]  
 RP SEQUENCE OF 1-15 FROM N.A.  
 RC STRAIN=Lt2;  
 RX MEDLINE=91358382; PubMed=1909324;  
 RA Hryniewicz M.M., Kredich N.M.;  
 RT "The cyst promoter of *Salmonella typhimurium*: characterization of two  
 RT binding sites for CysB protein, studies of in vivo transcription  
 RT initiation, and demonstration of the anti-inducer effects of  
 RT thiosulfate.";  
 RL J. Bacteriol. 173:5876-5886(1991).  
 CC -1- FUNCTION: Part of the ABC transporter complex CysAWTP (TC  
 CC 3.A.1.6.1) involved in sulfate/thiosulfate import. Probably  
 CC responsible for the translocation of the substrate across the  
 CC membrane (By similarity).  
 CC -1- SUBUNIT: The complex is composed of two ATP-binding proteins  
 CC (cysA), two transmembrane proteins (cysT and cysW) and a solute-  
 CC binding protein (cysB) (Probable).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM PERMEASE FAMILY. CYSTM SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AE008810; AAL21337.1; -;

DR StyGene; SG10520; cyst.  
DR InterPro; IPR000515; BPD\_transp.  
DR InterPro; IPR005667; Sulph\_transp2.  
DR Pfam; PF00528; BPD\_transp\_1.  
DR TIGRPFAMs; TIGR00965; ja0106802; 1.  
DR PROSITE; PS00402; BPD\_TRANSP\_INN\_MEMBER; 1.  
KW Transport; Sulfate transport; Membrane; Inner membrane; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 17 37 POTENTIAL.  
FT TRANSMEM 64 84 POTENTIAL.  
FT TRANSMEM 99 119 POTENTIAL.  
FT TRANSMEM 136 156 POTENTIAL.  
FT TRANSMEM 188 205 POTENTIAL.  
FT TRANSMEM 215 235 POTENTIAL.  
FT TRANSMEM 243 263 POTENTIAL.  
SQ SEQUENCE 277 AA; 30182 MW; 8C22531C99E50748 CRC64;  
  
Query Match 63.8%; Score 37; DB 1; Length 277;  
Best Local Similarity 62.5%; Pred. No. 43;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 TWGQYMAV 9  
Db 43 SMDQYMDV 50

Search completed: August 14, 2003, 09:06:17  
Job time : 15.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 09:05:40 ; Search time 60 Seconds  
(without alignments)  
38.708 Million cell updates/sec

Title: US-09-214-836-1

Perfect score: 58

Sequence: 1 KTWGQYWAV 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_23.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioph:\*  
17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	84.5	626	11 Q9CZB2	Q9CZB2 mus musculus
2	45	77.6	476	12 Q8QNG3	Q8QNG3 ectocarpus
3	42	72.4	98	16 Q8RD90	Q8RD90 thermoaer
4	42	72.4	290	16 Q8XGZ7	Q8XGZ7 salmoneia
5	42	72.4	310	8 Q8MHX9	Q8MHX9 psilorum nu
6	42	72.4	608	16 Q98R58	Q98R58 mycoplasma
7	41	70.7	116	3 Q8UVZ4	Q8UVZ4 gaumannomy
8	41	70.7	260	8 Q95DY2	Q95DY2 cucumis sat
9	41	70.7	458	5 Q18533	Q18533 schistosoma
10	40	69.0	214	5 Q81080	Q81080 crassostrea
11	40	69.0	216	5 Q81788	Q81788 crassostrea
12	40	69.0	216	5 Q810T4	Q810T4 crassostrea
13	40	69.0	222	2 Q8GB62	Q8GB62 pseudocaler
14	40	69.0	264	16 Q8XB36	Q8XB36 escherichia
15	40	69.0	276	17 Q9Y9N5	Q9Y9N5 aeropyrum p
16	40	69.0	281	16 Q9KPY3	Q9KPY3 vibrio chol

17	40	69.0	305	2 Q45818	Q45818 chloroflexu
18	40	69.0	400	16 P74474	P74474 synchocyst
19	40	69.0	401	5 Q9BJM3	Q9BJM3 onchocerca
20	40	69.0	518	5 Q02622	Q02622 crassostrea
21	40	69.0	520	5 Q8MSH2	Q8MSH2 crassostrea
22	40	69.0	549	16 Q8CV9	Q8CV9 escherichia
23	40	69.0	551	10 Q8SS55	Q8SS55 oryza sativ
24	40	69.0	746	2 Q8GF63	Q8GF63 zymomonas m
25	40	69.0	750	2 Q9REP1	Q9REP1 zymomonas m
26	40	69.0	1451	5 Q01737	Q01737 caenorhabd
27	39	67.2	73	12 Q8OR33	Q8OR33 human papil
28	39	67.2	73	12 Q9DMY8	Q9DMY8 human papil
29	39	67.2	191	2 Q9EW89	Q9EW89 streptomyce
30	39	67.2	228	2 Q59962	Q59962 streptomyce
31	39	67.2	236	16 Q9RXG5	Q9RXG5 deinococcus
32	39	67.2	282	16 Q8DE55	Q8DE55 vibrio vuln
33	39	67.2	335	2 Q08346	Q08346 streptomyce
34	39	67.2	335	2 Q9KMM4	Q9KMM4 streptomyce
35	39	67.2	347	16 Q985T4	Q985T4 thizobium 1
36	39	67.2	358	13 Q9W616	Q9W616 brachydantio
37	39	67.2	358	13 Q9PM55	Q9PM55 brachydantio
38	39	67.2	362	13 Q9W617	Q9W617 brachydantio
39	39	67.2	366	13 Q9DRC6	Q9DRC6 xenopus lae
40	39	67.2	367	13 Q9DD36	Q9DD36 xenopus lae
41	39	67.2	367	13 Q9DFC5	Q9DFC5 xenopus lae
42	39	67.2	406	9 Q8LTU1	Q8LTU1 baccharomon
43	39	67.2	432	14 Q8JZK3	Q8JZK3 uncultured
44	39	67.2	461	1 Q8NKR5	Q8NKR5 thermococcu
45	39	67.2	469	1 Q50200	Q50200 thermococcu

## ALIGNMENTS

RESULT 1	ID	Q9CZB2	PREDIMINARY;	PRT;	626 AA.
AC	Q9CZB2	Q9CZB2			
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)			
DE	N/A.				
GN	SI OR SI.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Embryo;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,				
RA	Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner U., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Hono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustigich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombetris P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,				
RA	Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,				
RA	Hayashizaki Y.,				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
DR	EMBL; AK012808; BAB28486.1; -.				
DR	MGI; MGI:98301; Sl.				

DR InterPro; IPR000601; PKD\_domain.  
DR Pfam; PF00801; PKD; 1.  
DR SMART; SM00089; PKD; 1.  
DR PROSITE; PS50093; PKD; 1.  
SQ SEQUENCE 626 AA; 66301 MW; 7EC0A06C63212674 CRC64;

Query Match 84.5%; Score 49; DB 11; Length 626;  
Best Local Similarity 77.8%; Pred. No. 9.2;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGYWAV 9  
Db 153 KTWGYWAV 161

## RESULT 2

Q8ONG3 PRELIMINARY; PRT; 476 AA.  
AC Q8ONG3;  
DT 01-JUN-2002 (TREMblrel. 21, Created)  
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE Esv-1-116.  
OS Ectocarpus siliculosus virus.  
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.  
OX NCBI\_TaxID=37665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Esv-1;  
RA Delarogue N., Boche G., Pohl T., Knippers R., Mueller D.G., Boland W.,  
RT "The complete nucleotide sequence of the Ectocarpus siliculosus virus  
genome."  
RL Submitted (MAR-2001) to the EMBL/genbank/DBJ databases.  
DR EMBL; AF204951; AAK14534.1;  
DR Pfam; PF04451; Capsid\_Tridovir; 1  
SQ SEQUENCE 476 AA; 53212 MW; A6F5C92F3C92526D CRC64;

Query Match 77.6%; Score 45; DB 12; Length 476;  
Best Local Similarity 75.0%; Pred. No. 29;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TWGYWAV 9  
Db 202 TWGYWAV 209

## RESULT 3

Q8RD90 PRELIMINARY; PRT; 98 AA.  
AC Q8RD90;  
DT 01-JUN-2002 (TREMblrel. 21, Created)  
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
DE Hypothetical protein TTE0156.  
GN TTE0156.  
OS Thermomicrobacter tengcongensis.  
OC Bacteria; Firmicutes; Clostridia; Thermomicrobacteriales;  
CC Thermomicrobacteriaceae; Thermomicrobacter.  
OX NCBI\_TaxID=119072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MB4 / JCM 11007;  
RA MEDLINE=21992816; PubMed=11997336;  
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
RT "A complete sequence of T. tengcongensis genome."  
RL Genome Res. 12:689-700(2002).  
DR EMBL; AE012988; AAM23457.1;  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 98 AA; 11135 MW; 01317FPC55898A13 CRC64;

Query Match 72.4%; Score 42; DB 16; Length 98;

Best Local Similarity 75.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTWGYWAV 8  
Db 35 KTWGYWAV 42

## RESULT 4

Q8XGZ7 PRELIMINARY; PRT; 290 AA.  
AC Q8XGZ7;  
DT 01-MAR-2002 (TREMblrel. 20, Created)  
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE P-hydroxybenzoate: octaprenyltransferase (EC 2.5.1.-)  
DE (4-hydroxybenzoate octaprenyl transferase).  
GN UBA OR STM4234 OR STY4430.  
OS Salmonella typhimurium, and  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
CC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=602, 601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S. typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McCelland M., Sanderson K.E., Spiehl J., Clifton S.W., Latreille P.,  
RA Courtney L., Portwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
LT2."  
RL Nature 413:852-856(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S. typhi; STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677609;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrett B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
enterica serovar Typhi CT18."  
RL Nature 413:848-852(2001).  
DR EMBL; AB008898; AAL23058.1;  
DR EMBL; AL627282; CAD09218.1;  
DR InterPro; IPR000537; UBA.  
DR InterPro; IPR006370; UBA\_proteo.  
DR Pfam; PF01040; UBA; 1.  
DR TIGRPFAMs; TIGR01474; ubaA\_proteo; 1.  
DR PROSITE; PS00943; UBA; 1.  
KM Transferase; Complete proteome.  
SQ SEQUENCE 290 AA; 32602 MW; 0BA199F02C6C673 CRC64;

Query Match 72.4%; Score 42; DB 16; Length 290;  
Best Local Similarity 85.7%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WGYWAV 9  
Db 237 WGYWAV 243

## RESULT 5

Q8WHX9 PRELIMINARY; PRT; 310 AA.  
AC Q8WHX9;



DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Cytochrome c biosynthesis protein.  
 GN CCSA.  
 OS Psilotum nudum (Whisk fern).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Psilotophyta; Psilotales; Psilotaceae; Psilotum.  
 NCBI\_TaxID=3240;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Kingyoku;  
 RA Makasugi T., Nishikawa A., Yamada K., Sugita M.;  
 RT "Complete nucleotide sequence of the chloroplast genome from a fern,  
 Psilotum nudum";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF004638; BAB64273.1; -.  
 DR InterPro; IPR002541; CytC\_asm.  
 DR Pfam; PF01578; CytC\_asm; I.  
 DR PRINTS; PR01386; CCMCBIOGNISIS.  
 KW Chloroplast.  
 SQ SEQUENCE 310 AA; 35848 MW; 35BDB639F1C44C43 CRC64;

Query Match 72.4%; Score 42; DB 8; Length 310;  
 Best Local Similarity 62.5%; Pred. No. 56;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYWA 8  
 Db 239 ETWGSYWS 246

## RESULT 6

ID Q98R58 PRELIMINARY; PRT; 608 AA.  
 AC Q98R58;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein MYPU\_1520.  
 GN MYPU\_1520.  
 OS Mycoplasma pulmonis.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 NCBI\_TaxID=2107;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UAB CTIP;  
 RX MEDLINE=21267165; PubMed=11353084;  
 RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,  
 RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.;  
 RA Blanchard A.;  
 RT "The complete genome sequence of the murine respiratory pathogen  
 Mycoplasma pulmonis";  
 RL Nucleic Acids Res. 29:2145-2153 (2001).  
 DR EMBL; AL445563; CAC13325.1; -.  
 DR Mypulist; MYPU\_1520; -.  
 DR InterPro; IPR001708; 60kDa\_innerneb.  
 DR Pfam; PF02096; 60kDa\_IMP; I.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 608 AA; 70134 MW; E49F2EFDE924E4AD CRC64;

Query Match 72.4%; Score 42; DB 16; Length 608;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TWGQYWA 7  
 Db 349 TWGQYWA 354

## RESULT 7

Q9UVZ4  
 ID Q9UVZ4 PRELIMINARY; PRT; 116 AA.  
 AC Q9UVZ4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Fragment).  
 GN AXYL2.  
 OS Gaeanomomyces graminis.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Gaeanomomyces.  
 NCBI\_TaxID=29850;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Emami K.;  
 RT "PCR-based characterization of fungal xylanase genes";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOMYXOLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 DR EMBL; AJ249160; CAB53513.1; -.  
 DR HSSP; P09850; XNB.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; I.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11.1; I.  
 KW Glycosidase; Hydrolase; Xylan degradation.  
 FT NON\_TER 1  
 FT TER 116  
 SQ SEQUENCE 116 AA; 12791 MW; DA7BA4FEA6770E9E CRC64;

Query Match 70.7%; Score 41; DB 3; Length 116;  
 Best Local Similarity 66.7%; Pred. No. 30;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTWGQYWA 9  
 Db 80 KTFNQYWA 88

## RESULT 8

ID Q95DY2 PRELIMINARY; PRT; 260 AA.  
 AC Q95DY2;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Putative cytochrome-c synthesis associated protein.  
 GN CCSA.  
 OS Cucumis sativus (Cucumber).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 NCBI\_TaxID=3659;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ullanat R., Jayabakaran C.;  
 RT "Evidence for a divergent gene-arrangement in the chloroplast genome  
 of cucumber";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ullanat R.;  
 RL Thesis (2000), Department of Biochemistry,  
 RL Indian Institute of Science, Bangalore, India.  
 DR EMBL; AJ318074; CAC41004.1; -.  
 DR InterPro; IPR002541; CytC\_asm.  
 DR Pfam; PF01578; CytC\_asm; I.  
 KW Chloroplast.  
 SQ SEQUENCE 260 AA; 29974 MW; 24018417B5C53731 CRC64;

Query Match 70.7%; Score 41; DB 8; Length 260;  
 Best Local Similarity 71.4%; Pred. No. 67;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYV 7  
 DB 187 ETWGSYV 193

## RESULT 9

ID 018533 PRELIMINARY; PRT; 458 AA.  
 AC 018533;  
 DT 01-JAN-1998 (Tremblrel. 05, Created)  
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Preprocathepsin C precursor (EC 3.4.14.1).  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Chinese;  
 RX MEDLINE=97442731; PubMed=9297696;  
 RA Brindley P.J., Kalina B.H., Dalton J.P., Day S.R., Wong J.Y.,  
 Snythe M.L., McManus D.P.;  
 RT "Proteolytic degradation of host hemoglobin by schistosomes.";  
 RL Mol. Biochem. Parasitol. 89:1-9(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Chinese;  
 RX MEDLINE=98409270;  
 RA Holja-Jamriska L., Tort J.F., Dalton J.P., Day S.R., Fan J., Aaskov J.,  
 Brindley P.J.;  
 RT "Cathepsin C from Schistosoma japonicum: cDNA encoding the  
 RT preprocathepsin and phylogenetic relationships.";  
 RL Eur. J. Biochem. 255:527-534(1998).  
 DR EMBL; U77932; AAC32040.1; -.  
 DR HSSP; P00787; ITHE.  
 DR MEROPS; C01.070; -.  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR InterPro; IPR000169; SHProl\_acsite.  
 DR Pfam; PF00112; Peptidase\_C1; 1.  
 DR PRINTS; PR00705; PAPAIN\_C1.  
 DR ProDom; PD000158; Peptidase\_C1; 1.  
 DR SMART; SM00645; Pept\_C1; 1.  
 DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; 1.  
 DR PROSITE; PS00639; THIOI\_PROTEASE\_HIS; 1.  
 KW Hydrolyase; Protease; Signal; Thiol protease.  
 FT SIGNAL 1 22  
 FT CHAIN 222 458 CATHEPSIN C.  
 SO SEQUENCE 458 AA; 52698 MW; AD976566C4142C CRC64.

Query Match 70.7%; Score 41; DB 5; Length 458;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 TWGQYV 7  
 DB 425 SWGQYV 430

## RESULT 10

ID 081080 PRELIMINARY; PRT; 214 AA.  
 AC 081080;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Alpha amylase (EC 3.2.1.1) (Fragment).  
 GN AMY.  
 OS Crassostrea gigas (Pacific oyster).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Ostreoida;  
 OC Ostreoida; Ostreidae; Crassostrea.  
 OX NCBI\_TaxID=29159;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van Wormhout A.E.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sellios D.A.;  
 RT "Structure of the amylase genes in populations of the pacific cupped  
 RT oyster Crassostrea gigas: tissue expression and allelic  
 RT polymorphism.";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ496599; CAD43098.1; -.  
 DR EMBL; AJ496601; CAD43100.1; -.  
 KW Glycosidase; Hydrolyase.  
 FT NON\_TER 1 1  
 FT NON\_TER 214 214  
 SO SEQUENCE 214 AA; 24314 MW; CFEF0577222394MD CRC64;

Query Match 69.0%; Score 40; DB 5; Length 214;  
 Best Local Similarity 55.6%; Pred. No. 79;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYVAV 9  
 DB 135 KTWGQYVAV 143

## RESULT 11

ID 08178 PRELIMINARY; PRT; 216 AA.  
 AC 08178;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Alpha amylase (EC 3.2.1.1) (Fragment).  
 GN AMY.  
 OS Crassostrea gigas (Pacific oyster).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Ostreoida;  
 OC Ostreoida; Ostreidae; Crassostrea.  
 OX NCBI\_TaxID=29159;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van Wormhout A.E.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sellios D.A.;  
 RT "Structure of the amylase genes in populations of the pacific cupped  
 RT oyster Crassostrea gigas: tissue expression and allelic  
 RT polymorphism.";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ496597; CAD43096.1; -.  
 KW Hydrolyase; Glycosidase.  
 FT NON\_TER 1 1  
 FT NON\_TER 216 216  
 SO SEQUENCE 216 AA; 24442 MW; FD285566E51AB3A CRC64;

Query Match 69.0%; Score 40; DB 5; Length 216;  
 Best Local Similarity 55.6%; Pred. No. 80;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTWGQYVAV 9  
 DB 135 KTWGQYVAV 143

## RESULT 12

ID 081074 PRELIMINARY; PRT; 216 AA.  
 AC 081074;

DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Alpha amylase (EC 3.2.1.1) (Fragment).  
 GN AMY.  
 OS Crassostrea gigas (Pacific oyster).  
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;  
 OC Ostreoidae; Ostreidae; Crassostrea.  
 OX NCBI\_TaxID=29159;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van Wormhout A.E.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Sello D.A.;  
 RL "Structure of the amylase genes in populations of the Pacific cupped  
 oyster Crassostrea gigas: tissue expression and allelic  
 polymorphism."  
 RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AJ496596; CAD43095.1; -  
 DR EMBL; AJ496598; CAD43097.1; -  
 DR EMBL; AJ496600; CAD43099.1; -  
 KM Glycosidase; Hydrolase.  
 FT NON\_TER  
 FT 1  
 SQ SEQUENCE 216 AA; 24428 MW; 082D0533EB04AB3C CRC64;

Query Match 69.0%; Score 40; DB 5; Length 216;  
 Best Local Similarity 55.6%; Pred. No. 80;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTWGOYMAV 9  
 |||||  
 Db 135 KTWGEQWGM 143

RESULT 13  
 Q8GB62  
 ID 08GB62 PRELIMINARY; PRT; 222 AA.  
 AC 08GB62  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Extracellular agarase precursor.  
 GN AGA.  
 OS Pseudalteromonas sp. CY24.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Pseudalteromonas.  
 OX NCBI\_TaxID=210426;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CY24.  
 RC Chu Y., Yu W.G., Han F.;  
 RT "Cloning and Sequencing of an Extracellular Agarase Gene from Marine  
 Pseudalteromonas sp. strain CY24."  
 RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AY150179; AAN39119.1; -  
 SQ SEQUENCE 222 AA; 25104 MW; 6DB2FA97E750F1C CRC64;

Query Match 69.0%; Score 40; DB 2; Length 222;  
 Best Local Similarity 83.3%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TWGOYV 7  
 |||||  
 Db 29 TWGNYW 34

RESULT 14  
 Q8XE36  
 ID 08XE36 PRELIMINARY; PRT; 264 AA.  
 AC 08XE36;

DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein 23480.  
 GN Z3480 OR EGS110.  
 OS Escherichia coli O157:H7.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RC MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boulton A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimelanta E.T., Potamous K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
 RL Nature 409:529-533(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=O157:H7 / RIMD 0509952;  
 RC MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasekawa C., Ogasawara N., Yasunaga T.,  
 RA Kunara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12";  
 RL DNA Res. 8:11-22(2001).  
 DR EMBL; AE005454; AAG57356.1; -  
 DR EMBL; AP002560; BAB36533.1; -  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 264 AA; 29288 MW; 257B81A5E4A9489 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WGOYV 7  
 |||||  
 Db 125 WGOYV 129

RESULT 15  
 Q9Y9N5  
 ID 09Y9N5 PRELIMINARY; PRT; 276 AA.  
 AC 09Y9N5;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE 276AA long hypothetical lactose transport system permease protein.  
 GN APE2253.  
 OS Aeropyrum pernix.  
 CC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcates;  
 OC Desulfurococcaceae; Aeropyrum.  
 OX NCBI\_TaxID=56636;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=KI;  
 RC MEDLINE=9310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Maeda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushida N., Ogunchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 crenarchaeon, Aeropyrum pernix KI";  
 RT DNA Res. 6:83-101(1999).  
 RL EMBL; AP000064; BAA81265.1; -

DR InterPro; IPR000515; BPD transp.  
 DR Pfam; PF00528; BPD\_transp; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 276 AA; 31573 MW; A94486CBP8032631 CRC64;

Query Match 69.0%; Score 40; DB 17; Length 276;  
 Best Local Similarity 55.6%; Pred. No. 1e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KTWGQYMAV 9  
 DB 215 KTWGQYMSL 223

RESULT 16  
 O9KPY3 PRELIMINARY; PRT; 281 AA.  
 AC O9KPY3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 GN Hypothetical protein VCC2229.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrrio.  
 OX NCBI\_TaxID=666;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=El Tor N16961 / Serotype O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Ermlaeva M.D., Yamachyan J., Bess S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Ustehack T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.;  
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
 cholerae";  
 RL Nature 406:477-483(2000).  
 DR EMBL; AE004294; AAF95373.1; -.  
 DR TIGR; VC2229; -.  
 DR InterPro; IPR000583; GATase\_2.  
 DR Pfam; PF00310; GATase\_2; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 281 AA; 31824 MW; 7CA75AD3494DFDD0 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGQYV 7  
 DB 99 WGQYV 103

RESULT 17  
 O45818 PRELIMINARY; PRT; 305 AA.  
 ID O45818;  
 AC O45818;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 GN Hypothetical 33.7 Kda protein (BCHGC).  
 OS Chloroflexus aurantiacus.  
 OC Bacteria; Chloroflexi; Chloroflexales; Chloroflexaceae; Chloroflexus.  
 OX NCBI\_TaxID=1108;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J10-FL;  
 RX MEDLINE=94192803; PubMed=7511541;

RA Niedermeier G., Shiozawa J.A., Lottspeich F., Feick R.G.;  
 RT "The primary structure of two chlorosome proteins from Chloroflexus  
 aurantiacus";  
 RL FEBS Lett. 342:61-65(1994).

Query Match 69.0%; Score 40; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGQYV 7  
 DB 246 WGQYV 250

RESULT 18  
 P74474 PRELIMINARY; PRT; 400 AA.  
 ID P74474;  
 AC P74474;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 GN D-alanyl-D-alanine carboxypeptidase.  
 SLR1924.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kikuta T.,  
 RA Hoshino T., Matsuura A., Muraki A., Nakazaki N., Naito K., Okumura S.,  
 RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions";  
 RL DNA Res 3:109-136(1996).  
 DR EMBL; D90915; BAA18575.1; -.  
 DR InterPro; IPR001466; Beta\_lactamase.  
 DR Pfam; PF00144; beta\_lactamase; 1.  
 KW Carboxypeptidase; Complete proteome.  
 SQ SEQUENCE 400 AA; 44316 MW; 75510481820E462F CRC64;

Query Match 69.0%; Score 40; DB 16; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WGQYV 7  
 DB 335 WGQYV 339

RESULT 19  
 O9BIM3 PRELIMINARY; PRT; 401 AA.  
 ID O9BIM3;  
 AC O9BIM3;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, last annotation update)  
 DE Cathepsin L-like cysteine proteinase.  
 OS Onchocerca volvulus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Onchocerca.  
 OX NCBI\_TaxID=6282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Guiliano D.B., Blaxter M.L., Williams S.A., Lustigman S.;  
 RT "Characterization of a Novel Developmentally Regulated Family of  
 Cysteine Proteinases from Filarial Nematodes".  
 RL Submitted (DSC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF31036; AAK16514.1; -.  
 DR HSSP; P43335; MEM.  
 DR MEROPS; C01.055; -.  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR InterPro; IPR000169; SHprot\_acctc.  
 DR Pfam; PF00112; Peptidase\_C1; 1.  
 DR PRINTS; PR00705; PAPA1N.  
 DR ProDom; PD000158; Peptidase\_C1; 1.  
 DR SMART; SM00645; Pept\_C1; 1.  
 DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; 1.  
 DR PROSITE; PS00639; THIOI\_PROTEASE\_HIS; 1.  
 DR HydroLase; Protease; Thiol protease.  
 KM SEQUENCE 401 AA; 45511 MW; 58E10CE3913A3F66 CRC64;  
 SQ

Query Match 69.0%; Score 40; DB 5; Length 401;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTMGOYNAV 9  
 Db 359 KTYGEYWI 367

RESULT 20  
 ID 002622 PRELIMINARY; PRT; 518 AA.  
 AC 002622;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Alpha-amyase precursor (EC 3.2.1.1) (Fragment).  
 GN Amy.  
 OS Crassostrea gigas (Pacific oyster).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;  
 OC Ostreoidae; Ostreidae; Crassostrea.  
 OX NCBI\_TaxID=29159;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Digestive gland.  
 RA Moal J., Daniel J.Y., Le Moine S., Sello D., Van Wormhoudt A.,  
 RA Samain J.F.;  
 RT "Control of the expression of the amyase by food in Crassostrea  
 gigas".  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y08370; CAA69658.1; -.  
 DR HSSP; P00690; LTF.  
 DR InterPro; IPR006048; Alpha\_amy1\_C.  
 DR InterPro; IPR006047; Alpha\_amy1\_cat.  
 DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amyase; 1.  
 DR Pfam; PF02806; alpha-amyase\_C; 1.  
 DR PRINTS; PR00110; ALPHAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 DR SMART; SM00632; Amy\_C; 1.  
 KM Glycosidase; HydroLase; Signal.  
 FT NON TER 1  
 FT SIGNAL <1 1  
 FT CHAIN 19 518 POTENTIAL.  
 FT SEQUENCE 518 AA; 57435 MW; 2F386491AE7278AC CRC64;  
 SQ

Query Match 69.0%; Score 40; DB 5; Length 518;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTMGOYNAV 9  
 Db 292 KTMGEQWGM 300

RESULT 21  
 ID 08WSH2 PRELIMINARY; PRT; 520 AA.  
 AC 08WSH2;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Alpha amyase A (EC 3.2.1.1).  
 OS Crassostrea gigas (Pacific oyster).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;  
 OC Ostreoidae; Ostreidae; Crassostrea.  
 OX NCBI\_TaxID=29159;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sello D.Y., Van Wormhoudt A.E.;  
 RT "Structure and polymorphism of the amyase genes in the oyster  
 Crassostrea gigas".  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF320688; AAL37183.1; -.  
 DR InterPro; IPR006048; Alpha\_amy1\_C.  
 DR InterPro; IPR006047; Alpha\_amy1\_cat.  
 DR InterPro; IPR006589; Alp\_amy1\_cat\_sub.  
 DR InterPro; IPR006046; Glyco\_hydro\_13.  
 DR Pfam; PF00128; alpha-amyase; 1.  
 DR Pfam; PF02806; alpha-amyase\_C; 1.  
 DR PRINTS; PR00110; ALPHAMYLASE.  
 DR SMART; SM00642; Amy; 1.  
 DR SMART; SM00632; Amy\_C; 1.  
 DR HydroLase; Glycosidase.  
 KM SEQUENCE 520 AA; 57713 MW; 59A33D914E726A9A CRC64;  
 SQ

Query Match 69.0%; Score 40; DB 5; Length 520;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTMGOYNAV 9  
 Db 294 KTMGEQWGM 302

RESULT 22  
 ID 08CV9 PRELIMINARY; PRT; 549 AA.  
 AC 08CV9;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Hypothetical protein yfaQ precursor.  
 GN YfaQ OR C2769.  
 OS Escherichia coli O6.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=217992;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=06:HI / CFT073 / ATCC 700928;  
 RC MEDLINE=22388234; PubMed=12471157;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosch P.,  
 RA Raebko D., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Domeneberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 of uropathogenic Escherichia coli".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).  
 SQ

DR EMBL; AE016763; AAN81223.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 549 AA; 61590 MW; FFEAB9B9CD22A8B6 CRC64;

Query Match 69.0%; Score 40; DB 16; Length 549;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WGOYV 7  
| | | | |  
Db 125 WGOYV 129

## RESULT 23

085555 PRELIMINARY; PRT; 551 AA.

AC 085555;  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Putative proton-dependent oligopeptide transport.  
GN OJ1208D02.10.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA KucComb W.R., Spiegel L., de la Bastide M., Preston R., Kirchhoff K.,  
RA McComb K., Nascimben L., Zutavern T., Ballja V., Bell M., Baker J.,  
RA Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,  
RA Dite S., O'Shaughnessy A., Palmer L., Dedhia N.;  
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone  
OJ1208D02, from chromosome 10, complete sequence."  
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC107314; AAM08619.1; -;  
DR Gramene; O85555; -;  
DR InterPro; IPR00109; PTR2.  
DR Pfam; PF00854; PTR2; 1.  
DR PROSITE; PS01023; PTR2; 1.  
SQ SEQUENCE 551 AA; 59912 MW; AD899A43ADF31BB6 CRC64;

Query Match 69.0%; Score 40; DB 10; Length 551;  
Best Local Similarity 71.4%; Pred. No. 2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WGOYV 9  
| | | | |  
Db 90 WGRYWTV 96

## RESULT 24

08GF63 PRELIMINARY; PRT; 746 AA.

AC 08GF63;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Zymomonas mobilis.  
OG Plasmid 1.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
OC Sphingomonadaceae; Zymomonas.  
OX NCBI\_TaxID=542;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ZM4;  
RA Seo J., Park H., Kim H., Wang K., Yoon K., Rhee H., Kang J., Jung C.,  
RA Kim M., Park C., An Y., Choi E.;  
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY057845; AAL36103.1; -;

KW Hypothetical protein; Plasmid.  
SQ SEQUENCE 746 AA; 81269 MW; 5F95F527307FF43B CRC64;

Query Match 69.0%; Score 40; DB 2; Length 746;  
Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGOYWA 8  
| | | | |  
Db 313 KMWGOYWA 320

## RESULT 25

09REPI PRELIMINARY; PRT; 750 AA.

AC 09REPI;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Ferrichrome receptor FcuA.  
GN FCUA.  
OS Zymomonas mobilis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
OC Sphingomonadaceae; Zymomonas.  
OX NCBI\_TaxID=542;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ZM4;  
RA Um H.W., Kang H.S.;  
RT "Sequence analysis of 4283 fosmid clone of Zymomonas mobilis."  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
CC -1 SUBCELLULAR LOCATION: OUTER MEMBRANE (BY SIMILARITY).  
DR EMBL; AF213822; AAF23804.1; -;  
DR InterPro; IPR000531; TonB\_box.  
DR Pfam; PF00593; TonB\_dep\_Rec; 1.  
DR Membrane; Outer membrane; Receptor; TonB box.  
SQ SEQUENCE 750 AA; 82315 MW; 272729049A69FCED CRC64;

Query Match 69.0%; Score 40; DB 2; Length 750;  
Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTWGOYWA 8  
| | | | |  
Db 313 KMWGOYWA 320

Search completed: August 14, 2003, 09:10:11  
Job time : 64 secs

09/214836

L1 FILE 'REGISTRY' ENTERED AT 15:32:20 ON 25 AUG 2003  
61 S.K[TV]WGQYW[AQ]V/SQSP

L2 FILE 'HCAPLUS' ENTERED AT 15:32:48 ON 25 AUG 2003  
86 S L1

L4 51 SEA ABB=ON PLU=ON L2(L)(?MELANOM? OR ?NEOPLAS? OR  
?CANCER? OR ?CARCIN? OR ?TUMOUR? OR ?TUMOR?)

L4 ANSWER 1 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2003:330613 HCAPLUS

DOCUMENT NUMBER: 139:99547

TITLE: Stimulation of tumor-reactive T lymphocytes  
using mixtures of synthetic peptides derived  
from tumor-associated antigens with diverse MHC  
binding affinities

AUTHOR(S): Riley, John P.; Rosenberg, Steven A.; Parkhurst,  
Maria R.

CORPORATE SOURCE: Surgery Branch, National Institutes of Health,  
National Cancer Institute, Bethesda, MD,  
20892-1502, USA

SOURCE: Journal of Immunological Methods (2003),  
276(1-2), 103-119

CODEN: JIMMBG; ISSN: 0022-1759

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The use of reverse immunol. may be necessary to identify new  
tumor-assocd. antigens, particularly for cancers, against which  
tumor-reactive T cell populations have been difficult to establish.  
One approach has been to screen peptides derived from a candidate  
antigen with high major histocompatibility complex (MHC) binding  
affinities for the induction of tumor-reactive T lymphocytes in  
vitro. However, many candidate antigens that are overexpressed in  
tumors are non-mutated self-proteins, and unlike foreign or mutated  
proteins, immunodominant epitopes may not be expressed at high d. on  
the surface of tumor cells. Therefore, to identify tumor-assocd.  
epitopes, it may be necessary to screen large panels of peptides  
with wide ranges of MHC binding affinities. The current methodol.  
of stimulating peripheral blood lymphocytes (PBL) from donors  
expressing the MHC mol. of interest with individual peptides is  
impractical for screening such large panels. Therefore, the authors  
evaluated the use of mixts. of peptides with variable MHC binding  
affinities for the induction of tumor-reactive T lymphocytes with  
the melanoma antigens gp100 and an alternate isoform of  
tyrosinase-related protein 2 (TRP2-6b) as models. A mixt. of 10  
known human leukocyte antigen (HLA)-A\*0201-restricted peptides from  
gp100 induced melanoma-reactive cytotoxic T lymphocyte (CTL) from  
multiple patients with metastatic melanoma. The majority of these T  
cell populations recognized the known immunodominant epitopes  
gp100:209-217 and gp100:280-288, even though the HLA-A\*0201 binding  
affinities of these peptides were much lower than other peptides in  
the mixt. Similarly, melanoma-reactive CTL were generated with a  
mixt. of HLA-A\*0201-restricted peptides from TRP2-6b, and these  
responses were directed against the previously identified  
tumor-assocd. epitopes TRP2-6b:180-188, TRP2-6b:288-296 and  
TRP2-6b:403-411. Thus, the use of peptide mixts. may facilitate the  
identification of new tumor-assocd. antigens through the application





09/214836

of reverse immunol.  
IT **162558-08-9**  
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(**tumor**-reactive T cells stimulation using mixts. of  
synthetic peptides derived from **tumor**-assocd. antigens  
with diverse MHC binding affinities for new antigens screening)  
REFERENCE COUNT: 71 THERE ARE 71 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L4 ANSWER 2 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2003:242452 HCAPLUS  
DOCUMENT NUMBER: 138:282427  
TITLE: Gene expression profiles useful in methods of  
diagnosis of cancer compositions and methods of  
screening for modulators of cancer  
INVENTOR(S): Afar, Daniel; Aziz, Natasha; Gish, Kurt C.;  
Hevezi, Peter A.; Mack, David H.; Wilson, Keith  
E.; Zlotnik, Albert  
PATENT ASSIGNEE(S): EOS Biotechnology, Inc., USA  
SOURCE: PCT Int. Appl., 767 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 36  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003025138	A2	20030327	WO 2002-US29560	20020917
WO 2003025138	A3	20030508		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2003025138	A2	20030327	WO 2002-XA29560	20020917
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
WO 2003025138	A2	20030327	WO 2002-XB29560	20020917
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,			



09/214836

GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,  
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ;  
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW,  
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,  
BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU,  
MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, ML, MR, NE, SN, TD, TG  
WO 2003025138 A2 20030327 WO 2002-XC29560 20020917  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,  
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,  
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,  
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW,  
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,  
BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU,  
MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, ML, MR, NE, SN, TD, TG  
WO 2003025138 A2 20030327 WO 2002-XD29560 20020917  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,  
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,  
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,  
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW,  
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,  
BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU,  
MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, ML, MR, NE, SN, TD, TG  
WO 2003025138 A2 20030327 WO 2002-XE29560 20020917  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,  
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,  
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,  
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW,  
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,  
BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU,  
MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, ML, MR, NE, SN, TD, TG  
WO 2003025138 A2 20030327 WO 2002-XF29560 20020917  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,  
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,  
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,  
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW,  
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,  
BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU,  
MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, ML, MR, NE, SN, TD, TG  
WO 2003025138 A2 20030327 WO 2002-XG29560 20020917



09/214836

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG  
WO 2003025138 A2 20030327 WO 2002-XH29560 20020917  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG  
PRIORITY APPLN. INFO.: US 2001-323469P P 20010917  
US 2001-323887P P 20010920  
US 2001-350666P P 20011113  
US 2002-355145P P 20020208  
US 2002-355257P P 20020208  
US 2002-372246P P 20020412  
WO 2002-US29560 A 20020917  
AB Described herein are genes whose expression are up-regulated or down-regulated in specific cancers, including acute lymphocytic leukemia, glioblastoma, glioblastoma multiforme, glioma, kidney cancer, stomach cancer, melanoma, and benign NEVI. Mol. profiles of various normal and cancerous tissues were detd. and analyzed using the Affymetrix/Eos Hu01 and Hu03 GeneChip microarrays contg. 35,403 and 59,680 probe sets, resp. Related methods and compns. that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.  
IT 503636-92-8  
RL: ANT (Analyte); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(amino acid sequence; gene expression profiles useful in methods of diagnosis of **cancer** compns. and methods of screening for modulators of **cancer**)

L4 ANSWER 3 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2003:197914 HCAPLUS

DOCUMENT NUMBER: 138:220360

TITLE: Generation of cytotoxic T-cells to tumor antigens

INVENTOR(S): Chaux, Pascal; Luiten, Rosalie; Demotte, Nathalie; Duffour, Marie-Therese; Lurquin, Christophe; Traversari, Catia; Stroobant, Vincent; Cornelis, Guy; Boon-Falleur, Thierry; Van Der Bruggen, Pierre



09/214836

PATENT ASSIGNEE(S): Ludwig Institute for Cancer Research, USA;  
Universite Catholique De Louvain  
SOURCE: U.S., 39 pp., Cont.-in-part of U.S. 6,407,063.  
CODEN: USXXAM  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 2  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6531451	B1	20030311	US 1999-289350	19990409
US 6407063	B1	20020618	US 1998-165863	19981002
WO 2000020445	A2	20000413	WO 1999-IB1664	19990915
WO 2000020445	A3	20000713		
W: AU, CA, CN, JP, KR, NZ, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9959929	A1	20000426	AU 1999-59929	19990915
EP 1117679	A2	20010725	EP 1999-970091	19990915
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003518911	T2	20030617	JP 2000-574556	19990915

PRIORITY APPLN. INFO.:  
US 1998-165863 A2 19981002  
US 1999-289350 A 19990409  
WO 1999-IB1664 W 19990915

AB The authors disclose a method for generation of cytotoxic T lymphocyte (CTL) clones. These CTL comprise clones that have been isolated by successive steps of stimulation and testing with different antigen presenting cells; these cells utilize various expression systems (e.g., from recombinant Yersinia, recombinant Salmonella, or recombinant viruses) for presentation of cognate antigen by HLA class I complexes. In particular, the present invention relates to isolated CTL clones that are specific for MAGE-1 and MAGE-4.

IT **162558-08-9**

RL: PRP (Properties)  
(unclaimed sequence; generation of cytotoxic T-cells to tumor antigens)

REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2003:91924 HCAPLUS

DOCUMENT NUMBER: 138:185978

TITLE: Priming of T cells with Ad-transduced DC followed by expansion with peptide-pulsed DC significantly enhances the induction of tumor-specific CD8+ T cells: implications for an efficient vaccination strategy

AUTHOR(S): Tuettenberg, A.; Jonuleit, H.; Tueting, T.; Brueck, J.; Knop, J.; Enk, A. H.

CORPORATE SOURCE: Dep. Dermatol., J.-Gutenberg Univ., Mainz, Germany

SOURCE: Gene Therapy (2003), 10(3), 243-250

CODEN: GETHEC; ISSN: 0969-7128

PUBLISHER: Nature Publishing Group

Searcher : Shears 308-4994





09/214836

DOCUMENT TYPE: Journal  
LANGUAGE: English

AB In recent years, vaccination strategies using antigen-presenting cells (APC) have been under investigation. Antigen delivery using genetic immunization through ex vivo transduction of dendritic cells (DC) is supposed to enhance the induction of antitumor responses in humans by activating a broad range of peptide-specific CD8+ T cells. In this study, we compared the potential of adenoviral (Ad)-transduced vs. peptide-pulsed DC to induce melanoma-antigen (Ag)-specific T-cell responses in vitro. Whereas gp100-peptide-pulsed DC induced long-lasting specific CD8+ T-cell responses against single peptides, Ad-transduced DC induced broad and strong, specific immunity against various peptides of the gp100-Ag. Surprisingly, several restimulations led to decreasing gp100-specific and in parallel to increasing anti-adenoviral T-cell responses. Nevertheless, those anti-adenoviral T-cell responses provided an adjuvant effect by inducing an early release of high amts. of IL-2/IFN-.gamma., therewith enhancing CTL induction in the initiation phase. Based on these data, we suggest a prime/boost vaccination strategy in melanoma patients - combining the use of Ad-DC and peptide-pulsed DC - to obtain efficient and long-term antitumor T-cell responses.

IT 162558-08-9

RL: BSU (Biological study; unclassified); BIOL (Biological study) (priming of T cells with Adenovirus-transduced DC followed by expansion with peptide-pulsed DC significantly enhances the induction of tumor-specific CD8+ T cells in vaccine)

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2003:76882 HCAPLUS

DOCUMENT NUMBER: 138:135820

TITLE: Epitope sequences derived from tumor-associated antigens for use in diagnosis and vaccines  
INVENTOR(S): Simard, John J. L.; Diamond, David C.; Liu, Liping; Xie, Zhidong

PATENT ASSIGNEE(S): CTL Immunotherapies Corp., USA

SOURCE: PCT Int. Appl., 239 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 6

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008537	A2	20030130	WO 2002-US10189	20020329
W: AU				
PRIORITY APPLN. INFO.:		US 2001-282211P	P	20010406
		US 2001-337017P	P	20011107
		US 2002-363210P	P	20020307

AB The present invention provides epitopes that have a high affinity for MHC class I, and that correspond to the processing specificity of the housekeeping proteasome, which is active in peripheral cells. These epitopes thus correspond to those presented on target cells, and are derived from tumor-assocd. antigens such as tyrosinase,



09/214836

SSX-2, PMSA (prostate-specific membrane antigen), GP100, MAGE-1, MAGE-2, MAGE-3, NY-ESO-1, PRAME (also known as MAPE, DAGE, and OIP4), PSA (prostate-specific antigen), and PSCA (prostate stem cell antigen). The use of such epitopes in vaccines can activate the cellular immune response to recognize the correctly processed tumor-assocd. antigen and can result in removal of target cells that present such epitopes. The housekeeping epitopes provided can be used in combination with immune epitopes, generating a cellular immune response that is competent to attack target cells both before and after interferon induction. The epitopes are also useful in diagnosis and monitoring of the target-assocd. disease and in the generation of immunol. reagents for such purposes. Disclosed herein are polypeptides, including epitopes, clusters, and antigens.

IT 481197-02-8, GenBank AAB19181

RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (amino acid sequence; epitope sequences derived from tumor-assocd. antigens for use in diagnosis and vaccines)

L4 ANSWER 6 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:795492 HCAPLUS

DOCUMENT NUMBER: 137:309110

TITLE: Modification of a tumor-derived peptide at an HLA-A2 anchor residue can alter the conformation of the MHC-peptide complex: probing with TCR-like recombinant antibodies

AUTHOR(S): Denkborg, Galit; Klechevsky, Eynav; Reiter, Yoram

CORPORATE SOURCE: Faculty of Biology, Technion-Israel Institute of Technology, Haifa, 32000, Israel

SOURCE: Journal of Immunology (2002), 169(8), 4399-4407  
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A common assumption about peptide binding to the class I MHC complex is that each residue in the peptide binds independently. Based on this assumption, modifications in class I MHC anchor positions were used to improve the binding properties of low-affinity peptides (termed altered peptide ligands), esp. in the case when tumor-assocd. peptides are used for immunotherapy. Using a new mol. tool in the form of recombinant Abs endowed with Ag-specific MHC-restricted specificity of T cells, the authors show that changes in the identity of anchor residues may have significant effects, such as altering the conformation of the peptide-MHC complex, and as a consequence, may affect the TCR-contacting residues. The authors herein demonstrate that the binding of TCR-like recombinant Abs, specific for the melanoma differentiation Ag T cell epitope G9-209, is entirely dependent on the identity of a single peptide anchor residue at position 2. An example is shown in which TCR-like Abs can recognize the specific complex only when a modified peptide, G9-209-2 M, with improved affinity to HLA-A2 was used, but not with the unmodified natural peptide. Importantly, these results demonstrate, using a novel mol. tool, that modifications at anchor residues can dramatically influence the conformation of the MHC peptide groove and thus may have a profound effect on TCR interactions. Moreover, these results may have important implications in designing modifications in peptides for cancer



09/214836

immunotherapy, because most such peptides studied are of low affinity.

IT 162558-08-9

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(modification of a **tumor**-derived peptide at HLA-A2 anchor residue can alter conformation of MHC-peptide complex)

REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 7 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:793764 HCAPLUS

DOCUMENT NUMBER: 137:309478

TITLE: anticancer vaccines comprising epitopes of tumor or neovasculature antigen

INVENTOR(S): Simard, John J. L.; Diamond, David C.; Liu, Liping; Xie, Zhidong

PATENT ASSIGNEE(S): CTL Immunotherapies Corp., USA; Mannkind Corporation

SOURCE: PCT Int. Appl., 352 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 6

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002081646	A2	20021017	WO 2002-US11101	20020404
WO 2002081646	A3	20030717		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: US 2001-282211P P 20010406  
US 2001-337017P P 20011107  
US 2002-363210P P 20020307

AB Disclosed herein are polypeptides, including epitopes, clusters, and antigens. Also disclosed are compns. that include said polypeptides and methods for their use for cancer diagnosis and therapy.

IT 471943-16-5, Protein (human gene pmell7)

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(amino acid sequence; **anticancer** vaccines comprising epitopes of **tumor** or neovasculature antigen)

L4 ANSWER 8 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:657918 HCAPLUS

DOCUMENT NUMBER: 137:200246

Searcher : Shears 308-4994



09/214836

TITLE: Préparation of tumor antigen-specific cytotoxic  
T lymphocytes for cancer therapy  
INVENTOR(S): Degraw, Juli; Moriarty, Ann; Leturcq, Didier J.;  
Jackson, Michael R.; Peterson, Per A.; Heiskala,  
Marja  
PATENT ASSIGNEE(S): Ortho-McNeil Pharmaceutical, Inc., USA  
SOURCE: PCT Int. Appl., 99 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002065992	A2	20020829	WO 2002-US5748	20020219
WO 2002065992	A3	20030213		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

US 2003077248 A1 20030424 US 2002-80013 20020219  
PRIORITY APPLN. INFO.: US 2001-270252P P 20010220  
AB T cell responses are often diminished in humans with a compromised immune system. We have developed a method to isolate, stimulate and expand naive cytotoxic T lymphocyte precursors (CTLp) to antigen-specific effectors, capable of lysing tumor cells in vivo. This ex vivo protocol produces fully functional effectors. Artificial antigen presenting cells (AAPCs; Drosophila melanogaster) transfected with human HLA class I and defined accessory mols., are used to stimulate CD8+ T cells from both normal donors and cancer patients. The class I mols. expressed to a high d. on the surface of the Drosophila cells are empty, allowing for efficient loading of multiple peptides that results in the generation of polyclonal responses recognizing tumor cells endogenously expressing the specific peptides. The responses generated are robust, antigen-specific and reproducible if the peptide epitope is a defined immunogen. This artificial antigen expression system can be adapted to treat most cancers in a significant majority of the population.

IT 162558-08-9

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(prepn. of **tumor** antigen-specific cytotoxic T lymphocytes for **cancer** therapy)

L4 ANSWER 9 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:536421 HCAPLUS

DOCUMENT NUMBER: 137:114479

TITLE: Pharmaceutical compositions for treating or preventing cancer, especially melanoma

Searcher : Shears 308-4994





09/214836

INVENTOR(S): Moelling, Karin; Nawrath, Michael; Pavlovic, Jovan  
PATENT ASSIGNEE(S): Universitaet Zuerich Institut Fuer Medizinische Virologie, Switz.  
SOURCE: Eur. Pat. Appl., 34 pp.  
CODEN: EPXXDW  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1222928	A2	20020717	EP 2002-185	20020109
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2002177547	A1	20021128	US 2002-47539	20020115
PRIORITY APPLN. INFO.: EP 2001-100914 A 20010116				
AB The present invention relates to a pharmaceutical or vaccine compn. comprising a nucleic acid mol. encoding a tumor-assocd. antigen and at least one peptide comprising a region corresponding to a putative cytotoxic T cell, helper T cell or B cell epitope of a tumor-assocd. antigen and/or cells pulsed with such peptides, optionally in combination with a pharmaceutically acceptable carrier. Such pharmaceutical compns. can be used for the treatment of cancer or for the vaccination against cancer.				
IT <b>162558-08-9</b> RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (pharmaceutical compns. for treating or preventing <b>cancer</b> , esp. <b>melanoma</b> )				
IT <b>442701-70-4</b> RL: PRP (Properties) (unclaimed protein sequence; pharmaceutical compns. for treating or preventing <b>cancer</b> , esp. <b>melanoma</b> )				

L4 ANSWER 10 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2002:416216 HCAPLUS  
DOCUMENT NUMBER: 138:23273  
TITLE: Induction of HLA-A2-restricted CTL responses by a tubular structure carrying human melanoma epitopes  
AUTHOR(S): Ghosh, Mrinal K.; Li, Cui-Ling; Fayolle, Catherine; Dadaglio, Gilles; Murphy, Aileen; Lemonnier, Francois A.; Roy, Polly; Leclerc, Claude  
CORPORATE SOURCE: School of Medicine, Department of Medicine, Division of Geographic Medicine, University of Alabama at Birmingham, Birmingham, AL, 35294, USA  
SOURCE: Vaccine (2002), 20(19-20), 2463-2473  
CODEN: VACCDE; ISSN: 0264-410X  
PUBLISHER: Elsevier Science Ltd.  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
AB Epitope-based vaccination strategies designed to induce strong tumor-specific CD8+ T cell responses are being widely considered for cancer immunotherapy. Here, two recombinant tubular structures,



09/214836

NS1-Mela 1 and NS1-Mela 2, carrying, resp. two HLA-A2 epitopes derived from human melanoma antigens were constructed and their capability to induce CTL responses in vivo were studied in HLA-A2 transgenic mice. Strong CTL responses specific for GnP-V/NA 17-A and gp100 (154-162) epitopes were generated in HLA-A2 transgenic mice immunized by the construct NS1-Mela 1 carrying these two epitopes. The second construct NS1-Mela 2 carrying both Tyrosinase (369-377 Da) and Melan-A/Mart-1 (27-35) epitopes induced a weak Tyrosinase-specific CTL response in mice but failed to induce specific CTL responses against the Melan-A/Mart-1 (27-35) epitope in the tested mice. Thus, recombinant tubular structures contg. multiple tumoral epitopes may lead to new strategies for the induction of strong tumor-specific CTL responses in cancer patients.

IT 162558-08-9

RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(induction of HLA-A2-restricted CTL responses by a tubular structure carrying human melanoma epitopes)

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L4 ANSWER 11 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:353300 HCAPLUS

DOCUMENT NUMBER: 136:368444

TITLE: Polynucleotides expressing fusion protein of  
human .beta.2 microglobulin and cancer or  
non-cancer epitopes for cancer therapy

INVENTOR(S): Tafuro, Sabrina; Meier, Ute-Christiane;  
McMichael, Andrew James; Bell, John Irving;  
Layton, Guy; Hunter, Michael

PATENT ASSIGNEE(S): Isis Innovation Limited, UK

SOURCE: PCT Int. Appl., 46 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002036146	A2	20020510	WO 2001-GB4844	20011101
WO 2002036146	A3	20021017		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
AU 2002012472	A5	20020515	AU 2002-12472	20011101
EP 1330259	A2	20030730	EP 2001-980679	20011101
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
PRIORITY APPLN. INFO.:			GB 2000-26812	A 20001102

Searcher : Shears 308-4994



WO 2001-GB4844 W 20011101

AB The present invention relates to polynucleotides for use in cancer therapy. In particular, the invention provides a polynucleotide capable of expressing an epitope-.beta.2m fusion protein; for use in the generation of cytotoxic T lymphocyte (CTL) responses against a tumor; and a polynucleotide capable of expressing an epitope-.beta.2m fusion protein; for use in a method of restoring antigen presentation in the tumor of a host. The epitope is derived from latent membrane protein, EBNA-3C antigen, BZLF1 or BMLF1 of Epstein-Barr virus; lower matrix protein pp65 of cytomegalovirus; nucleoprotein or matrix protein of influenza; and tumor antigens of human.

IT 162558-08-9

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(polynucleotides expressing fusion protein of human .beta.2 microglobulin and **cancer** or non-**cancer** epitopes for **cancer** therapy)

L4 ANSWER 12 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:51038 HCAPLUS

DOCUMENT NUMBER: 137:45640

TITLE: Human dendritic cells genetically engineered to express a melanoma polyepitope.DNA vaccine induce multiple cytotoxic T-cell responses  
AUTHOR(S): Smith, Steven Gerard; Patel, Poulam Manubhai; Porte, Joanne; Selby, Peter John; Jackson, Andrew Mark

CORPORATE SOURCE: Applied Immunology Group, St. James's University Hospital, Leeds, LS9 7TF, UK

SOURCE: Clinical Cancer Research (2001), 7(12), 4253-4261

CODEN: CCREF4; ISSN: 1078-0432

PUBLISHER: American Association for Cancer Research

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Purpose: To assess the therapeutic potential of a melanoma polyepitope vaccine in human cells. Polyepitope DNA vaccines encoding T-cell epitopes have been demonstrated in murine systems to generate multiple cytotoxic T-cell responses to different antigens. Here, for the first time the authors demonstrate the ability of a melanoma polyepitope to stimulate lymphocytes from normal human donors to simultaneously generate multiple antigen-specific responses. Exptl. Design: Human dendritic cells (DC), transduced with a melanoma-polyepitope cDNA, were used to activate autologous lymphocytes from naive donors as an in vitro model of DNA vaccination. Lymphocytes were primed with polyepitope or mock-transduced DC, boosted with peptide, then measured for antigen-specific cytotoxicity. Results: Lymphocytes primed with polyepitope-transduced DC and boosted with peptide generated multiple cytotoxic responses. By contrast lymphocytes primed with mock-transfected DCs and boosted with peptide gave no specific cytotoxicity. However, when lymphocytes were repeatedly stimulated with polyepitope-transduced DCs immunodominance was seen with CTLs being generated to only one epitope, MART27-35. Conclusions: the authors show in a human system that a melanoma polyepitope primes CTL to multiple epitopes. However, repeated stimulation by the polyepitope restricts the response to only the MART1 epitope. Thus,



09/214836

although polyepitope vaccines are an effective way of priming multiple naive T-cell responses, continual boosting with polyepitope vaccines may, as a result of immunodominance, restrict the CTL. These findings have important implications for the use of DNA polyepitope vaccines in cancer immunotherapy.

IT 162558-08-9P

RL: PAC (Pharmacological activity); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(human dendritic cells genetically engineered to express a melanoma polyepitope induce multiple cytotoxic T-cell responses)

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 13 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:886174 HCAPLUS

DOCUMENT NUMBER: 136:31665

TITLE: Therapeutic anti-melanoma compounds

INVENTOR(S): Nicolette, Charles A.

PATENT ASSIGNEE(S): Genzyme Corp., USA

SOURCE: PCT Int. Appl., 69 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001092294	A2	20011206	WO 2001-US16417	20010521
WO 2001092294	A3	20020613		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
US 2002082217	A1	20020627	US 2001-862260	20010521
EP 1284996	A2	20030226	EP 2001-939224	20010521
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
PRIORITY APPLN. INFO.:			US 2000-208955P P	20000531
			US 2001-267877P P	20010209
			WO 2001-US16417 W	20010521

AB The present invention provides synthetic compds., antibodies that recognize and bind to these compds., polynucleotides that encode these compds., and immune effector cells raised in response to presentation of these epitopes. The invention further provides methods for inducing an immune response and administering immunotherapy to a subject by delivering the compn. of the invention.





09/214836

IT 155422-80-3

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(amino acid sequence; therapeutic anti-melanoma  
comps.)

L4 ANSWER 14 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:780623 HCAPLUS

DOCUMENT NUMBER: 135:343268

TITLE: Methods and compositions for heat shock protein  
mediated immunotherapy of melanoma

INVENTOR(S): Houghton, Alan; Livingston, Philip; Al-Awqati,  
Qais; Mayhew, Mark; Hoe, Mee

PATENT ASSIGNEE(S): USA

SOURCE: PCT Int. Appl., 150 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001078655	A2	20011025	WO 2001-US12449	20010417
WO 2001078655	A3	20020314		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 2001057072	A5	20011030	AU 2001-57072	20010417
PRIORITY APPLN. INFO.:			US 2000-197462P P	20000417
			WO 2001-US12449 W	20010417

AB The present invention relates to immunotherapeutic comps. comprising an effective amt. of a mol. chaperone such as a heat shock protein, preferably hsp70, non-covalently bound to one or more javelinized melanoma antigens and to methods of using the immunotherapeutic comps. to induce an immune response against melanoma in a subject. The immunotherapeutic compn. may contain one or more heat shock proteins, such as one or more of hsp70, hsp90, gp96, BiP, and hsp40, and may contain one or more javelinized melanoma antigens.

IT 162558-08-9 370891-72-8 370891-73-9  
370891-74-0 370891-75-1 370891-76-2  
370891-77-3 370891-78-4 370891-79-5  
371771-64-1 371771-65-2 371772-22-4  
371772-23-5 371772-24-6 371772-37-1  
371772-38-2 371772-39-3 371772-40-6  
371772-41-7 371772-42-8 371772-43-9

RL: BSU (Biological study, unclassified); PRP (Properties); THU  
(Therapeutic use); BIOL (Biological study); USES (Uses)  
(heat shock protein and melanoma antigen for



09/214836

immunotherapy of melanoma)

L4 ANSWER 15 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2001:713374 HCAPLUS  
DOCUMENT NUMBER: 135:267217  
TITLE: Synthetic antigenic peptide sequences for gp100  
positive melanoma and uses for cancer vaccines  
INVENTOR(S): Nicolette, Charles A.  
PATENT ASSIGNEE(S): Genzyme Corporation, USA  
SOURCE: PCT Int. Appl., 67 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001070767	A2	20010927	WO 2001-US8919	20010319
WO 2001070767	A3	20020124		
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
US 2002169132	A1	20021114	US 2001-812238	20010319
EP 1268542	A2	20030102	EP 2001-959922	20010319
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
PRIORITY APPLN. INFO.:			US 2000-190750P	P 20000320
			US 2000-255019P	P 20001212
			WO 2001-US8919	W 20010319

AB The present invention provides synthetic compds., antibodies that recognize and bind to these compds., polynucleotides that encode these compds., and immune effector cells raised in response to presentation of these epitopes. In particular, this invention provides novel, synthetic antigenic peptide sequences, which are useful as components of anti-cancer vaccines and to expand immune effector cells that are specific for cancers characterized by expression of the melanoma antigen gp100. The invention further provides methods for inducing an immune response and administering immunotherapy to a subject by delivering the compns. of the invention. In one embodiment, the altered ligands of the invention have comparable affinity for MHC binding as the native ligand.

IT 155422-80-3

RL: PRP (Properties)  
(unclaimed protein sequence; synthetic antigenic peptide sequences for gp100 pos. melanoma and uses for cancer vaccines)

L4 ANSWER 16 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2001:544451 HCAPLUS  
DOCUMENT NUMBER: 135:240560  
TITLE: Detection and quantification of CD8+ T cells specific for HLA-A\*0201-binding melanoma and viral peptides by the IFN-.gamma.-ELISPOT assay  
AUTHOR(S): Griffioen, Marieke; Borghi, Martina; Schrier, Peter I.; Osanto, Susanne  
CORPORATE SOURCE: Department of Clinical Oncology, Leiden University Medical Center, Leiden, 2300 RC,



09/214836

SOURCE: Neth.  
International Journal of Cancer (2001), 93(4),  
549-555  
CODEN: IJCNW; ISSN: 0020-7136  
PUBLISHER: Wiley-Liss, Inc.  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB Blood lymphocytes from HLA-A\*0201-subtyped melanoma patients and healthy controls were screened for the presence of T cells specific for HLA-A\*0201-binding melanoma and viral peptide antigens by the enzyme-linked immunoSPOT (ELISPOT) assay. CD8+ cells were tested for peptide-specific IFN-.gamma. release immediately after selection as well as after 2 wk of in vitro stimulation. After in vitro stimulation, CD8+ T cells specific for influenza were measured in all patients and controls, whereas these T cells could be detected among nonstimulated CD8+ cells in only 52% of individuals. Similarly, T cells specific for EBV were more frequently measured among in vitro-stimulated than nonstimulated CD8+ cells. In nonstimulated CD8+ cells, T cells specific for MART-1/Melan-A, gp100, tyrosinase and CAMEL were present in 4 (33%), 1 (8%), 1 (8%) and 3 (25%) of 12 patients, resp. Only MART-1/Melan-A-specific CD8+ T cells were found in 1 (11%) of 9 healthy controls. CD8+ T cells specific for MAGE-2 were not obsd. After in vitro stimulation, CD8+ T cells specific for MART-1/Melan-A could be demonstrated in 6 (46%) of 13 patients and 2 (20%) of 10 controls. CD8+ T cells specific for gp100 were detected in 1 patient after in vitro stimulation. No CD8+ T cells specific for tyrosinase, MAGE-2 or CAMEL could be measured after in vitro stimulation. These data show that the ELISPOT assay allows direct ex vivo detection of CD8+ T cells specific for viral and melanoma antigens. Furthermore, the data show that the sensitivity of the ELISPOT assay to measure influenza- and EBV-specific CD8+ T cells can be enhanced by a short in vitro stimulation step, whereas opposing effects on nos. of CD8+ T cells specific for melanoma antigens have been obsd.

IT 162558-08-9P

RL: BPR (Biological process); BSU (Biological study, unclassified);  
SPN (Synthetic preparation); BIOL (Biological study); PREP  
(Preparation); PROC (Process)  
(detection and quantification of CD8+ T cells specific for  
HLA-A\*0201-binding melanoma and viral peptides by the  
IFN-.gamma.-ELISPOT assay)

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L4 ANSWER 17 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:427335 HCAPLUS

DOCUMENT NUMBER: 135:32376

TITLE: DNA and protein sequence of tumor associated  
antigen gene 3.8 and its therapeutic and  
diagnostic uses

INVENTOR(S): Martelange, Valerie; De Smet, Charles;  
Boon-Falleur, Thierry

PATENT ASSIGNEE(S): Ludwig Institute for Cancer Research, USA

SOURCE: U.S., 34 pp., Cont.-in-part of U.S. Ser. No.  
122,989, abandoned.  
CODEN: USXXAM

DOCUMENT TYPE: Patent

Searcher : Shears 308-4994



09/214836

LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 2  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6245525	B1	20010612	US 1998-183706	19981030
WO 9953061	A2	19991021	WO 1999-US8163	19990414
WO 9953061	A3	20000323		
W: AU, CA, CN, JP, KR, NZ, ZA				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9935603	A1	19991101	AU 1999-35603	19990414
EP 1073734	A2	20010207	EP 1999-917493	19990414
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002511266	T2	20020416	JP 2000-543609	19990414
US 6303756	B1	20011016	US 2000-567995	20000510
US 2002115142	A1	20020822	US 2001-923831	20010807

PRIORITY APPLN. INFO.:

	US 1998-122989	B2	19980727
	US 1998-60706	A	19980415
	US 1998-183706	A	19981030
	US 1998-183789	A	19981030
	WO 1999-US8163	W	19990414
	US 2000-567995	A3	20000510

AB The invention provides the cDNA and deduced protein sequence of tumor assocd. gene sdp3.8 (HEGA) from human sarcoma cell line LB-23. The sdp3.8 gene is expressed in normal testis tissue and several tumoral cells. This invention also provides the the predicted HLA binding motifs in HAGE(sdp3.8) peptides and the gene bank search results of HAGE (sdp3.8) sequence homologs. Methods and products also are provided for diagnosing and treating conditions characterized by expression of a sdp3.8 gene product.

IT **162558-08-9**  
RL: PRP (Properties)  
(unclaimed sequence; dNA and protein sequence of **tumor** assocd. antigen gene 3.8 and its therapeutic and diagnostic uses)

REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 18 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:387198 HCAPLUS

DOCUMENT NUMBER: 136:100793

TITLE: Synergistic effect of a combined DNA and peptide vaccine against gp100 in a malignant melanoma mouse model

AUTHOR(S): Nawrath, Michael; Pavlovic, Jovan; Moelling, Karin

CORPORATE SOURCE: Institute of Medical Virology, University of Zurich, Zurich, 8028, Switz.

SOURCE: Journal of Molecular Medicine (Berlin, Germany) (2001), 79(2-3), 133-142  
CODEN: JMLME8; ISSN: 0946-2716

PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Vaccination against tumors relies on tumor-assocd. antigens, and has





been quite successful with synthetic peptides used as immunogens. Gp100 is a human melanoma-associated antigen (hgpl00) with a highly homologous mouse counterpart, pmel17/gp100 (mgpl00), that is expressed in melanocytes and highly tumorigenic B16 melanoma cells. Since mgpl00 is poorly immunogenic in mice, we used a xenoimmunization approach and vaccinated with the hgpl00 immunogen. To that end, plasmid DNA encoding hgpl00 was applied as a vaccine in combination with three synthetic peptides corresponding to putative cytotoxic T cell epitopes of hgpl00. Immunization with DNA and peptide-pulsed spleen cells had a synergistic effect and provided significant protection against a challenge with poorly immunogenic B16-F0 malignant melanoma cells in the syngeneic C57BL/6 mouse model. Vaccination with either plasmid DNA or peptides alone delayed the onset of tumor formation, and reduced tumor growth 2-fold and 30-fold, resp. However, while all animals vaccinated with DNA encoding hgpl00 or with peptides eventually developed tumors, 30% of the animals treated with both vaccines remained tumor free and survived for the entire observation period of 150 days. Depletion of T cell subsets revealed that the protective effect obsd. after vaccination with plasmid DNA was mediated by CD4+ and CD8+ T cells, while protection following vaccination with DNA encoding hgpl00 in combination with peptides appears to depend on CD4+ T cells only. Furthermore, we could also demonstrate a therapeutic effect of the combined DNA/peptide regime. A single treatment cycle consisting of injections of plasmid DNA and peptide-pulsed spleen cells led to a fourfold redn. in the growth rate of preexisting tumors. The data presented demonstrate that immunization with xenoantigens induces cross-species priming leading to an immunol. response against the tumor-specific antigens.

IT 162558-08-9

RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(combined DNA and peptide vaccine against gp100 in a malignant melanoma)

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L4 ANSWER 19 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:319754 HCAPLUS

DOCUMENT NUMBER: 134:339527

TITLE: Method of inducing and/or enhancing an immune response to tumor antigens

INVENTOR(S): Berinstein, Neil; Tartaglia, James; Moingeon, Philippe; Barber, Brian

PATENT ASSIGNEE(S): Aventis Pasteur Limited, Can.

SOURCE: PCT Int. Appl., 60 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001030382	A1	20010503	WO 2000-CA1253	20001020
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,				



09/214836

LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,  
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,  
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,  
TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,  
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,  
BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG  
WO 2001030847 A1 20010503 WO 2000-CA1254 20001020  
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH,  
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,  
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,  
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,  
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,  
TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,  
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,  
BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG  
EP 1227837 A1 20020807 EP 2000-971184 20001020  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,  
PT, IE, SI, LT, LV, FI, RO, MK, CY, AL  
EP 1228095 A1 20020807 EP 2000-971185 20001020  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,  
PT, IE, SI, LT, LV, FI, RO, MK, CY, AL  
JP 2003512437 T2 20030402 JP 2001-532799 20001020  
JP 2003512829 T2 20030408 JP 2001-533844 20001020  
PRIORITY APPLN. INFO.: US 1999-160879P P 19991022  
US 2000-223325P P 20000807  
WO 2000-CA1253 W 20001020  
WO 2000-CA1254 W 20001020  
AB An improved method of inducing and/or enhancing an immune response  
to a tumor antigen is disclosed. The method involves administering  
the tumor antigen, nucleic acid coding therefor, vectors and/or  
cells comprising said nucleic acid, or vaccines comprising the  
aforementioned to a lymphatic site.  
IT **337989-60-3**  
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(amino acid sequence; vector encoding **tumor** antigen as  
vaccine at lymphatic site for **cancer** immunotherapy)  
IT **337916-59-3**  
RL: PRP (Properties)  
(unclaimed sequence; method of inducing and/or enhancing an  
immune response to **tumor** antigens)  
REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR  
THIS RECORD. ALL CITATIONS AVAILABLE IN  
THE RE FORMAT  
L4 ANSWER 20 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2001:284118 HCAPLUS  
DOCUMENT NUMBER: 134:309695  
TITLE: Hepatitis B virus preS2 proteins containing  
tumor or pathogen epitopes and DNA constructs  
encoding them for use in induction of CTL  
response  
INVENTOR(S): Firat, Hueseyin; Lemonnier, Francois;  
Langlade-Demoyen, Pierre  
PATENT ASSIGNEE(S): Institut Pasteur, Fr.



09/214836

SOURCE: PCT Int. Appl., 70 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001027291	A1	20010419	WO 2000-EP9902	20000929
WO 2001027291	C2	20020906		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
US 2002164721	A1	20021107	US 2002-106487	20020327
PRIORITY APPLN. INFO.:			US 1999-158356P	P 19991012
			US 2000-675673	B1 20000929

AB Polyepitope proteins comprising an hepatitis B preS2 antigen into which is inserted epitopes of viral, fungal, bacterial or tumor antigens are disclosed. Also disclosed are nucleotide sequences encoding such hybrid proteins, vectors contg. these sequences, and the use of the polyepitope proteins or nucleotide sequences encoding them for induction of CTL responses. H-2 class I neg., HLA-A2.1 transgenic HHD mice were used for a comparative evaluation of the immunogenicity of HLA-A2.1 restricted human tumor-assocd. CTL epitopes and HIV 1-derived epitopes. A hierarchy was established among these epitopic peptides injected into mice in IFA which correlates globally with their capacity to bind and stabilize HLA-A2.1 mols. A tyrosine substitution in position 1 of the HIV 1-derived epitopic peptides, which increases both their affinity for and their HLA-A2.1 mol. stabilizing capacity, was introduced in a significant proportion of them. DNA immunizations were performed using a construct comprising nucleic acids encoding the epitopes inserted into the pre-S2 segment of the hepatitis B middle glycoprotein. CTL responses against most of the inserted epitopes could be elicited simultaneously in a single animal.

IT 162558-08-9 332959-83-8

RL: PRP (Properties)

(unclaimed sequence; hepatitis B virus preS2 proteins contg.

tumor or pathogen epitopes and DNA constructs encoding

them for use in induction of CTL response)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 21 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:247508 HCAPLUS

DOCUMENT NUMBER: 134:279565

TITLE: Comparative evaluation of the immunogenicity of HLA-A2.1 restricted human tumor-assocd. CTL epitopes comprising hepatitis B virus sequences



09/214836

using H-2 class I negative HLA-A2.1 transgenic HHD mice.

INVENTOR(S): Firat, Hueseyin; Lemonnier, Francois;  
Langlade-Demoyen, Pierre; Michel, Marie-Louise;  
Suhrbier, Andreas A.

PATENT ASSIGNEE(S): Institut Pasteur, Fr.

SOURCE: PCT Int. Appl., 36 pp.  
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001023577	A2	20010405	WO 2000-EP9900	20000929
WO 2001023577	A3	20010517		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-156945P P 19990930

AB H-2 class I neg., HLA-A2.1 transgenic HHD mice were used for a comparative evaluation of the immunogenicity of HLA-A2.1 restricted human tumor-assocd. CTL epitopes. A hierarchy was established among these epitopic peptides injected into mice in IFA which correlates globally with their capacity to bind and stabilize HLA-A2.1 mols. Co-injection of a helper peptide enhanced most CTL responses. In contrast, classical HLA class I transgenic mice which still express their own class I mols. did not, in most cases, develop H.A.-A2.1-restricted CTL responses under the same exptl. conditions. Different monoepitopic immunization strategies of acceptable clin. usage were compared in HHD mice. Recombinant Ty-virus-like particles, or DNA encoding epitopes fused to the hepatitis B virus middle envelope protein gave the best results. Using this latter approach and a melanoma-based polyepitope construct, CTL responses against five distinct epitopes could be elicited simultaneously in a single animal. Thus, HHD mice provide a versatile animal model for preclin. evaluation of peptide-based cancer immunotherapy. In addn., this invention provides polynucleotides contg. at least part of the coding sequence of the middle glycoprotein of the hepatitis B virus in which is inserted a DNA sequence coding for an epitope comprising at least one tumoral epitope of a tumor antigen.

IT 162558-08-9

RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)  
(epitopic peptide sequence; comparative evaluation of immunogenicity of HLA-A2.1 restricted human **tumor** -assocd. CTL epitopes comprising hepatitis B virus sequences using H-2 class I neg. HLA-A2.1 transgenic HHD mice)

IT 332959-83-8

RL: PRP (Properties)





09/214836

(unclaimed protein sequence; comparative evaluation of the immunogenicity of HLA-A2.1 restricted human **tumor**-assocd. CTL epitopes comprising hepatitis B virus sequences using H-2 class I neg. HLA-A2.1 transgenic HHD mice)

IT **332959-84-9**

RL: PRP (Properties)

(unclaimed sequence; comparative evaluation of the immunogenicity of HLA-A2.1 restricted human **tumor**-assocd. CTL epitopes comprising hepatitis B virus sequences using H-2 class I neg. HLA-A2.1 transgenic HHD mice)

L4 ANSWER 22 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:384405 HCAPLUS

DOCUMENT NUMBER: 133:29604

TITLE: Tumor rejection antigens MAGE-A10 and MAGE-A8 able to complex with HLA-A2.1

INVENTOR(S): Huang, Lan-Qing; Van Pel, Aline; Brasseur, Francis; De Plaen, Etienne; Boon, Thierry

PATENT ASSIGNEE(S): Ludwig Institute for Cancer Research, USA

SOURCE: PCT Int. Appl., 80 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000032769	A2	20000608	WO 1999-IB2018	19991126
WO 2000032769	A3	20001019		
W: AU, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1131426	A2	20010912	EP 1999-958438	19991126
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002531088	T2	20020924	JP 2000-585400	19991126
PRIORITY APPLN. INFO.:			GB 1998-26143	A 19981127
			WO 1999-IB2018	W 19991126

AB Autologous cytolytic T lymphocyte clones are obtained from a melanoma patient, LB 1751, which recognize and hallow the identification of hitherto unknown HLA-A2.1-presented tumor rejection antigens encoded by MAGE-A10 and MAGE-A8. The cDNA and deduced amino acid sequences of MAGE-A10 and MAGE-A8 are provided.

IT **162558-08-9**

RL: PRP (Properties)

(unclaimed sequence; **tumor** rejection antigens MAGE-A10 and MAGE-A8 able to complex with HLA-A2.1)

L4 ANSWER 23 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:261711 HCAPLUS

DOCUMENT NUMBER: 133:29405

TITLE: Dendritic cells infected with a vaccinia vector carrying the human gp100 gene simultaneously present multiple specificities and elicit high-affinity T cells reactive to multiple epitopes and restricted by HLA-A2 and -A3

AUTHOR(S): Yang, Sixun; Kittlesen, David; Slingluff, Craig



09/214836

CORPORATE SOURCE: L., Jr.; Vervaert, Carol E.; Seigler, Hilliard F.; Darrow, Timothy L.  
SOURCE: Department of Surgery, Duke University Medical Center, Durham, NC, 27710, USA  
JOURNAL OF IMMUNOLOGY (2000), 164(8), 4204-4211  
CODEN: JOIMA3; ISSN: 0022-1767  
PUBLISHER: American Association of Immunologists  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB To investigate the ability of human dendritic cells (DC) to process and present multiple epitopes from the gp100 melanoma tumor-associated Ags (TAA), DC from melanoma patients expressing HLA-A2 and HLA-A3 were pulsed with gp100-derived peptides G9154, G9209, or G9280 or were infected with a vaccinia vector (Vac-Pmel/gp100) containing the gene for gp100 and used to elicit CTL from autologous PBL. CTL were also generated after stimulation of PBL with autologous tumor. CTL induced with autologous tumor stimulation demonstrated HLA-A2-restricted, gp100-specific lysis of autologous and allogeneic tumors and no lysis of HLA-A3-expressing, gp100+ target cells. CTL generated by G9154, G9209, or G9280 peptide-pulsed, DC-lysed, HLA-A2-matched EBV transformed B cells pulsed with the corresponding peptide. CTL generated by Vac-Pmel/gp100-infected DC (DC/Pmel) lysed HLA-A2- or HLA-A3-matched B cell lines pulsed with the HLA-A2-restricted G9154, G9209, or G9280 or with the HLA-A3-restricted G917 peptide derived from gp100. Furthermore, these DC/Pmel-induced CTL demonstrated potent cytotoxicity against allogeneic HLA-A2- or HLA-A3-matched gp100+ melanoma cells and autologous tumor. The authors conclude that DC-expressing TAA present multiple gp100 epitopes in the context of multiple HLA class I-restricting alleles and elicit CTL that recognize multiple gp100-derived peptides in the context of multiple HLA class I alleles. The data suggest that for tumor immunotherapy, genetically modified DC that express an entire TAA may present the full array of possible CTL epitopes in the context of all possible HLA alleles and may be superior to DC pulsed with limited nos. of defined peptides.

IT 162558-08-9

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dendritic cells transduced with **melanoma** gp100 gene elicit both HLA-A2- and HLA-A3-restricted cytotoxic T-cells to)

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 24 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:241272 HCAPLUS

DOCUMENT NUMBER: 132:292703

TITLE: Tumor antigens and CTL clones isolated by a novel procedure

INVENTOR(S): Chaux, Pascal; Luiten, Rosalie; Demotte, Nathalie; Duffour, Marie-therese; Lurquin, Christophe; Traversari, Catia; Stroobant, Vincent; Cornelis, Guy R.; Boon-falleur, Thierry; Van Der Bruggen, Pierre; Schultz, Erwin; Warnier, Guy; et al.

PATENT ASSIGNEE(S): Belg.

SOURCE: PCT Int. Appl., 99 pp.  
CODEN: PIXXD2



09/214836

DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 2  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000020445	A2	20000413	WO 1999-IB1664	19990915
WO 2000020445	A3	20000713		
W: AU, CA, CN, JP, KR, NZ, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6407063	B1	20020618	US 1998-165863	19981002
US 6531451	B1	20030311	US 1999-289350	19990409
AU 9959929	A1	20000426	AU 1999-59929	19990915
EP 1117679	A2	20010725	EP 1999-970091	19990915
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003518911	T2	20030617	JP 2000-574556	19990915

PRIORITY APPLN. INFO.:  
US 1998-165863 A 19981002  
US 1999-289350 A 19990409  
WO 1999-IB1664 W 19990915

AB The present invention relates to isolation of cytotoxic T lymphocyte (CTL) clones. In particular, the present invention relates to isolated CTL clones that are specific for proteins of the MAGE family. The CTL clones of the present invention have been isolated by successive steps of stimulation and testing of lymphocytes with antigen presenting cells which present antigens derived from different expression systems, e.g., from recombinant Yersinia, recombinant Salmonella, or recombinant viruses. The present invention further relates to antigenic peptides as well as the peptide/HLA complexes which are recognized by the isolated CTL clones.

IT 162558-08-9

RL: PRP (Properties)  
(unclaimed sequence; **tumor** antigens and CTL clones isolated by a novel procedure)

L4 ANSWER 25 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:175691 HCAPLUS

DOCUMENT NUMBER: 132:220880

TITLE: A tumor rejection antigen encoded by an alternative open reading frame of the human macrophage colony-stimulating factor gene and its role in renal cell carcinomas

INVENTOR(S): Probst-Kepper, Michael; Van Den Eynde, Benoit; Boon-Falleur, Thierry

PATENT ASSIGNEE(S): Ludwig Institute for Cancer Research, USA

SOURCE: PCT Int. Appl., 74 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000013699	A1	20000316	WO 1999-US20344	19990903

Searcher : Shears 308-4994



09/214836

W: AU, JP, US  
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC,  
NL, PT, SE  
AU 9960273 A1 20000327 AU 1999-60273 19990903  
EP 1109568 A1 20010627 EP 1999-968629 19990903  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,  
PT, IE, FI  
PRIORITY APPLN. INFO.: US 1998-99077P P 19980904  
US 1998-99077 P 19980904  
WO 1999-US20344 W 19990903

AB A tumor rejection antigen encoded by an alternative open reading frame of the macrophage colony stimulating factor gene that is expressed in renal cell carcinoma is identified and characterized. The antigen can be used in the diagnosis, prophylaxis and treatment of renal cell carcinoma. The antigen was identified as one recognized by cytotoxic T-lymphocytes and a cDNA was cloned by screening an expression library in 293-EBNA cells using cells expressing HLA-B\*3501 and HLA-Cw\*0401 genes from the cytotoxic T-lymphocytes. Sequencing of the cDNA showed that it was derived from a splice variant of the macrophage colony-stimulating factor transcript. AN HLA-B35-binding peptide of the antigen was identified. The antigen was found in normal renal tubular cells and hepatocytes but not in other major tissues tested. Expression was regulated independently from that of macrophage colony-stimulating factor.

IT 162558-08-9

RL: PRP (Properties)

(unclaimed sequence; **tumor** rejection antigen encoded by an alternative open reading frame of the human macrophage colony-stimulating factor gene and its role in renal cell **carcinomas**)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 26 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:146226 HCAPLUS

DOCUMENT NUMBER: 132:292403

TITLE: The density of peptides displayed by dendritic cells affects immune responses to human tyrosinase and gp100 in HLA-A2 transgenic mice  
AUTHOR(S): Bullock, Timothy N. J.; Colella, Teresa A.; Engelhard, Victor H.

CORPORATE SOURCE: Department of Microbiology and Carter Immunology Center, University of Virginia, Charlottesville, VA, 22908, USA

SOURCE: Journal of Immunology (2000), 164(5), 2354-2361  
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Several HLA-A\*0201-restricted peptide epitopes that can be used as targets for active immunotherapy have been identified within melanocyte differentiation proteins. However, uncertainty exists as to the most effective way to elicit CD8+ T cells with these epitopes in vivo. The authors report the use of transgenic mice expressing a deriv. of HLA-A\*0201, and dendritic cells, to enhance the activation of CD8+ T cells that recognize peptide epitopes derived from human

The first part of the report deals with the general situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The second part of the report deals with the financial situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The third part of the report deals with the social situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The fourth part of the report deals with the economic situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The fifth part of the report deals with the political situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The sixth part of the report deals with the cultural situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The seventh part of the report deals with the educational situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The eighth part of the report deals with the health situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The ninth part of the report deals with the environment situation of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.

The tenth part of the report deals with the foreign relations of the country and the progress of the work. It is followed by a detailed account of the various projects and the results achieved. The report concludes with a summary of the work done and the prospects for the future.



tyrosinase and glycoprotein 100. The authors find that by altering the cell surface d. of the immunizing peptide on the dendritic cells, either by pulsing with higher concns. of peptide, or by changing the MHC-peptide-binding affinity by generating variants of the parent peptides, the size of the activated CD8+ T cell populations can be modulated in vivo. Significantly, the d. of peptide that produced the largest response was less than the max. d. achievable through short-term peptide pulsing. The authors have also found, however, that while some variant peptides are effective at eliciting both primary and recall CD8+ T cell responses that can recognize the parental epitope, other variant epitopes lead to the outgrowth of CD8+ T cells that only recognize the variant. HLA-A\*0201 transgenic mice provide an important model to define which peptide variants are most likely to stimulate CD8+ T cell populations that recognize the parental, melanoma-specific peptide.

IT 162558-08-9

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(peptide d. on dendritic cells affects T-cell responses to HLA-A2-restricted **melanoma** antigens in transgenic mouse)

REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 27 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
 ACCESSION NUMBER: 2000:98598 HCAPLUS  
 DOCUMENT NUMBER: 132:150600  
 TITLE: Endogenous retrovirus tumor associated nucleic acids and antigens  
 INVENTOR(S): Coulie, Pierre; Boon-Falleur, Thierry  
 PATENT ASSIGNEE(S): Ludwig Institute for Cancer Research, USA  
 SOURCE: PCT Int. Appl., 78 pp.  
 CODEN: PIXXD2  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 1  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000006598	A1	20000210	WO 1999-US16236	19990715
W: AU, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9950028	A1	20000221	AU 1999-50028	19990715
EP 1100817	A1	20010523	EP 1999-934130	19990715
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002521051	T2	20020716	JP 2000-562394	19990715
PRIORITY APPLN. INFO.:			US 1998-124398	A 19980729
			US 1998-91243P	P 19980729
			WO 1999-US16236	W 19990715

AB The invention describes HERV-AVL3-B tumor assocd. genes, including fragments and biol. functional variants thereof. Also included are polypeptides and fragments thereof encoded by such genes, and antibodies relating thereto. Methods and products also are provided



09/214836

for diagnosing and treating conditions characterized by expression of a HERV-AVL3-B gene product.

IT 162558-08-9

RL: PRP (Properties)

(unclaimed sequence; endogenous retrovirus **tumor**  
assocd. nucleic acids and antigens)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR  
THIS RECORD. ALL CITATIONS AVAILABLE IN  
THE RE FORMAT

L4 ANSWER 28 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:13836 HCAPLUS

DOCUMENT NUMBER: 132:333090

TITLE: Competition for binding between peptides in  
peptide-based vaccines

AUTHOR(S): Thompson, Lee W.; Brinckerhoff, Laurence H.;  
Slingluff, Craig L., Jr.

CORPORATE SOURCE: Department of Surgery, University of Virginia,  
Charlottesville, VA, USA

SOURCE: Surgical Forum (1998), 49, 458-460

CODEN: SUFOAX; ISSN: 0071-8041

PUBLISHER: American College of Surgeons

DOCUMENT TYPE: Journal

LANGUAGE: English

AB When mixts. of peptides in multivalent vaccines are used, a key question is whether the peptides with a higher affinity for binding to the MHC will competitively block MHC binding of other peptides below the threshold necessary for T cell recognition. Here, a high-affinity peptide epitope for melanoma-reactive cytotoxic T cells (gp10054-162) and a high affinity peptide epitope for flu-reactive CTLs (influenza M158-66) were combined and these peptides were pulsed at various ratios onto antigen-presenting cells. At equimolar concns. of high-affinity peptides, no blocking of T cell recognition could be seen. Only with a 100-fold excess of M1 was the response to melanoma-reactive CTLs to gp100-peptide reduced. These data suggest that the use of mixts. of peptide in peptide-based vaccines may not cause significant competitive inhibition of MHC binding as long as the peptides are used at equimolar concns.

IT 162558-08-9P

RL: BPR (Biological process); BSU (Biological study, unclassified);  
PRP (Properties); SPN (Synthetic preparation); BIOL (Biological  
study); PREP (Preparation); PROC (Process)

(**melanoma**-high affinity gp100; competition for binding  
between peptides in peptide-based vaccines)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR  
THIS RECORD. ALL CITATIONS AVAILABLE IN  
THE RE FORMAT

L4 ANSWER 29 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:677539 HCAPLUS

DOCUMENT NUMBER: 132:48743

TITLE: H-2 class I knockout, HLA-A2.1-transgenic mice.  
A versatile animal model for preclinical  
evaluation of antitumor immunotherapeutic  
strategies

AUTHOR(S): Firat, Huseyin; Garcia-Pons, Francisco; Tourdot,  
Sophie; Pascolo, Steve; Scardino, Antonio;



09/214836

CORPORATE SOURCE: Garcia, Zacarias; Michel, Marie-Louise; Jack, Ralph Williams; Jung, Gunther; Kosmatopoulos, Konstadinos; Mateo, Luis; Suhrbier, Andreas; Lemonnier, Francois A.; Langlade-Demoyen, Pierre  
Unite Immunité Cellulaire Antivirale, Dep. SIDA-Retrovirus, Institut Pasteur, Paris, F-75724, Fr.  
SOURCE: European Journal of Immunology (1999), 29(10), 3112-3121  
CODEN: EJIMAF; ISSN: 0014-2980  
PUBLISHER: Wiley-VCH Verlag GmbH  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB H-2 class I-neg., HLA-A2.1-transgenic HHD mice were used for a comparative evaluation of the immunogenicity of HLA-A2.1-restricted human tumor-assocd. cytotoxic T lymphocyte (CTL) epitopes. A hierarchy was established among these peptides injected into mice in incomplete Freund's adjuvant which correlates globally with their capacity to bind and stabilize HLA-A2.1 mols. Co-injection of a helper peptide enhanced most CTL responses. In contrast, classical HLA class I-transgenic mice which still express their own class I mols. did not, in most cases, develop HLA-A2.1-restricted CTL responses under the same exptl. conditions. Different monoepitope immunization strategies of acceptable clin. usage were compared in HHD mice. Recombinant Ty-virus-like particles, or DNA encoding epitopes fused to the hepatitis B virus middle envelope protein gave the best results. Using this latter approach and a melanoma-based polyepitope construct, CTL responses against 5 distinct epitopes could be elicited simultaneously in a single animal. Thus, HHD mice provide a versatile animal model for preclin. evaluation of peptide-based cancer immunotherapy.

IT 162558-08-9

RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)  
(preclin. evaluation of peptide-based **cancer** immunotherapy using HLA-A2.1-restricted **tumor**-assocd. CTL epitopes)

REFERENCE COUNT: 32 . THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 30 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:673033 HCAPLUS

DOCUMENT NUMBER: 131:321139

TITLE: Genes expressed in tumors encoding tumor rejection antigen precursors and their diagnostic and therapeutic uses

INVENTOR(S): Martelange, Valerie; De Smet, Charles; Boon-Falleur, Thierry

PATENT ASSIGNEE(S): Ludwig Institute for Cancer Research, USA

SOURCE: PCT Int. Appl., 93 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:



09/214836

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9953061	A2	19991021	WO 1999-US8163	19990414
WO 9953061	A3	20000323		
W: AU, CA, CN, JP, KR, NZ, ZA				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6245525	B1	20010612	US 1998-183706	19981030
AU 9935603	A1	19991101	AU 1999-35603	19990414
EP 1073734	A2	20010207	EP 1999-917493	19990414
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002511266	T2	20020416	JP 2000-543609	19990414
PRIORITY APPLN. INFO.:				
			US 1998-60706	A 19980415
			US 1998-122989	A 19980727
			US 1998-183706	A 19981030
			US 1998-183789	A 19981030
			WO 1999-US8163	W 19990414
AB	Genes encoding tumor rejection antigen precursors SAGE (sdph3.10), sdph3.5 and HAGE (sdph3.8) are cloned and their products characterized for therapeutic use. Methods and products also are provided for diagnosing and treating conditions characterized by expression of sdph3.10, sdph3.5 and/or sdph3.8 gene products. Genes specific to a sarcoma were identified by representational difference anal. Many were found to be genes normally assocd. with cell proliferation, and of the remainder, three showed ectopic expression in tumors, i.e. were expressed in a tumor, not in the corresponding normal tissue, but were expressed in other normal tissues. The genes showed normal expression in tissues of the reproductive system (uterus, mammary gland, testis) and skin.			
IT	162558-08-9 RL: PRP (Properties) (unclaimed sequence; genes expressed in <b>tumors</b> encoding <b>tumor</b> rejection antigen precursors and their diagnostic and therapeutic uses)			
L4	ANSWER 31 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN			
ACCESSION NUMBER:	1999:628118 HCAPLUS			
DOCUMENT NUMBER:	131:350041			
TITLE:	An HLA-A2 polyepitope vaccine for melanoma immunotherapy			
AUTHOR(S):	Mateo, Luis; Gardner, Joy; Chen, Qiyan; Schmidt, Christopher; Down, Michelle; Elliott, Suzanne L.; Pye, Stephanie J.; Firat, Huseyin; Lemonnier, Francois A.; Cebon, Jonathon; Suhrbier, Andreas			
CORPORATE SOURCE:	Australian Centre for International and Tropical Health and Nutrition, Co-operative Research Centre for Vaccine Technology, Queensland Institute of Medical Research and University of Queensland, Queensland, Australia			
SOURCE:	Journal of Immunology (1999), 163(7), 4058-4063 CODEN: JOIMA3; ISSN: 0022-1767			
PUBLISHER:	American Association of Immunologists			
DOCUMENT TYPE:	Journal			
LANGUAGE:	English			
AB	Epitope-based vaccination strategies designed to induce tumor-specific CD8 CTL are being widely considered for cancer			





09/214836

immunotherapy. Here the authors describe a recombinant poxvirus vaccine that codes for 10 HLA-A2-restricted epitopes derived from 5 melanoma Ags conjoined in an artificial polyepitope or polytope construct. Target cells infected with the melanoma polytope vaccinia were recognized by 3 different epitope-specific CTL lines derived from HLA-A2 melanoma patients, and CTL responses to 7 of the epitopes were generated in at least one of 6 HLA-A2-transgenic mice immunized with the construct. CTL lines derived from vaccinated transgenic mice were also able to kill melanoma cells in vitro. Multiple epitopes within the polytope construct were therefore shown to be individually immunogenic, illustrating the feasibility of the polytope approach for melanoma immunotherapy. Tumor escape from CTL surveillance, through down regulation of individual tumor Ags and MHC alleles, might be overcome by polytope vaccines, which simultaneously target multiple cancer Ags.

IT 162558-08-9

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(HLA-A2 polyepitope vaccine for **melanoma** immunotherapy)

IT 250672-73-2

RL: PRP (Properties)  
(amino acid sequence; HLA-A2 polyepitope vaccine for **melanoma** immunotherapy)

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 32 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:613608 HCAPLUS

DOCUMENT NUMBER: 131:256325

TITLE: Methods for enhanced antigen presentation on antigen-presenting cells and compositions produced thereby

INVENTOR(S): Nicolette, Charles A.; Kaplan, Johanne

PATENT ASSIGNEE(S): Genzyme Corporation, USA

SOURCE: PCT Int. Appl., 67 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9947102	A2	19990923	WO 1999-US6031	19990319
WO 9947102	A3	19991021		
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2322750	AA	19990923	CA 1999-2322750	19990319
AU 9931023	A1	19991011	AU 1999-31023	19990319
AU 755156	B2	20021205		
EP 1063891	A2	20010103	EP 1999-912710	19990319
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002506622	T2	20020305	JP 2000-536343	19990319
PRIORITY APPLN. INFO.:			US 1998-78880P P	19980320

Searcher : Shears 308-4994



WO 1999-US6031 W 19990319

AB The present invention provides compns. and methods for improved immunotherapy and cancer vaccine, and in particular for inducing an immune response against an antigen in a patient. Thus, in one aspect, this invention provides genetically modified antigen-presenting cells which are more potent presenters of exogenous peptide than parental antigen-presenting cells. Compns. comprising these genetically modified cells and a carrier, such as pharmaceutically acceptable carrier, are further provided by this invention. The genetically modified antigen-presenting cells of this invention can be used in adoptive immunotherapy or to expand a substantially pure population of immune effector cells. Methods for expansion of the substantially pure population of cells are also provided by this invention. Described were cytotoxic T cell epitopes of HSV-1 and HSV-2 ICP47 peptides, melanoma antigen gp100 and MART1, and human tyrosinase-related protein 2.

IT 244224-43-9

RL: PRP (Properties)

(amino acid sequence; methods for enhanced antigen presentation on antigen-presenting cells and compns. for immunotherapy and as **cancer** vaccine)

L4 ANSWER 33 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:600664 HCAPLUS

DOCUMENT NUMBER: 132:106619

TITLE: Establishment of gp100 and MART-1/Melan-A-specific cytotoxic T lymphocyte clones using in vitro immunization against preselected highly immunogenic melanoma cell clones

AUTHOR(S): Kirkin, Alexei F.; Straten, Per thor; Hansen, Mia Riise; Barfoed, Annette; Dzhandzhugazyan, Karine N.; Zeuthen, Jesper

CORPORATE SOURCE: Department of Tumour Cell Biology, Institute of Cancer Biology, Danish Cancer Society, Copenhagen, DK-2100, Den.

SOURCE: Cancer Immunology Immunotherapy (1999), 48(5), 239-246

CODEN: CIIMDN; ISSN: 0340-7004

PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The induction of an in vitro T cell response against tumor-assocd. antigens with subsequent expansion of the individual cytotoxic T lymphocyte (CTL) clones still is not routine and the only tumor-assocd. antigen that has been found to easily induce the establishment of CTL clones is the MART-1/Melan-A antigen. In this paper, we describe a new approach for in vitro immunization based on the use of preselected melanoma cell clones. The human melanoma cell subline FM3.P was cloned and the immunol. properties of individual clones were compared. Melanoma cell clone FM3.29, having a high level of expression of melanoma differentiation antigens, as well as high levels of the HLA class I and class II antigens and adhesion mols., was used for the establishment of a CTL line that was subsequently cloned. For optimization of the conditions of growth of established CTL clones, a particular melanoma subline FM3.D/40 was selected for supporting the proliferation of CTL clones. The majority of the established CTL clones recognized the melanoma-assocd. differentiation antigens gp100 and MART-1/Melan-A.



09/214836

Epitope anal. indicated that two different epitopes derived from gp100 (154-162 and 280-288) and a single epitope from MART-1/Melan-A (27-35) were recognized by these CTL clones. The gp100-specific CTL clones were found to be significantly more sensitive to the culture conditions than the MART-1/Melan-A-specific CTL clones. In addn., the presence of excess peptide in the culture medium induced autokilling of the gp100-specific, but not the MART-1/Melan-A-specific CTL clones. These results demonstrate that, by careful preselection of melanoma cell lines and clones both for the induction of CTL line from patients' peripheral blood lymphocytes and subsequent cloning, it is possible to obtain a large no. of stable CTL clones even against such an inherently "difficult" differentiation antigen as gp100.

IT 162558-08-9

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(**melanoma**-assocd. antigen; establishment of gp100 and MART-1/Melan-A-specific cytotoxic T lymphocyte clones using in vitro immunization against highly immunogenic **melanoma** cell clones)

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 34 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:366631 HCAPLUS

DOCUMENT NUMBER: 131:156878

TITLE: Characterization of circulating T cells specific for tumor-associated antigens in melanoma patients

AUTHOR(S): Lee, Peter P.; Yee, Cassian; Savage, Peter A.; Fong, Lawrence; Brockstedt, Dirk; Weber, Jeffrey S.; Johnson, Denise; Swetter, Susan; Thompson, John; Greenberg, Philip D.; Roederer, Mario; Davis, Mark M.

CORPORATE SOURCE: Howard Hughes Medical Institute/Department of Microbiology and Immunology, Stanford University, Stanford, CA, 94305, USA

SOURCE: Nature Medicine (New York) (1999), 5(6), 677-685  
CODEN: NAMEFI; ISSN: 1078-8956

PUBLISHER: Nature America

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The authors identified circulating CD8+ T-cell populations specific for the tumor-assocd. antigens (TAAs) MART-1 (27-35) or tyrosinase (368-376) in 6 of 11 patients with metastatic melanoma using peptide/HLA-A\*0201 tetramers. These TAA-specific populations were of 2 phenotypically distinct types: one, typical for memory/effector T cells; the other, a previously undescribed phenotype expressing both naive and effector cell markers. This latter type represented >2% of the total CD8+ T cells in one patient, permitting detailed phenotypic and functional anal. Although these cells have many of the hallmarks of effector T cells, they were functionally unresponsive, unable to directly lyse melanoma target cells or produce cytokines in response to mitogens. In contrast, CD8+ T cells from the same patient were able to lyse EBV-pulsed target cells and showed robust allogeneic responses. Thus, the clonally



09/214836

expanded TAA-specific population seems to have been selectively rendered anergic in vivo. Peptide stimulation of the TAA-specific T-cell populations in other patients failed to induce substantial upregulation of CD69 expression, indicating that these cells may also have functional defects, leading to blunted activation responses. Thus, systemic TAA-specific T-cell responses can develop de novo in cancer patients, but antigen-specific unresponsiveness may explain why such cells are unable to control tumor growth.

IT 162558-08-9

RL: PRP (Properties)

(circulating T cells characterization specific for tumor  
-assocd. antigens in melanoma patients)

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L4 ANSWER 35 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:107655 HCAPLUS

DOCUMENT NUMBER: 130:280522

TITLE: Isolation of high avidity melanoma-reactive CTL  
from heterogeneous populations using peptide-MHC  
tetramers

AUTHOR(S): Yee, Cassian; Savage, Peter A.; Lee, Peter P.;  
Davis, Mark M.; Greenberg, Philip D.

CORPORATE SOURCE: Clinical Research Division, Fred Hutchinson  
Cancer Research Center, and Departments of  
Medicine and Immunology, University of  
Washington, Seattle, WA, 98109, USA

SOURCE: Journal of Immunology (1999), 162(4), 2227-2234  
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Immunogenic peptides of human tumor Ag have been used to generate antigen-specific CTL. However, the vast majority of these peptide-specific CTL clones are of low avidity and are peptide, but not tumor, reactive. Peptide-MHC tetramers have been shown to bind specific TCRs with sufficient affinity to be useful reagents for flow cytometry. In this paper the authors demonstrate that peptide-MHC tetramers can also be used to selectively identify high avidity tumor-reactive CTL and enrich, from a heterogeneous population, the subpopulation of peptide-reactive T cells that can lyse tumor targets. The melanoma proteins, MART-1 and gp100, were used to induce potentially tumor-reactive T cells, and the intensity of T cell staining by TCR binding of specific peptide-MHC tetramers was assessed. A range of fluorescence intensity was detected, and the magnitude of tetramer binding was correlated with T cell avidity. The population of peptide-reactive T cells was phenotypically similar with regard to expression of TCR and adhesion mols., suggesting that this differential avidity for tumor cells reflected differential affinity of the TCR for its peptide-MHC ligand. Sorting, cloning, and expansion of tetramerhigh CTL from a heterogeneous population of peptide-stimulated PBMCs enabled rapid selection of high avidity tumor-reactive CTL clones, which retained their functional and tetramerhigh phenotype on re-expansion. These results demonstrate that the avidity of a T cell for its tumor target is due to the specific affinity of the TCR for its peptide-MHC ligand, that this interaction can be described using





09/214836

peptide-MHC tetramers and used to isolate high avidity  
tumor-reactive CTL.  
IT **162558-08-9D**, MHC class I tetramers  
RL: BUU (Biological use, unclassified); BIOL (Biological study);  
USES (Uses)  
(isolation of high avidity **melanoma**-reactive human  
cytotoxic T-cells by)  
REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L4 ANSWER 36 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 1998:799700 HCAPLUS  
DOCUMENT NUMBER: 130:37302  
TITLE: Melanoma antigens and their use in diagnostic  
and therapeutic methods  
INVENTOR(S): Kawakami, Yutaka; Rosenberg, Steven A.  
PATENT ASSIGNEE(S): United States Dept. of Health and Human  
Services, USA  
SOURCE: U.S., 76 pp., Cont.-in-part of U.S. Ser. No.  
231,565.  
CODEN: USXXAM  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 2  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5844075	A	19981201	US 1995-417174	19950405
US 5874560	A	19990223	US 1994-231565	19940422
CA 2188432	AA	19951102	CA 1995-2188432	19950421
WO 9529193	A2	19951102	WO 1995-US5063	19950421
WO 9529193	A3	19960104		
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TT, UA				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9523958	A1	19951116	AU 1995-23958	19950421
AU 706443	B2	19990617		
EP 756604	A1	19970205	EP 1995-917151	19950421
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 10505481	T2	19980602	JP 1995-527821	19950421
FI 9604235	A	19961220	FI 1996-4235	19961021
US 5994523	A	19991130	US 1998-7961	19980116
US 6537560	B1	20030325	US 1998-73138	19980505
US 6270778	B1	20010807	US 1999-267439	19990312
US 2003144482	A1	20030731	US 2001-898860	20010703
PRIORITY APPLN. INFO.:				
			US 1994-231565	A2 19940422
			US 1995-417174	A 19950405
			WO 1995-US5063	W 19950421
			US 1998-73138	A3 19980505
			US 1999-267439	A3 19990312
AB The present invention provides a nucleic acid sequence encoding a				



09/214836

melanoma antigen recognized by T lymphocytes, designated MART-1. This invention further relates to bioassays using the nucleic acid sequence, protein or antibodies of this invention to diagnose, assess or prognoses a mammal afflicted with melanoma or metastatic melanoma. This invention also provides immunogenic peptides derived from the MART-1 melanoma antigen and a second melanoma antigen designated gp100. This invention further provides immunogenic peptides derived from the MART-1 melanoma antigen or gp100 antigen which have been modified to enhance their immunogenicity. The proteins and peptides provided can serve as an immunogen or vaccine to prevent or treat melanoma.

IT 162558-08-9 162558-09-0

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(**melanoma**-assocd. antigens MART-1 and gp100 and epitopes and antibodies for diagnosis and therapy  
**melanoma** and metastasis)

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 37 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:71219 HCAPLUS

DOCUMENT NUMBER: 128:139756

TITLE: Melanoma-associated peptide analogs and vaccines against melanoma

INVENTOR(S): Figdor, Carl Gustav; Adema, Gosse Jan

PATENT ASSIGNEE(S): Akzo Nobel N.V., Neth.; Figdor, Carl Gustav; Adema, Gosse Jan

SOURCE: PCT Int. Appl., 47 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9802538	A1	19980122	WO 1997-EP3712	19970708
W: AU, CA, JP, KR, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
ZA 9705858	A	19980901	ZA 1997-5858	19970701
CA 2259944	AA	19980122	CA 1997-2259944	19970708
AU 9736938	A1	19980209	AU 1997-36938	19970708
EP 934405	A1	19990811	EP 1997-933664	19970708
EP 934405	B1	20011010		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2000515739	T2	20001128	JP 1998-505606	19970708
AT 206759	E	20011015	AT 1997-933664	19970708
ES 2165619	T3	20020316	ES 1997-933664	19970708

PRIORITY APPLN. INFO.: EP 1996-201945 A 19960711  
WO 1997-EP3712 W 19970708

AB The MHC class-I binding affinity of an epitope is an important parameter detg. the immunogenicity of the peptide-MHC complex. To improve the immunogenicity of an epitope derived from melanocyte lineage-specific antigen gp100 and Melan-A/MART-1, amino acid



substitutions were performed within the epitope and both HLA-A\*0201 binding and CTL recognition were assayed. Anchor replacements towards the HLA-A\*0201 peptide-binding motif gave rise to peptides with higher HLA-A\*0201 binding capacity compared to the wild-type epitope. In addn., several of the gp100 154-162 epitope-analogs were more efficient at target-cell sensitization for lysis by anti-gp100 154-162 CTL compared to the wild-type epitope. These altered gp100 154-162 epitopes were subsequently tested for their capacity to induce CTL responses in vivo using HLA-A\*0201/Kb transgenic mice, and in vitro using HLA-A\*0201+ donor-derived lymphocytes. Interestingly, the peptide-specific CTL obtained, which were raised against the different gp100 154-162 epitope-analogs, displayed cross-reactivity with target cells endogenously processing and presenting the native epitope. These data demonstrate that altered epitopes can be exploited to elicit native epitope-reactive CTL. The use of epitope-analogs with improved immunogenicity may contribute to the development of CTL-epitope based vaccines in viral disease and cancer.

IT 162558-08-9 187974-51-2 202393-35-9

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(analogs of cytotoxic T lymphocyte epitopes with improved MHC class-I binding capacity elicit anti-melanoma CTL recognizing wild-type epitope)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 38 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:401143 HCAPLUS

DOCUMENT NUMBER: 127:134628

TITLE: TCR .beta.-chain variable region-driven selection and massive expansion of HLA class I-restricted antitumor CTL lines from HLA-A\*0201+ melanoma patients

AUTHOR(S): Maccalli, Cristina; Farina, Cinthia; Sensi, Marialuisa; Parmiani, Giorgio; Anichini, Andrea  
CORPORATE SOURCE: Div. Experimental Oncol. D, Natl. Tumor Inst., Milan, 20133, Italy

SOURCE: Journal of Immunology (1997), 158(12), 5902-5913  
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Recognition of a given melanoma antigen (Ag) involves a limited array of T cell clones bearing a structurally defined TCR. The aim here was to verify whether this information can be used to isolate and expand such antitumor effectors from fresh lymphocyte populations. The authors found that 1-3 different TCR .beta.-chain variable (TCRBV) regions were expanded in 4-wk mixed lymphocyte-tumor cultures (MLTC) from 6 HLA-A\*0201+ melanoma patients, and that the T cells expressing the expanded TCRBV regions were involved in HLA class I-restricted lysis of the tumor. T cell activation by mAbs to MLTC-selected TCRBV region and CD28 resulted in large scale expansion (1-10.times.109 cells) of T cell lines, highly enriched for the expression of a single TCRBV region and for CD8+ T cells. The TCRBV-driven selection was equally effective when



09/214836

applied to patients' or healthy donors' lymphocytes, and the T cell lines isolated from melanoma patients exerted HLA class I-restricted lysis of the autologous tumor. MLTC and TCRBV-selected lines recognized allogeneic melanomas sharing HLA-A and -B alleles with the autologous tumor, but only 2 of the HLA-A2-restricted lines were directed to a known peptide from melanoma-assocd. Ags. Single-strand conformation polymorphism anal. indicated a polyclonal compn. of both MLTC and TCRBV-selected lines, but expansion of clonotypes with identical CDR3 length was obsd. only in the MLTC lines. Thus, TCRBV-driven selection can be exploited to obtain large scale expansion of antitumor CTL lines from melanoma patients.

IT 162558-08-9

RL: PRP (Properties)

(peptides from **melanoma**-assocd. antigens recognition by mixed lymphocyte **tumor** culture vs. TCR .beta.-chain variable region-selected cytotoxic T cells)

L4 ANSWER 39 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:169342 HCAPLUS

DOCUMENT NUMBER: 126:249922

TITLE: Anti-melanoma cytotoxic T lymphocytes (CTL) recognize numerous antigenic peptides having 'self' sequences: autoimmune nature of the anti-melanoma CTL response

AUTHOR(S): Tsomides, Theodore J.; Reilly, Edward B.; Eisen, Herman N.

CORPORATE SOURCE: Center Cancer Res. and Dep. Biol., Massachusetts Inst. Tech., Cambridge, MA, 02139, USA

SOURCE: International Immunology (1997), 9(2), 327-338

CODEN: INIMEN; ISSN: 0953-8178

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A line of tumor-infiltrating lymphocytes (660TIL) specifically lysed the autologous HLA-A2+ melanoma (660MEL) and also most A2+ melanoma cell lines. The authors immunopptd. A2 from a large no. (>1012) OF 660MEL cells, extd. naturally processed peptides, fractionated them by HPLC, screened the fractions for recognition by 660TIL, and found a single predominant and a minor peak of activity. Although too little was recovered of the major 660MEL peptide to establish its sequence, HPLC fingerprinting showed that it did not correspond to any of the known A2-assocd. melanoma peptides recognized by T cells, including peptides from tyrosinase, MART-1/Melan-A, gp100, and MAGE-3. The major 660MEL antigenic peptide appears to be derived from MART-1/Melan-A but is neither AAGIGILTV nor ILTVILGVL nor any other MART-1/Melan-A peptide contg. the A2 consensus motif. The multiplicity of melanoma peptides recognized by CD8+ T cells, most of which are non-mutated (including most likely the present 660MEL peptide), suggests the existence of unknown mechanisms, perhaps similar to those operating in autoimmune disorders, whereby T cell that recognize normal self sequences become activated.

IT 162558-08-9

RL: PRP (Properties)

(autoimmune nature of anti-**melanoma** cytotoxic T lymphocytes response to antigenic peptides)

L4 ANSWER 40 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:167497 HCAPLUS





09/214836

DOCUMENT NUMBER: 126:210733  
TITLE: Analogs of CTL epitopes with improved MHC class-I binding capacity elicit anti-melanoma CTL recognizing the wild-type epitope  
AUTHOR(S): Bakker, Alexander B.H.; Van Der Burg, Sjoerd H.; Huijbens, Richard J.F.; Drijfhout, Jan-Wouter; Melief, Cornelis J.M.; Adema, Gosse J.; Figdor, Carl G.  
CORPORATE SOURCE: Department of Tumor Immunology, University Hospital Nijmegen St. Radboud, Nijmegen, Neth.  
SOURCE: International Journal of Cancer (1997), 70(3), 302-309  
CODEN: IJCNAW; ISSN: 0020-7136  
PUBLISHER: Wiley-Liss  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB The MHC class-I binding affinity of an epitope is an important parameter detg. the immunogenicity of the peptide-MHC complex. To improve the immunogenicity of an epitope derived from melanocyte lineage-specific antigen gp100, we performed amino-acid substitutions within the epitope and assayed both HLA-A\*0201 binding and CTL recognition. Anchor replacements towards the HLA-A\*0201 peptide-binding motif gave rise to peptides with higher HLA-A\*0201 binding capacity compared to the wild-type epitope. In addn., several of the gp100 154-162 epitope-analogs were more efficient at target-cell sensitization for lysis by anti-gp100 154-162 CTL compared to the wild-type epitope. These altered gp100 154-162 epitopes were subsequently tested for their capacity to induce CTL responses in vivo using HLA-A\*0201/Kb transgenic mice, and in vitro using HLA-A\*0201+ donor-derived lymphocytes. Interestingly, the peptide-specific CTL obtained, which were raised against the different gp100 154-162 epitope-analogs, displayed cross-reactivity with target cells endogenously processing and presenting the native epitope. These data demonstrate that altered epitopes can be exploited to elicit native epitope-reactive CTL. The use of epitope-analogs with improved immunogenicity may contribute to the development of CTL-epitope based vaccines in viral disease and cancer.

IT 162558-08-9 (187974-51-2)  
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)  
(analogs of cytotoxic T lymphocyte epitopes with improved MHC class-I binding capacity elicit anti-melanoma CTL recognizing wild-type epitope)

L4 ANSWER 41 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:119427 HCAPLUS  
DOCUMENT NUMBER: 126:210701  
TITLE: Identification of subdominant CTL epitopes of the gp100 melanoma-associated tumor antigen by primary in vitro immunization with peptide-pulsed dendritic cells  
AUTHOR(S): Tsai, Van; Southwood, Scott; Sidney, John; Sakaguchi, Kazuyasu; Kawakami, Yutaka; Appella, Ettore; Sette, Alessandro; Celis, Esteban  
CORPORATE SOURCE: Cytel Corp., San Diego, CA, 92121, USA  
SOURCE: Journal of Immunology (1997), 158(4), 1796-1802



09/214836

CODEN: JOIMA3; ISSN: 0022-1767  
PUBLISHER: American Association of Immunologists  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB The gp100 melanoma-assocd. tumor antigen (Ag) was selected as a model system to study the diversity of human antitumor cytotoxic T cell responses. First, peptides corresponding to dominant gp100 HLA-A2.1-restricted CTL epitopes were tested using lymphocytes from normal volunteers and an in vitro priming protocol that uses peptide-pulsed dendritic cells as APCs and IL-7 and IL-10 as immune-enhancing cytokines. High CTL activity toward both peptide-pulsed target cells and gp100+ melanoma cells was obtained with 4 out of 5 peptides tested. Second, HLA-A2.1-binding peptides from gp100 that do not appear to represent CTL epitopes in melanoma patients were also tested for their capacity to induce CTL using the in vitro priming protocol. Three of 6 peptides tested induced CTL in lymphocytes from normal volunteers. One of these peptides was also immunogenic for lymphocytes derived from a melanoma patient in remission. Because these 3 CTL epitopes were not recognized in the natural immune response in melanoma patients but do appear as immunogens when peptides are used to induce the T cell response, they may be considered as typical "subdominant" epitopes. The results are discussed in the context of the usefulness of this approach to detail the immunol. potential of a given tumor-assocd. Ag and its relevance for the design of effective immune-based therapies.

IT 162558-08-9

RL: PRP (Properties)  
(subdominant cytotoxic T cell epitopes of gp100 melanoma -assocd. tumor antigen identification by primary in vitro immunization with peptide-pulsed dendritic cells)

L4 ANSWER 42 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:649156 HCAPLUS

DOCUMENT NUMBER: 125:298993

TITLE: Immunization against epitopes in the human melanoma antigen gp100 following patient immunization with synthetic peptides

AUTHOR(S): Salgaller, Michael L.; Marincola, Francesco M.; Cormier, Janice N.; Rosenberg, Steven A.

CORPORATE SOURCE: Surgery Branch, Natl. Cancer Inst., Bethesda, MD, 20892, USA

SOURCE: Cancer Research (1996), 56(20), 4749-4757

CODEN: CNREA8; ISSN: 0008-5472

PUBLISHER: American Association for Cancer Research

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The gp100 glycoprotein is a melanocytic lineage-specific antigen recognized by tumor-infiltrating lymphocytes, the adoptive transfer of which is assocd. with tumor regression in melanoma patients. In this study, peripheral blood mononuclear cells (PBMCs) were harvested from HLA-A2+ melanoma patients before and after immunization with G9-209 (ITDQVPFSY), G9-280 (YLEPGPVTA), or G9-154 (KTWGQYWQV) peptides in Incomplete Freund's Adjuvant and were tested for the ability to be sensitized in vitro using PBMCs pulsed with the native peptides. In addn., PBMCs from patients receiving the G9-209 or G9-280 peptide were stimulated in vitro with peptides modified at anchor residues to enhance binding to HLA-A2: G9-209/2M



(IMDQVPFSY) or G9-280-9V (YLEPGPVTV). In patients immunized with G9-209, a single in vitro restimulation with G9-209, a single in vitro restimulation with G9-209/2m resulted in the generation of specific antipeptide lymphocytes from 7 of 7 postimmune PBMCs and only 3 of 7 preimmune PBMCs. In patients immunized with G9-280, a single in vitro restimulation with G9-280/9V resulted in the generation of specific antipeptide lymphocytes from 5 of 6 postimmune PBMCs and 4 of 6 preimmune PBMCs. In almost all cases, CTLs raised against modified epitopes were capable of recognizing targets displaying the native nonamers. Several anti-G9-209 and anti-G9-209/2M CTLs also demonstrated specific lysis of, and specific IFN- $\gamma$  release in response to, gp100+ -established cell lines. Thus, using peptides modified to enhance immunogenicity for in vitro stimulation improved the sensitivity of immune monitoring of patients immunized with synthetic peptides. These results demonstrate that immunization with a peptide derived from a tumor-assocd. protein such as gp100 can provoke a measurable antitumor immune response in cancer patients.

IT **162558-08-9P**

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(immune response to human **melanoma** antigen gp100 following patient immunization with synthetic peptides)

L4 ANSWER 43 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:562140 HCAPLUS

DOCUMENT NUMBER: 125:219058

TITLE: Improved induction of melanoma-reactive CTL with peptides from the melanoma antigen gp100 modified at HLA-A\*0201-binding residues

AUTHOR(S): Parkhurst, Maria R.; Salgaller, Michael L.; Southwood, Scott; Robbins, Paul F.; Sette, Alessandro; Rosenberg, Steven A.; Kawakami, Yutaka

CORPORATE SOURCE: National Cancer Institute, National Institutes of Health, Bethesda, MD, 20892, USA

SOURCE: Journal of Immunology (1996), 157(6), 2539-2548  
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Recognition of the melanoma Ag gp100 by tumor-infiltrating lymphocytes (TIL) in vitro has been correlated with tumor regression in patients with metastatic melanoma treated with the adoptive transfer of TIL plus IL-2. Three common gp100 epitopes have been identified that are recognized in the context of HLA-A2 by TIL from different patients: G9154 (KTWGQYWQV), G9209 (ITDQVPFSV), and G9280 (YLEPGPVTA). Upon stimulation with these peptides, melanoma-reactive CTL could be induced in vitro from PBL of some HLA-A2+ melanoma patients. However, numerous restimulations were required, and specific reactivity could not be generated in many patients. Therefore, to enhance the immunogenicity of gp100 peptides, amino acid substitutions were introduced into G9154, G9209, and G9280 at HLA-A\*0201-binding anchor positions, but not at TCR contact residues, to increase peptide class I MHC-binding affinity. Several modified gp100 peptides bound with greater



affinity to HLA-A\*0201 than unmodified peptides and were recognized by TIL specific for the neutral epitopes. These peptides were used to sensitize PBL from HLA-A2+ melanoma patients in vitro using peptide-pulsed autologous PBMC as stimulators. After five weekly restimulations with either the native G9209 or G9280 peptide, melanoma-reactive CTL could only be induced from two of seven patients. However, amino acid substitutions in these peptides enabled the induction of melanoma-reactive CTL from all seven patients. These results suggest that modified gp100 peptides may be more immunogenic than the native epitopes, and may be useful in immunotherapy protocols for patients with melanoma.

IT 162558-08-9

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(melanoma-reactive human cytotoxic T-cells are induced by gp100-derived peptides modified for enhanced HLA-A2 binding)

L4 ANSWER 44 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:282522 HCAPLUS

DOCUMENT NUMBER: 124:314539

TITLE: Binding and presentation of peptides derived from melanoma antigens MART-1 and glycoprotein-100 by HLA-A2 subtypes.

AUTHOR(S): Implications for peptide-based immunotherapy Rivoltini, Licia; Loftus, Douglas J.;

Barracchini, Kathleen; Arienti, Flavio;

Mazzocchi, Arabella; Biddison, William E.;

Salgaller, Michael L.; Appella, Ettore;

Parmiani, Giorgio; Marincola, Francesco M.

CORPORATE SOURCE: Surgery Branch, National Institutes Health, Bethesda, MD, 20892, USA

SOURCE: Journal of Immunology (1996), 156(10), 3882-3891  
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Cellular immune responses to melanoma-assocd. Ags are the focus of ongoing studies aimed at developing immunotherapies for treatment of malignant melanoma. Melanoma predominantly affects Caucasians, a population in whom expression of HLA-A2 is prevalent. Among HLA-A2 subtypes, HLA-A\*0201 is widely expressed, and HLA-A\*0201-restricted, tumor-reactive CTL responses are well studied. We have obsd. in a group of melanoma patients an unexpectedly high frequency (.apprx.20%) of non-HLA-A\*0201 subtypes (\*0202, \*0204, and \*0205), and little is known regarding antimelanoma response profiles in patients expressing such subtypes. We analyzed non-HLA-A\*0201 peptide response profiles using HLA-A\*0201-restricted epitopes from melanoma Ags MART-1/Melan A and glycoprotein 100. Most of these peptides bound to the majority of subtypes tested with 50% inhibitory concns. less than 500 nM. Recognition of cells pulsed with different peptides (MART-1 G9154, and G9280 Flu M158-66) and expressing different subtype mols. by HLA-A\*0201-restricted CTL was limited to only a subset of non-HLA-A\*0201 mols., and the peptide/subtype complexes recognized varied among the effector populations tested. CTL responses elicited from PBL of patients and healthy donors expressing subtypes HLA-A\*0202 and HLA-A\*0205 suggested significant differences among HLA-A2 subtype function in





09/214836

the context of melanoma Ag presentation. These observations imply the necessity of subtyping patients considered for peptide-based protocols and highlight the need for further study of melanoma-directed cellular responses among patients expressing non-HLA-A\*0201 subtypes.

IT 162558-08-9

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(binding and presentation of peptides derived from  
**melanoma** antigens MART-1 and glycoprotein-100 by HLA-A2 subtypes)

L4 ANSWER 45 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:998386 HCAPLUS

DOCUMENT NUMBER: 124:84888

TITLE: Melanoma antigens recognized by tumor infiltrating lymphocyte

INVENTOR(S): Kawakami, Yutaka; Rosenberg, Steven A.

PATENT ASSIGNEE(S): United States Dept. of Health and Human Services, USA

SOURCE: PCT Int. Appl., 183 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9529193	A2	19951102	WO 1995-US5063	19950421
WO 9529193	A3	19960104		
W:	AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TT, UA			
RW:	KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG			
US 5874560	A	19990223	US 1994-231565	19940422
US 5844075	A	19981201	US 1995-417174	19950405
AU 9523958	A1	19951116	AU 1995-23958	19950421
AU 706443	B2	19990617		
EP 756604	A1	19970205	EP 1995-917151	19950421
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE			
JP 10505481	T2	19980602	JP 1995-527821	19950421
FI 9604235	A	19961220	FI 1996-4235	19961021
US 2003144482	A1	20030731	US 2001-898860	20010703
PRIORITY APPLN. INFO.:			US 1994-231565	A 19940422
			US 1995-417174	A 19950405
			WO 1995-US5063	W 19950421
			US 1999-267439	A3 19990312

OTHER SOURCE(S): MARPAT 124:84888

AB The present invention provides a nucleic acid sequence encoding a melanoma antigen recognized by T lymphocytes, designated MART-1. This invention further relates to bioassays using the nucleic acid sequence, protein or antibodies of this invention to diagnose, assess or prognose a mammal afflicted with melanoma or metastatic



09/214836

melanoma. This invention also provides immunogenic peptides derived from the MART-1 melanoma antigen and a second melanoma antigen designated gp100. This invention further provides immunogenic peptides derived from the MART-1 melanoma antigen of gp100 antigen which have been modified to enhance their immunogenicity. The proteins and peptides can serve as an immunogen or vaccine to prevent or treat melanoma. In example, cytotoxic T lymphocytes and culture of cell lines were prepd., immunogenic epitopes of MART-1 were characterized, and a second human melanoma antigen recognized by tumor infiltrating lymphocytes assocd. with in vivo tumor rejection was also identified. In addn., recognition of multiple epitopes in human melanoma antigen by tumor infiltrating lymphocytes, modified melanoma epitopes with improved immunogenicity, use of the improved epitopes as vaccine for treating melanoma in mammals, and use of lymphocytes sensitized to immunogenic peptides derived from melanoma antigens for therapeutically treating mammals afflicted with melanoma were demonstrated.

IT 155422-80-3

RL: PRP (Properties)

(amino acid sequence; **melanoma** antigens MART1 and gp100 epitopes recognized by **tumor**-infiltrating lymphocyte as vaccine for treating **melanoma** in mammals)

IT 162558-08-9 162558-09-0

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(**melanoma** antigens MART1 and gp100 epitopes recognized by **tumor**-infiltrating lymphocyte as vaccine for treating **melanoma** in mammals)

L4 ANSWER 46 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:916208 HCAPLUS

DOCUMENT NUMBER: 123:311939

TITLE: Recognition of multiple epitopes in the human melanoma antigen gp100 by peripheral blood lymphocytes stimulated in vitro with synthetic peptides

AUTHOR(S): Salgaller, Micheal L.; Afshar, Alireza; Marincola, Francesco M.; Rivoltini, Licia; Kawakami, Yutaka; Rosenberg, Steven A.

CORPORATE SOURCE: Surgery Branch, National Institutes Health, Bethesda, MD, 20892, USA

SOURCE: Cancer Research (1995), 55(21), 4972-9  
CODEN: CNREA8; ISSN: 0008-5472

PUBLISHER: American Association for Cancer Research

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Gp100 is a melanocyte lineage-specific antigen recognized by tumor-infiltration lymphocytes whose adoptive transfer has been assocd. with tumor regression in patients with metastatic melanoma. The peripheral blood mononuclear cells of five melanoma patients were sensitized in vitro with synthetic peptides to elicit antigen-specific cytotoxic T lymphocyte (CTL) lines against four gp100 epitopes. These epitope-specific CTL lines were generated following weekly in vitro stimulation with the synthetic decamer G10476 (V-L-Y-R-Y-G-S-F-S-V) or the nonamers G9280 (Y-L-E-P-G-P-V-T-A), G9154 (K-T-W-G-Q-Y-W-Q-V), or G9209 (I-T-D-Q-V-P-F-S-V) pulsed onto autologous irradiated peripheral



09/214836

blood mononuclear cells. These lines grew as long as 4 mo in culture in low-dose interleukin 2 (30 IU/mL) and exhibited antigen-specific, MHC class I-restricted lysis of peptide-pulsed T2 cells and HLA-A2+, gp100+ established melanoma cell lines. G10476- and G9280-specific CTLs demonstrated specific release of granulocyte-macrophage-colony-stimulating factor and tumor necrosis factor .alpha. in response to T2 cells pulsed with relevant peptide, as well as to gp100+ melanoma cell lines. These results demonstrate that several peptides derived from the gp100 protein are presented on the surface of melanoma cells and are sufficiently immunogenic to generate, in vitro, potent CTLs capable of cytolysis and the secretion of cytokines. Therefore, for HLA-A2+ melanoma patients, these and possibly other gp100 peptides could represent good candidates for antigen-specific immunotherapy either singly or in a multivalent regimen.

IT 162558-08-9

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(gp100-derived peptides stimulate cytotoxic T lymphocytes to release cytokines and lyse melanoma cells expressing gp100-derived peptides)

L4 ANSWER 47 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:913438 HCAPLUS

DOCUMENT NUMBER: 123:312226

TITLE: Melanoma associated antigenic polypeptide, epitopes thereof and vaccines against melanoma

INVENTOR(S): Adema, Gosse Jan; Figdor, Carl Gustav

PATENT ASSIGNEE(S): Akzo Nobel N. V., Neth.

SOURCE: Eur. Pat. Appl., 41 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 668350	A1	19950823	EP 1995-200348	19950214
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
CA 2142575	AA	19950817	CA 1995-2142575	19950215
FI 9500665	A	19950817	FI 1995-665	19950215
AU 9512272	A1	19950824	AU 1995-12272	19950215
AU 697267	B2	19981001		
ZA 9501239	A	19951019	ZA 1995-1239	19950215
US 6500919	B1	20021231	US 1995-388852	19950215
JP 07278193	A2	19951024	JP 1995-28387	19950216
PRIORITY APPLN. INFO.:			EP 1994-200337	A 19940216
			EP 1994-203709	A 19941221

AB The present invention describes a melanoma associated antigen known as gp100. Furthermore, peptides derived from said antigen are claimed. Gp100 and its peptides can be used in vaccines for the treatment of melanoma. Another aspect of the invention are host cells capable of expression of gp100 or the gp100-derived peptides. Furthermore, tumor infiltrating lymphocytes (TIL's) specifically recognizing gp100 are claimed, as are vaccines with these TIL's.



09/214836

Furthermore, diagnostics for the detection of melanoma and for the monitoring of vaccination form part of the invention.

IT 155422-80-3P

RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(amino acid sequence of; **melanoma** assocd. antigenic polypeptide, epitopes thereof and vaccines against **melanoma**)

IT 162558-08-9 162558-09-0 167635-39-4  
170153-76-1

RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(**melanoma** assocd. antigenic polypeptide, epitopes thereof and vaccines against **melanoma**)

L4 ANSWER 48 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:724076 HCAPLUS

DOCUMENT NUMBER: 123:196160

TITLE: Identification of a novel peptide derived from the melanocyte-specific GP100 antigen as the dominant epitope recognized by an

AUTHOR(S): Bakker, Alexander B.H.; Schreurs, Marco W.J.; Tafazzul, Gaalda; de Boer, Annemiek J.; Kawakami, Yutaka; Adema, Gosse J.; Figdor, Carl G.

CORPORATE SOURCE: Department of Tumor Immunology, University Hospital Nijmegen, Nijmegen, Neth.

SOURCE: International Journal of Cancer (1995), 62(1), 97-102

CODEN: IJCNAW; ISSN: 0020-7136

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Cytotoxic T lymphocytes (CTL) reactive with human melanoma tumor cells occasionally display cross-reactivity with normal melanocytes. Previously, we identified the melanocyte lineage-specific antigen gp100 that is expressed by both melanoma cells and normal melanocytes, as a target antigen for tumor-infiltrating lymphocytes derived from a melanoma patient (TIL 1200). Here, we demonstrate that the oligoclonal HLA-A2.1-restricted TIL 1200 line is reactive with 2 distinct peptides derived from the gp100 protein. Apart from the peptide corresponding to gp100 amino acids 457-466, we identified the gp100 peptide 154-162 as a second epitope recognized by TIL 1200. A 100-fold lower concn. of this novel gp100 peptide was required for target-cell sensitization compared to peptide 457-466, indicating that the 154-162 peptide is the dominant gp100 epitope for TIL 1200. Together with the recently described gp100 280-288 epitope, 3 distinct CTL epitopes have now been identified in gp100, all presented in the context of HLA-A2.1. Therefore, gp100 is an attractive target antigen in the development of immuno-therapeutic protocols against melanoma.

IT 162558-08-9 162558-09-0 167635-39-4

RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)

(peptide from the melanocyte-specific GP100 antigen as the dominant epitope recognized by an HLA-A2.1-restricted anti-**melanoma** CTL line)





09/214836

L4 ANSWER 49 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 1995:497876 HCAPLUS  
DOCUMENT NUMBER: 122:263119  
TITLE: Recognition of multiple epitopes in the human melanoma antigen gp100 by tumor-infiltrating T lymphocytes associated with in vivo tumor regression  
AUTHOR(S): Kawakami, Yutaka; Eliyahu, Siona; Jennings, Christopher; Sakaguchi, Kazuyasu; Kang, Xiaoqiang; Southwood, Scott; Robbins, Paul F.; Sette, Alexxandro; Apella, Ettore; Rosenberg, Steven A.  
CORPORATE SOURCE: Surg. Branch, Nat. Inst. Health, Bethesda, MD, 20892, USA  
SOURCE: Journal of Immunology (1995), 154(8), 3961-8  
CODEN: JOIMA3; ISSN: 0022-1767  
PUBLISHER: American Association of Immunologists  
DOCUMENT TYPE: Journal  
LANGUAGE: English  
AB Four of ten HLA-A2-restricted melanoma specific CTL that were derived from tumor-infiltrating lymphocytes (TIL) and administered to patients recognized the gp100 melanoma Ag and nine of ten recognized the MART-1 Ag. Adoptive transfer of the four gp100-reactive CTL, but not the other TIL, resulted in tumor regression when infused into autologous patients along with IL-2. Tumor regression was thus correlated with the recognition of gp100 by the administered T cells. To identify the epitopes recognized by these four gp100-reactive CTL, 169 peptides contg. HLA-A2.1 binding motifs were synthesized and screened for their recognition by TIL using cytotoxicity and IFN-.gamma. release assays. Five gp100 epitopes (two for TIL620, three for TIL550, one for TIL1143, and two for TIL1200) were recognized by CTL derived from different patients. Five of eight HLA-A2 binding melanoma epitopes (five gp100, one MART-1/Melan-A, two tyrosinase) had intermediate binding affinity to HLA-A2.1. These gp100 epitopes may be responsible for mediating tumor rejection in vivo and thus may be useful for the development of immunotherapies for patients with melanoma.  
IT 162558-08-9 162558-09-0  
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)  
(recognition of epitopes in human melanoma antigen gp100 by HLA-A2-restricted cytotoxic T lymphocytes assocd. with in vivo tumor regression)

L4 ANSWER 50 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 1994:697583 HCAPLUS  
DOCUMENT NUMBER: 121:297583  
TITLE: Molecular characterization of the melanocyte lineage-specific antigen gp100  
AUTHOR(S): Adema, Gosse J.; de Boer, Annemiek J.; Vogel, Arthur M.; Loenen, Wil A. M.; Figdor, Carl G.  
CORPORATE SOURCE: Div. Immunology, Netherlands Cancer Inst., Amsterdam, 1066 CX, Neth.  
SOURCE: Journal of Biological Chemistry (1994), 269(31), 20126-33



CODEN: JBCHA3; ISSN: 0021-9258

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The glycoproteins recognized by monoclonal antibody (mAb) NKI-beteb are among the best diagnostic markers for human melanoma because their expression is restricted to melanocytic cells. Recently, the authors isolated a cDNA clone, termed gp100-cl, which confers immunoreactivity not only to mAb NKI-beteb, but also to two other mAbs used to diagnose malignant melanoma, HMB-50 and HMB-45. In this report, the authors demonstrate that gp100-cl cDNA encodes glycoproteins of 100 kDa (gp100) and 10 kDa (gp10) which are recognized by these mAbs in human melanoma cells. The translation product deduced from the open reading frame persistent in gp100-cl cDNA is highly homologous to another melanocyte-specific protein, Pmel17. Nucleotide sequence anal. of genomic DNA indicates that the transcripts corresponding to gp100 and Pmel17 cDNAs originate from a single gene via alternative splicing. In all normal and malignant melanocytic cells analyzed, gp100 and Pmel17 RNAs are simultaneously expressed.

IT 155422-80-3, Antigen gp100 (human melanocyte precursor clone gp100-cl)

RL: PRP (Properties)

(amino acid sequence of, mRNA alternative splicing and melanoma diagnosis in relation to)

L4 ANSWER 51 OF 51 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:476416 HCAPLUS

DOCUMENT NUMBER: 121:76416

TITLE: Cloning and expression of the gene for the melanoma-associated ME20 antigen

AUTHOR(S): Maresh, Grace A.; Marken, John S.; Neubauer, Michael; Aruffo, Alejandro; Hellstrom, Ingegerd; Hellstrom, Karl Erik; Marquardt, Hans

CORPORATE SOURCE: Bristol-Myers Squibb Pharm. Res. Inst., Seattle, WA, 98121, USA

SOURCE: DNA and Cell Biology (1994), 13(2), 87-95

CODEN: DCEBE8; ISSN: 1044-5498

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Human melanoma cells, but not tumor cells of other histol. origin, express a unique membrane-assocd. glycoprotein, designated ME2-M, and secrete glycoprotein, designated ME20-S, defined by monoclonal antibody ME20. Here the authors report the isolation and characterization of a cDNA clone that when transfected into COS cells directs the expression of ME20-M and ME20-S. This cDNA contains an open reading frame which encodes a 661-amino-acid-long precursor that contains a 23-amino-acid signal peptide and a 26-amino-acid transmembrane domain, sepd. by a hydrophilic region contg. 5 potential Asn-linked and 14 predicted Pro-assocd., Thr-linked glycosylation sites. The transmembrane domain is followed by a carboxy-terminal 45-amino-acid putative intracellular domain rich in Ser residues. Anal. of ME20-M by amino acid sequencing identified the proteolytic processing site. Signal peptide cleavage occurs at the Thr-24-Lys-25 peptide bond of the precursor and results in the 637-amino-acid ME20-M with calcd. mol. wt. of 67,782. ME20-M is derived from a single 3.3- to 3.4-kb mRNA transcript that is expressed at varying levels in melanoma cell lines, correlating with immunofluorescence detn. of protein

W0



09/214836

expression. The amino acid sequence of the ME20 antigen deduced from the cDNA differs from the human neonatal melanocyte-specific Pmel 17 gene product by a single amino acid substitution and deletion of 7 amino acid residues, and it is 80 homologous with the bovine retinal pigment RPE1 cDNA. The obsd. differences in the sequence of the melanoma-derived and normal melanocyte-derived gene products may suggest that ME20-M is a unique tumor antigen or, alternatively, an oncofetal self-antigen, if the differences in the sequences are the result of a germ-line-encoded polymorphism.

IT **155422-80-3, Melanoma-associated ME20 antigen**  
(Human clone HF12-2 gene ME20 precursor ME20-S)  
RL: BIOL (Biological study)  
(amino acid sequence and signal peptide and C-terminal  
transmembrane domain and intracellular serine-rich domain and  
proteolytic processing site of)

E1 THROUGH E37 ASSIGNED

FILE 'REGISTRY' ENTERED AT 15:36:49 ON 25 AUG 2003

L5 37 SEA FILE=REGISTRY ABB=ON PLU=ON (162558-08-9/BI OR  
155422-80-3/BI OR 162558-09-0/BI OR 167635-39-4/BI OR  
187974-51-2/BI OR 332959-83-8/BI OR 170153-76-1/BI OR  
202393-35-9/BI OR 244224-43-9/BI OR 250672-73-2/BI OR  
332959-84-9/BI OR 337916-59-3/BI OR 337989-60-3/BI OR  
370891-72-8/BI OR 370891-73-9/BI OR 370891-74-0/BI OR  
370891-75-1/BI OR 370891-76-2/BI OR 370891-77-3/BI OR  
370891-78-4/BI OR 370891-79-5/BI OR 371771-64-1/BI OR  
371771-65-2/BI OR 371772-22-4/BI OR 371772-23-5/BI OR  
371772-24-6/BI OR 371772-37-1/BI OR 371772-38-2/BI OR  
371772-39-3/BI OR 371772-40-6/BI OR 371772-41-7/BI OR  
371772-42-8/BI OR 371772-43-9/BI OR 442701-70-4/BI OR  
471943-16-5/BI OR 481197-02-8/BI OR 503636-92-8/BI)

=> s 15 and 11

L6 37 L5 AND L1

L6 ANSWER 1 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN **503636-92-8** REGISTRY

CN Tumor-associated protein (human clone WO03025138-SEQID-331) (9CI)  
(CA INDEX NAME)

OTHER NAMES:

CN 331: PN: WO03025138 SEQID: 331 claimed protein

CI MAN

SQL 661

SEQ 1 MDLVLRKCLL HLAIVIGALLA VGATKVPNRQ DWLGVSRLR TKAWNRLYP  
51 EWTEAQRLLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG  
101 QVIWVNNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV  
151 YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL  
===== ==  
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY  
251 LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS  
301 CGSSPVPGBT DGHRTAEAP NTTAQVPTT EVVGTTPGQA PTAEPSGTTT  
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM  
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMTESI  
451 TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ  
501 AVPSGEGDAF ELTVSCQGL PKEACMEISS PGCQPPAQL CQVLPSPAC



09/214836

551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV  
601 GILLVLMMAV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG  
651 ENSPLLSGQQ V  
HITS AT: 154-162

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:282427

L6 ANSWER 2 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 481197-02-8 REGISTRY  
CN Glycoprotein gp100 (human) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN GenBank AAB19181  
CN GenBank AAB19181 (Translated from: GenBank U20093)  
CI MAN  
SQL 661

SEQ 1 MDLVLRCLL HLAIVIGALLA VGATKVP RNQ DWLGVSRLR TKAWNRLYP  
51 EWTEAQR LDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVL PDG  
101 QVIWVNN TII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV  
151 YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTYH RRGSR SYVPL  
===== ==  
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY  
251 LAEADLSYTW DFGDSSGT LI SRAPVVTHY LEPGPVTAQV VLQAAIPLTS  
301 CGSSPVP GTT DGHRTAEAP NTTAGQVPTT EVVGTPGQA PTAEPSGTTS  
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM  
401 TPAEVSIVVL SGT TAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI  
451 TGS LGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ  
501 AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQL CQPVLPSPAC  
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV  
601 GILLVLMMAV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG  
651 ENSPLLSGQQ V  
HITS AT: 154-162

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:135820

L6 ANSWER 3 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 471943-16-5 REGISTRY  
CN Protein (human gene pmel17) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 8: PN: WO02081646 SEQID: 70 claimed protein  
CI MAN  
SQL 661

SEQ 1 MDLVLRCLL HLAIVIGALLA VGATKVP RNQ DWLGVSRLR TKAWNRLYP  
51 EWTEAQR LDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVL PDG  
101 QVIWVNN TII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV  
151 YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTYH RRGSR SYVPL  
===== ==  
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY  
251 LAEADLSYTW DFGDSSGT LI SRAPVVTHY LEPGPVTAQV VLQAAIPLTS  
301 CGSSPVP GTT DGHRTAEAP NTTAGQVPTT EVVGTPGQA PTAEPSGTTS  
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM  
401 TPAEVSIVVL SGT TAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI  
451 TGS LGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ





09/214836

501 AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQL CQVLPSPAC  
551 QLVVHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV  
601 GILLVLMVAV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG  
651 ENSPLLSGQQ V

HITS AT: 154-162

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:309478

L6 ANSWER 4 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 442701-70-4 REGISTRY  
CN 5: PN: EP1222928 SEQID: 4 unclaimed protein (9CI) (CA INDEX NAME)  
CI MAN  
SQL 668

SEQ 1 MDLVLRCLL HLAIVIGALLA VGATKVPNRQ DWLGVSRLR TKAWNRLYP  
51 EWTEAQRDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG  
101 QVIWVNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV  
151 YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTYH RGRSRSYVPL  
=====

201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY  
251 LAEADLSYTW DFGDSSGTLI SRAPVVTHY LEPGPVTAQV VLQAAIPLTS  
301 CGSSPVPVGT DGHRTAEAP NTTAGQVPTT EVVGTPGQA PTAEPSGTTS  
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM  
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI  
451 TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ  
501 AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQL CQVLPSPAC  
551 QLVVHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPVPG ILLTGQEAGL  
601 GQVRLIVGIL LVLMAVVLAS LIYRRRLMKQ DFSVPQLPHS SSHWLRLPRI  
651 FCSCPIGENS PLLSGQQV

HITS AT: 154-162

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:114479

L6 ANSWER 5 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 371772-43-9 REGISTRY  
CN Peptide, (His-Trp-Asp-Phe-Ala-Trp-Pro-Trp-Xaa-Xaa-Xaa-Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Leu-Xaa-Xaa-Trp-Pro-Trp-Ala-Phe-Asp-Trp-His) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 53: PN: W00178655 SEQID: 311 claimed protein  
CI MAN  
SQL 32

SEQ 1 HWDFAWPWXX XKTWGQYWQV LXXXWPWAFD WH  
=====

HITS AT: 12-20

REFERENCE 1: 135:343268

L6 ANSWER 6 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 371772-42-8 REGISTRY  
CN Peptide, (Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Leu-Xaa-Xaa-Trp-Pro-Trp-Ala-Phe-Asp-Trp-His) (9CI) (CA INDEX NAME)  
OTHER NAMES:



09/214836

CN 52: PN: WO0178655 SEQID: 310 claimed protein  
CI MAN  
SQL 21

SEQ 1 KTWGQYWQVL XXXWPWAFDW H  
=====

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 7 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 371772-41-7 REGISTRY  
CN Peptide, (His-Trp-Asp-Phe-Ala-Trp-Pro-Trp-Xaa-Xaa-Xaa-Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Leu-Xaa-Xaa-Xaa-His-Trp-Asp-Phe-Ala-Trp-Pro-Trp) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 50: PN: WO0178655 SEQID: 306 claimed protein  
CI MAN  
SQL 32

SEQ 1 HWDFAWPWXX XKTWGQYWQV LXXXHWDFAW PW  
=====

HITS AT: 12-20

REFERENCE 1: 135:343268

L6 ANSWER 8 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 371772-40-6 REGISTRY  
CN Peptide, (Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Leu-Xaa-Xaa-Xaa-His-Trp-Asp-Phe-Ala-Trp-Pro-Trp) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 49: PN: WO0178655 SEQID: 305 claimed protein  
CI MAN  
SQL 21

SEQ 1 KTWGQYWQVL XXXHWDFAWP W  
=====

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 9 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 371772-39-3 REGISTRY  
CN Peptide, (His-Trp-Asp-Phe-Ala-Trp-Pro-Trp-Xaa-Xaa-Xaa-Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Leu) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 48: PN: WO0178655 SEQID: 304 claimed protein  
CI MAN  
SQL 21

SEQ 1 HWDFAWPWXX XKTWGQYWQV L  
=====

HITS AT: 12-20

REFERENCE 1: 135:343268

L6 ANSWER 10 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 371772-38-2 REGISTRY



09/214836

CN Peptide, (His-Trp-Asp-Phe-Ala-Trp-Pro-Trp-Xaa-Xaa-Xaa-Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Xaa-Xaa-Xaa-Trp-Pro-Trp-Ala-Phe-Asp-Trp-His)  
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 47: PN: WO0178655 SEQID: 301 claimed protein

CI MAN

SQL 31

SEQ 1 HWDFAWPWXX XKTWGQYWQV XXXWPWAFDW H  
=====

HITS AT: 12-20

REFERENCE 1: 135:343268

L6 ANSWER 11 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN 371772-37-1 REGISTRY

CN Peptide, (Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Xaa-Xaa-Xaa-Trp-Pro-Trp-Ala-Phe-Asp-Trp-His) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 46: PN: WO0178655 SEQID: 300 claimed protein

CI MAN

SQL 20

SEQ 1 KTWGQYWQVX XXWPWAFDWH  
=====

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 12 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN 371772-24-6 REGISTRY

CN Peptide, (His-Trp-Asp-Phe-Ala-Trp-Pro-Trp-Xaa-Xaa-Xaa-Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Xaa-Xaa-Xaa-His-Trp-Asp-Phe-Ala-Trp-Pro-Trp)  
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 440: PN: WO0178655 SEQID: 296 claimed sequence

CN 45: PN: WO0178655 SEQID: 296 claimed protein

CI MAN

SQL 31

SEQ 1 HWDFAWPWXX XKTWGQYWQV XXXHWDFAWP W  
=====

HITS AT: 12-20

REFERENCE 1: 135:343268

L6 ANSWER 13 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN 371772-23-5 REGISTRY

CN Peptide, (Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val-Xaa-Xaa-Xaa-His-Trp-Asp-Phe-Ala-Trp-Pro-Trp) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 439: PN: WO0178655 SEQID: 295 claimed sequence

CN 44: PN: WO0178655 SEQID: 295 claimed protein

CI MAN

SQL 20

SEQ 1 KTWGQYWQVX XXHWDFAWPW  
=====



09/214836

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 14 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **371772-22-4** REGISTRY  
CN Peptide, (His-Trp-Asp-Phe-Ala-Trp-Pro-Trp-Xaa-Xaa-Xaa-Lys-Thr-Trp-Gly-Gln-Tyr-Trp-Gln-Val) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 438: PN: WO0178655 SEQID: 294 claimed sequence  
CN 43: PN: WO0178655 SEQID: 294 claimed protein  
CI MAN  
SQL 20

SEQ 1 HWDFAWPWXX XKTWGQYWQV  
=====

HITS AT: 12-20

REFERENCE 1: 135:343268

L6 ANSWER 15 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **371771-65-2** REGISTRY  
CN L-Histidine, L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyL-L-tyrosyl-L-tryptophyl-L-glutaminyL-L-valyl-L-leucyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-.alpha.-aspartyl-L-tryptophyl- (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 54: PN: WO0178655 SEQID: 313 claimed protein  
CI MAN  
SQL 26

SEQ 1 HWDFAWPWKT WGQYWQVLWP WAFDWH  
== =====

HITS AT: 9-17

REFERENCE 1: 135:343268

L6 ANSWER 16 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **371771-64-1** REGISTRY  
CN L-Tryptophan, L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyL-L-tyrosyl-L-tryptophyl-L-glutaminyL-L-valyl-L-leucyl-L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl- (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 51: PN: WO0178655 SEQID: 309 claimed protein  
CI MAN  
SQL 26

SEQ 1 HWDFAWPWKT WGQYWQVLHW DFAWPW  
== =====

HITS AT: 9-17

REFERENCE 1: 135:343268





09/214836

L6 ANSWER 17 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN **370891-79-5** REGISTRY

CN L-Histidine, L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl-L-valyl-L-leucyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-.alpha.-aspartyl-L-tryptophyl- (9CI) (CA INDEX NAME)

SQL 18

SEQ 1 KTWGQYWQVL WPWAFDWH

=====

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 18 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN **370891-78-4** REGISTRY

CN L-Tryptophan, L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl-L-valyl-L-leucyl-L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 452: PN: WO0178655 SEQID: 308 claimed sequence

SQL 18

SEQ 1 KTWGQYWQVL HWDFAWPW

=====

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 19 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN **370891-77-3** REGISTRY

CN L-Leucine, L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl-L-valyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 451: PN: WO0178655 SEQID: 307 claimed sequence

SQL 18

SEQ 1 HWDFAWPWKT WGQYWQVL

== =====

HITS AT: 9-17

REFERENCE 1: 135:343268

L6 ANSWER 20 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN **370891-76-2** REGISTRY

CN L-Histidine, L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl-L-valyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-.alpha.-aspartyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 447: PN: WO0178655 SEQID: 303 claimed sequence

SQL 25

SEQ 1 HWDFAWPWKT WGQYWQVWPW AFDWH



09/214836

HITS AT: 9-17

REFERENCE 1: 135:343268

L6 ANSWER 21 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 370891-75-1 REGISTRY  
CN L-Histidine, L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyL-L-tyrosyl-L-tryptophyl-L-glutaminyL-L-valyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-.alpha.-aspartyl-L-tryptophyl-(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 446: PN: WO0178655 SEQID: 302 claimed sequence  
SQL 17

SEQ 1 KTWGQYWQVW PWAFDWH

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 22 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 370891-74-0 REGISTRY  
CN L-Tryptophan, L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyL-L-tyrosyl-L-tryptophyl-L-glutaminyL-L-valyl-L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 443: PN: WO0178655 SEQID: 299 claimed sequence  
SQL 25

SEQ 1 HWDFAWPWKT WGQYWQVHWD FAWPW

HITS AT: 9-17

REFERENCE 1: 135:343268

L6 ANSWER 23 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 370891-73-9 REGISTRY  
CN L-Tryptophan, L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyL-L-tyrosyl-L-tryptophyl-L-glutaminyL-L-valyl-L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl-(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 442: PN: WO0178655 SEQID: 298 claimed sequence  
SQL 17

SEQ 1 KTWGQYWQVH WDFAWPW

HITS AT: 1-9

REFERENCE 1: 135:343268

L6 ANSWER 24 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 370891-72-8 REGISTRY  
CN L-Valine, L-histidyl-L-tryptophyl-L-.alpha.-aspartyl-L-phenylalanyl-L-alanyl-L-tryptophyl-L-prolyl-L-tryptophyl-L-lysyl-L-threonyl-L-



09/214836

tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl-  
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 441: PN: WO0178655 SEQID: 297 claimed sequence

SQL 17

SEQ 1 HWDFAWPWKT WGQYWQV

== =====

HITS AT: 9-17

REFERENCE 1: 135:343268

L6 ANSWER 25 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN 337989-60-3 REGISTRY

CN Tumor-associated antigen gp100 (human derivative) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 109: PN: WO0130382 SEQID: 110 claimed protein

CN 2: PN: WO0149317 SEQID: 2 claimed protein

CN Glycoprotein gp100 (synthetic human)

CI MAN

SQL 661

SEQ 1 MDLVLRCLL HLAIVIGALLA VGATKVPNRQ DWLGVSRLR TKAWNRLYP  
51 EWTEAQRDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG  
101 QVIWVNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV  
151 YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTYH RRGSRSYVPL

=====

201 AHSSSAFTIM DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY  
251 LAEADLSYTW DFGDSSGTLI SRALVVTHY LEPGPVTQV VLQAAIPLTS  
301 CGSSPVPVGT DGHRTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSTTS  
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM  
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI  
451 TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ  
501 AVPSGEGDAF ELTVSCQGL PKEACMEISS PGCQPPAQL CQVLPSPAC  
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV  
601 GILLVLMVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG  
651 ENSPLLSGQ V

HITS AT: 154-162

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 135:106284

REFERENCE 2: 134:339527

L6 ANSWER 26 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN 337916-59-3 REGISTRY

CN Glycine, L-tyrosyl-L-valyl-L-tryptophyl-L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl-L-valyl-L-leucylglycyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 25: PN: WO0130382 TABLE: 4 unclaimed sequence

SQL 15

SEQ 1 YVWKTWGQYW QVLGG

=====

HITS AT: 4-12



09/214836

REFERENCE 1: 134:339527

L6 ANSWER 27 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **332959-84-9** REGISTRY  
CN 3: PN: WO0123577 FIGURE: 1 unclaimed sequence (9CI) (CA INDEX NAME)  
CI MAN  
SQL 92

SEQ 1 AAGIGILTVF LWGPRALVML LAVLYCLLLD GTATLRLKTW GQYWQVYMDG  
=====

51 TMSQYITDQV PFSVYLPPGT VTAILTVILG VLVLPDVFIR CV  
HITS AT: 38-46

REFERENCE 1: 134:279565

L6 ANSWER 28 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **332959-83-8** REGISTRY  
CN 2: PN: WO0123577 SEQID: 24 unclaimed protein (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 23: PN: WO0127291 SEQID: 24 unclaimed sequence  
CI MAN  
SQL 92

SEQ 1 AAGIGILTVF LWGPRALVME LAVLYCLLLD GTATLRLKTW GQYWQVYMDG  
=====

51 TMSDVITDQV PFSVYLEFGP VTAILTVILG VLVLPDVFIR CV  
HITS AT: 38-46

REFERENCE 1: 134:309695

REFERENCE 2: 134:279565

L6 ANSWER 29 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **250672-73-2** REGISTRY  
CN Antigen (synthetic human melanoma-associated polypeptide) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 93

SEQ 1 MAAGIGILTV FLWGPRALVM LLAVLYCLLL DGTATLRLKT WGQYWQVYMD  
=====

51 GTMSQVITDQ VPFSVYLEPG PVTAILTVIL GVLVLPDVFIR RCV  
HITS AT: 39-47

REFERENCE 1: 131:350041

L6 ANSWER 30 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **244224-43-9** REGISTRY  
CN Melanoma-associated antigen gp100 (human) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN PN: WO9947102 SEQID: 6 claimed protein  
CI MAN  
SQL 662

SEQ 1 MDLVLRCLL HLAIVIGALLA VGATKVPNRQ DWLGVSRLR TKAWNRLQYP  
51 EWTEAQRLLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG  
101 QVIWVNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV





09/214836

151 YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL  
===== ==  
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY  
251 LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS  
301 CGSSPVPGETT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS  
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM  
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI  
451 TGSGLPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ  
501 AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQL CQVLPSPAC  
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV  
601 GILLVLMVAV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG  
651 ENSPLLSGQQ VX

HITS AT: 154-162

REFERENCE 1: 131:256325

L6 ANSWER 31 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **202393-35-9** REGISTRY  
CN L-Valine, L-lysyl-L-valyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-  
L-tryptophyl-L-alanyl- (9CI) (CA INDEX NAME)  
SQL 9

SEQ 1 KVWGQYWAV  
=====

HITS AT: 1-9

REFERENCE 1: 128:139756

L6 ANSWER 32 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **187974-51-2** REGISTRY  
CN L-Valine, L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-  
tyrosyl-L-tryptophyl-L-alanyl- (9CI) (CA INDEX NAME)  
SQL 9

SEQ 1 KTWGQYWAV  
=====

HITS AT: 1-9

REFERENCE 1: 128:139756

REFERENCE 2: 126:210733

L6 ANSWER 33 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN **170153-76-1** REGISTRY  
CN L-Leucine, N-[N-[N2-[N-[N-[N2-[N-[N-[N-[N2-(N-L-valyl-L-tryptophyl)-  
L-lysyl]-L-threonyl]-L-tryptophyl]glycyl]-L-glutaminyl]-L-tyrosyl]-L-  
tryptophyl]-L-glutaminyl]-L-valyl]- (9CI) (CA INDEX NAME)  
SQL 12

SEQ 1 VWKTWGQYWQ VL  
===== =

HITS AT: 3-11

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 123:312226

L6 ANSWER 34 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

Searcher : Shears 308-4994



09/214836

RN 167635-39-4 REGISTRY  
CN L-Valine, N-[N2-[N-[N-[N2-[N-[N-[N2-(N-L-valyl-L-tryptophyl)-L-lysyl]-L-threonyl]-L-tryptophyl]glycyl]-L-glutaminyl]-L-tyrosyl]-L-tryptophyl]-L-glutaminyl]- (9CI) (CA INDEX NAME)  
SQL 11

SEQ 1 VWKTWGQYWQ V  
=====

HITS AT: 3-11

REFERENCE 1: 123:312226

REFERENCE 2: 123:196160

L6 ANSWER 35 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN 162558-09-0 REGISTRY  
CN L-Leucine, L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl-L-valyl- (9CI) (CA INDEX NAME)  
OTHER CA INDEX NAMES:

CN L-Leucine, N-[N-[N2-[N-[N-[N2-[N-[N-(N-L-lysyl-L-threonyl)-L-tryptophyl]glycyl]-L-glutaminyl]-L-tyrosyl]-L-tryptophyl]-L-glutaminyl]-L-valyl]-  
SQL 10

SEQ 1 KTWGQYWQVL  
=====

HITS AT: 1-9

REFERENCE 1: 130:37302

REFERENCE 2: 124:84888

REFERENCE 3: 123:312226

REFERENCE 4: 123:196160

REFERENCE 5: 122:263119

L6 ANSWER 36 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN

RN 162558-08-9 REGISTRY  
CN L-Valine, L-lysyl-L-threonyl-L-tryptophylglycyl-L-glutaminyl-L-tyrosyl-L-tryptophyl-L-glutaminyl- (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN L-Valine, N-[N2-[N-[N-[N2-[N-[N-(N-L-lysyl-L-threonyl)-L-tryptophyl]glycyl]-L-glutaminyl]-L-tyrosyl]-L-tryptophyl]-L-glutaminyl]-

OTHER NAMES:

CN 11: PN: WO03024480 PAGE: 84 unclaimed sequence  
CN 15: PN: WO0119408 SEQID: 15 unclaimed sequence  
CN 161: PN: WO0178655 SEQID: 14 claimed sequence  
CN 16: PN: FR2812087 SEQID: 15 unclaimed sequence  
CN 22: PN: WO0053161 SEQID: 61 unclaimed sequence  
CN 26: PN: US6531451 SEQID: 26 unclaimed sequence  
CN 29: PN: WO0236146 SEQID: 29 claimed sequence  
CN 30: PN: WO0193835 SEQID: 61 unclaimed sequence  
CN 32: PN: WO0021551 SEQID: 32 claimed sequence  
CN 335: PN: US20020007173 SEQID: 378 unclaimed sequence  
CN 34: PN: WO0050589 SEQID: 34 unclaimed sequence



09/214836

CN 35: PN: US6291430 SEQID: 71 unclaimed sequence  
CN 35: PN: WO0006598 SEQID: 36 unclaimed sequence  
CN 36: PN: US6245525 SEQID: 30 unclaimed sequence  
CN 36: PN: WO0020445 SEQID: 26 unclaimed sequence  
CN 37: PN: WO0129220 SEQID: 35 unclaimed sequence  
CN 45: PN: WO0127291 SEQID: 2 unclaimed sequence  
CN 46: PN: WO0013699 SEQID: 42 unclaimed sequence  
CN 4: PN: WO0123577 SEQID: 2 claimed sequence  
CN 56: PN: WO0020581 SEQID: 71 unclaimed sequence  
CN 57: PN: WO0153833 SEQID: 42 unclaimed sequence  
CN 5: PN: WO02065992 SEQID: 5 claimed sequence  
CN 67: PN: WO0078806 SEQID: 67 unclaimed sequence  
CN 68: PN: WO0032785 SEQID: 34 unclaimed sequence  
CN PN: WO9950637 SEQID: 30 unclaimed protein  
CN PN: WO9953061 SEQID: 30 unclaimed sequence  
CN PN: WO9955892 FIGURE: 15 unclaimed sequence  
SQL 9

SEQ 1 KTWGQYWQV

=====

HITS AT: 1-9

REFERENCE 1: 139:99547  
REFERENCE 2: 138:270293  
REFERENCE 3: 138:220360  
REFERENCE 4: 138:185978  
REFERENCE 5: 138:23273  
REFERENCE 6: 137:309110  
REFERENCE 7: 137:246573  
REFERENCE 8: 137:200246  
REFERENCE 9: 137:123841  
REFERENCE 10: 137:114479

L6 ANSWER 37 OF 37 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 155422-80-3 REGISTRY  
CN Antigen ME 20 (human clone hf12-2 precursor reduced) (9CI) (CA  
INDEX NAME)

OTHER NAMES:

CN 215: PN: WO0190197 SEQID: 817 unclaimed protein  
CN 2: PN: WO0170767 SEQID: 2 unclaimed protein  
CN 2: PN: WO0192294 SEQID: 2 claimed protein  
CN Antigen (human melanoma gene gp100)  
CN Antigen gp 100 (human clone gp100-cl precursor reduced)  
CN Antigen gp 100 (human melanoma-associated)  
CN Antigen MAA (human melanoma-assocd. antigen)  
CN Melanoma-associated ME20 antigen (Human clone HF12-2 gene ME20  
precursor ME20-S)  
CN Protein Pmel 17 (human reduced)  
CI MAN



09/214836

SQL 661

```
SEQ      1 MDLVLRCLL HLAIVIGALLA VGATKVPNRQ DWLGVSRLR TKAWNRLYP
      51 EWTEAQRDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG
     101 QVIWVNNITII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
     151 YVWKTWGQYW QVLGGPVSGL SIGTGRAMLG THTMEVTYH RRGSRSYVPL
          =====
     201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
     251 LAEADLSYTW DFGDSSGTLI SRALVVTHY LEPGPVTAQV VLQAAIPLTS
     301 CGSSPVP GTT DHRPTAEAP NTTAGQVPTT EVVGTPGQA PTAEPSTTS
     351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
     401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
     451 TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
     501 AVPSGEGDAF ELTVSCQGL PKEACMEISS PGCQPPAQL CQVLPSPAC
     551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
     601 GILLVLMVAV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
     651 ENSPLLSGQQ V
```

HITS AT: 154-162

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 136:49291

REFERENCE 2: 136:31665

REFERENCE 3: 135:267217

REFERENCE 4: 124:222382

REFERENCE 5: 124:84888

REFERENCE 6: 123:312226

REFERENCE 7: 121:297583

REFERENCE 8: 121:76416

FILE 'HOME' ENTERED AT 15:37:29 ON 25 AUG 2003

